



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 8, 2026 – 06:58 PM JST

PDB ID : 9VFL / pdb\_00009vfl  
Title : Crystal structure of PLCG1 SH2(C) domain with a triple Tyr phosphorylated peptide derived from NTRK1  
Authors : Weng, Y.; Zheng, Q.; Pan, M.; Chen, P.; Tian, R.  
Deposited on : 2025-06-11  
Resolution : 2.40 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

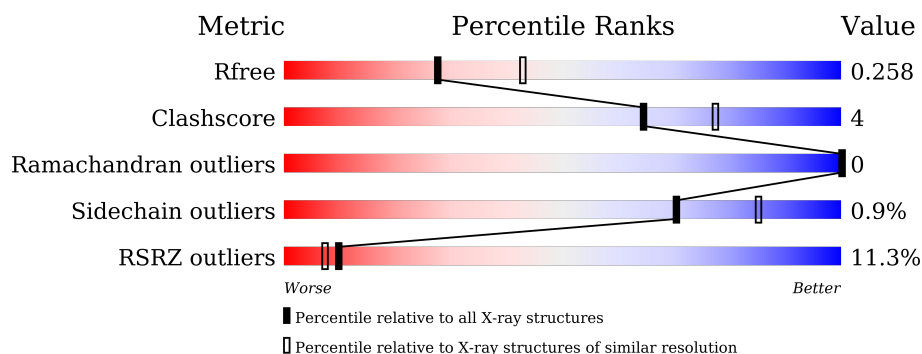
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.40 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	180053	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	96	<div> <div>5%</div> <div>93%</div> <div>6%</div> </div>
1	C	96	<div> <div>10%</div> <div>89%</div> <div>9%</div> </div>
1	E	96	<div> <div>6%</div> <div>91%</div> <div>7%</div> </div>
1	G	96	<div> <div>16%</div> <div>84%</div> <div>16%</div> </div>
1	I	96	<div> <div>20%</div> <div>86%</div> <div>8%</div> <div>5%</div> </div>
1	K	96	<div> <div>4%</div> <div>85%</div> <div>14%</div> </div>

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Mol	Chain	Length	Quality of chain
1	M	96	
1	O	96	
1	Q	96	
1	S	96	
1	U	96	
1	W	96	
2	B	16	
2	D	16	
2	F	16	
2	H	16	
2	J	16	
2	L	16	
2	N	16	
2	P	16	
2	R	16	
2	T	16	
2	V	16	
2	X	16	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	CL	G	103	-	-	X	-

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 11376 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	95	Total	C	N	O	S	0	1	0
			794	505	145	138	6			
1	C	94	Total	C	N	O	S	0	2	0
			800	509	147	138	6			
1	E	94	Total	C	N	O	S	0	1	0
			786	501	141	138	6			
1	G	96	Total	C	N	O	S	0	1	0
			798	507	146	139	6			
1	I	91	Total	C	N	O	S	0	1	0
			765	485	141	133	6			
1	K	95	Total	C	N	O	S	0	1	0
			796	507	145	139	5			
1	M	94	Total	C	N	O	S	0	0	0
			789	502	144	138	5			
1	O	95	Total	C	N	O	S	0	0	0
			790	503	145	137	5			
1	Q	92	Total	C	N	O	S	0	0	0
			773	492	142	134	5			
1	S	95	Total	C	N	O	S	0	0	0
			795	505	145	140	5			
1	U	96	Total	C	N	O	S	0	0	0
			799	507	146	141	5			
1	W	94	Total	C	N	O	S	0	1	0
			788	502	144	136	6			

There are 60 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	2	GLY	-	expression tag	UNP P19174
A	3	SER	-	expression tag	UNP P19174
A	4	PRO	-	expression tag	UNP P19174
A	5	GLU	-	expression tag	UNP P19174

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Chain	Residue	Modelled	Actual	Comment	Reference
A	6	PHE	-	expression tag	UNP P19174
C	2	GLY	-	expression tag	UNP P19174
C	3	SER	-	expression tag	UNP P19174
C	4	PRO	-	expression tag	UNP P19174
C	5	GLU	-	expression tag	UNP P19174
C	6	PHE	-	expression tag	UNP P19174
E	2	GLY	-	expression tag	UNP P19174
E	3	SER	-	expression tag	UNP P19174
E	4	PRO	-	expression tag	UNP P19174
E	5	GLU	-	expression tag	UNP P19174
E	6	PHE	-	expression tag	UNP P19174
G	2	GLY	-	expression tag	UNP P19174
G	3	SER	-	expression tag	UNP P19174
G	4	PRO	-	expression tag	UNP P19174
G	5	GLU	-	expression tag	UNP P19174
G	6	PHE	-	expression tag	UNP P19174
I	2	GLY	-	expression tag	UNP P19174
I	3	SER	-	expression tag	UNP P19174
I	4	PRO	-	expression tag	UNP P19174
I	5	GLU	-	expression tag	UNP P19174
I	6	PHE	-	expression tag	UNP P19174
K	2	GLY	-	expression tag	UNP P19174
K	3	SER	-	expression tag	UNP P19174
K	4	PRO	-	expression tag	UNP P19174
K	5	GLU	-	expression tag	UNP P19174
K	6	PHE	-	expression tag	UNP P19174
M	2	GLY	-	expression tag	UNP P19174
M	3	SER	-	expression tag	UNP P19174
M	4	PRO	-	expression tag	UNP P19174
M	5	GLU	-	expression tag	UNP P19174
M	6	PHE	-	expression tag	UNP P19174
O	2	GLY	-	expression tag	UNP P19174
O	3	SER	-	expression tag	UNP P19174
O	4	PRO	-	expression tag	UNP P19174
O	5	GLU	-	expression tag	UNP P19174
O	6	PHE	-	expression tag	UNP P19174
Q	2	GLY	-	expression tag	UNP P19174
Q	3	SER	-	expression tag	UNP P19174
Q	4	PRO	-	expression tag	UNP P19174
Q	5	GLU	-	expression tag	UNP P19174
Q	6	PHE	-	expression tag	UNP P19174
S	2	GLY	-	expression tag	UNP P19174

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Chain	Residue	Modelled	Actual	Comment	Reference
S	3	SER	-	expression tag	UNP P19174
S	4	PRO	-	expression tag	UNP P19174
S	5	GLU	-	expression tag	UNP P19174
S	6	PHE	-	expression tag	UNP P19174
U	2	GLY	-	expression tag	UNP P19174
U	3	SER	-	expression tag	UNP P19174
U	4	PRO	-	expression tag	UNP P19174
U	5	GLU	-	expression tag	UNP P19174
U	6	PHE	-	expression tag	UNP P19174
W	2	GLY	-	expression tag	UNP P19174
W	3	SER	-	expression tag	UNP P19174
W	4	PRO	-	expression tag	UNP P19174
W	5	GLU	-	expression tag	UNP P19174
W	6	PHE	-	expression tag	UNP P19174

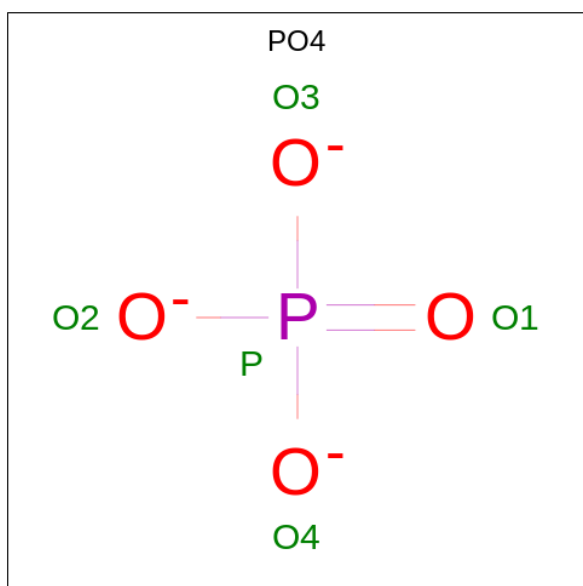
- Molecule 2 is a protein called High affinity nerve growth factor receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	13	Total	C	N	O	P	0	0	0
			122	69	19	31	3			
2	D	14	Total	C	N	O	P	0	0	0
			127	72	20	32	3			
2	F	13	Total	C	N	O	P	0	1	0
			135	77	19	35	4			
2	H	15	Total	C	N	O	P	0	0	0
			138	78	24	33	3			
2	J	13	Total	C	N	O	P	0	1	0
			135	77	19	35	4			
2	L	12	Total	C	N	O	P	0	0	0
			112	64	15	30	3			
2	N	12	Total	C	N	O	P	0	0	0
			111	63	15	30	3			
2	P	14	Total	C	N	O	P	0	0	0
			127	72	20	32	3			
2	R	12	Total	C	N	O	P	0	1	0
			124	71	15	34	4			
2	T	13	Total	C	N	O	P	0	0	0
			122	69	19	31	3			
2	V	15	Total	C	N	O	P	0	0	0
			134	76	21	34	3			
2	X	12	Total	C	N	O	P	0	0	0
			112	64	15	30	3			

- Molecule 3 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Cl	0	0
			1	1		
3	C	1	Total	Cl	0	0
			1	1		
3	D	1	Total	Cl	0	0
			1	1		
3	E	1	Total	Cl	0	0
			1	1		
3	G	3	Total	Cl	0	0
			3	3		
3	L	1	Total	Cl	0	0
			1	1		
3	M	1	Total	Cl	0	0
			1	1		
3	O	1	Total	Cl	0	0
			1	1		
3	Q	1	Total	Cl	0	0
			1	1		
3	U	2	Total	Cl	0	0
			2	2		

- Molecule 4 is PHOSPHATE ION (CCD ID: PO4) (formula: O<sub>4</sub>P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	C	1	Total	O	P	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	E	1	Total	O	P	0	0
			5	4	1		
4	E	1	Total	O	P	0	0
			5	4	1		
4	G	1	Total	O	P	0	0
			5	4	1		
4	G	1	Total	O	P	0	0
			5	4	1		
4	I	1	Total	O	P	0	0
			5	4	1		
4	M	1	Total	O	P	0	0
			5	4	1		
4	Q	1	Total	O	P	0	0
			5	4	1		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	34	Total	O	0	0
			34	34		
5	B	7	Total	O	0	0
			7	7		
5	C	24	Total	O	0	0
			24	24		
5	D	10	Total	O	0	0
			10	10		
5	E	31	Total	O	0	0
			31	31		
5	F	7	Total	O	0	0
			7	7		
5	G	21	Total	O	0	0
			21	21		
5	H	7	Total	O	0	0
			7	7		
5	I	8	Total	O	0	0
			8	8		
5	J	7	Total	O	0	0
			7	7		
5	K	15	Total	O	0	0
			15	15		
5	L	6	Total	O	0	0
			6	6		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	M	22	Total 22	O 22	0	0
5	N	7	Total 7	O 7	0	0
5	O	23	Total 23	O 23	0	0
5	P	6	Total 6	O 6	0	0
5	Q	17	Total 17	O 17	0	0
5	R	4	Total 4	O 4	0	0
5	S	16	Total 16	O 16	0	0
5	T	9	Total 9	O 9	0	0
5	U	44	Total 44	O 44	0	0
5	V	10	Total 10	O 10	0	0
5	W	9	Total 9	O 9	0	0
5	X	7	Total 7	O 7	0	0

### 3 Residue-property plots [i](#)

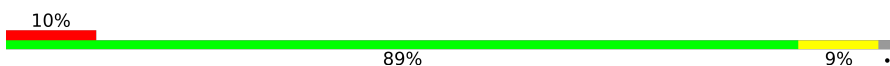
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

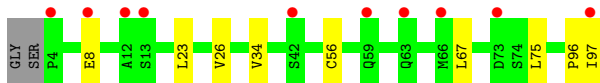
- Molecule 1: 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1

Chain A: 



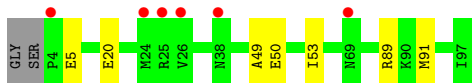
- Molecule 1: 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1

Chain C: 




- Molecule 1: 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1

Chain E: 




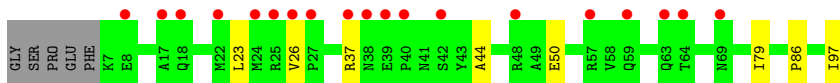
- Molecule 1: 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1

Chain G: 

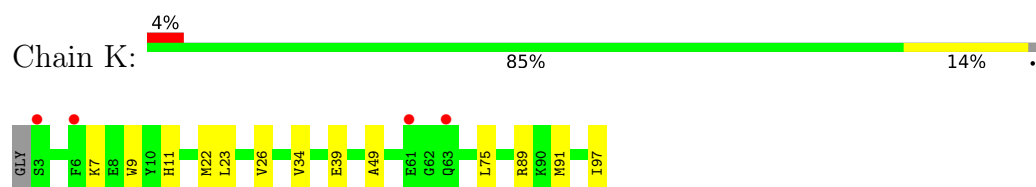


- Molecule 1: 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1

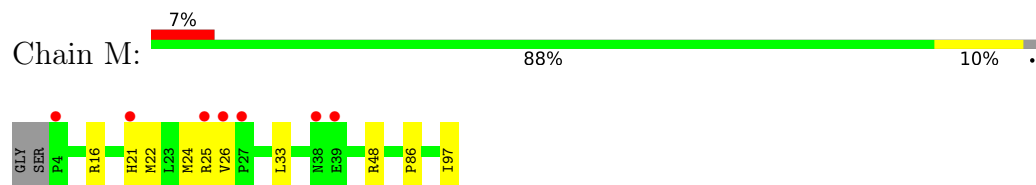
Chain I: 



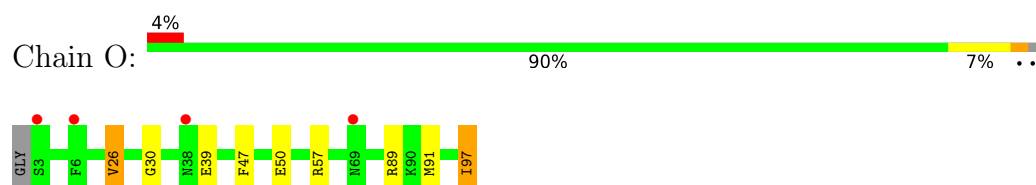
- Molecule 1: 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1



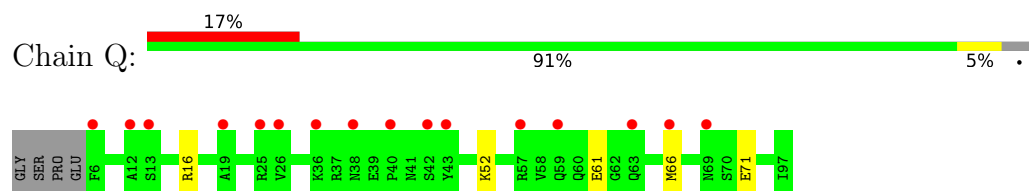
- Molecule 1: 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1



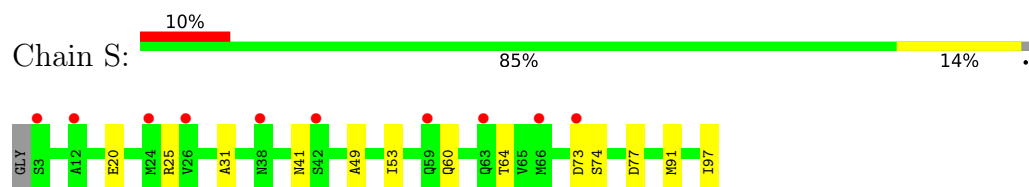
- Molecule 1: 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1



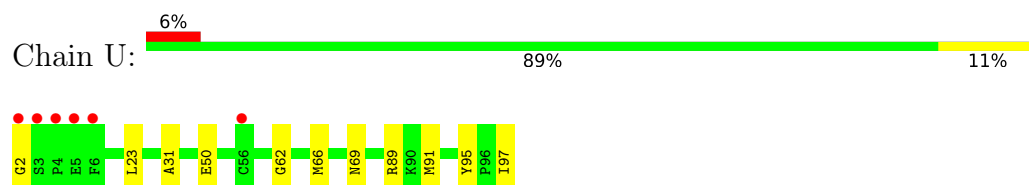
- Molecule 1: 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1



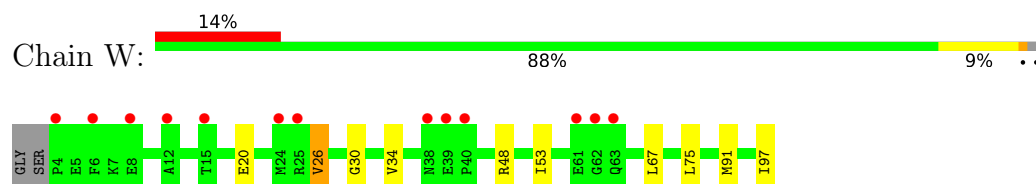
- Molecule 1: 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1



- Molecule 1: 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1



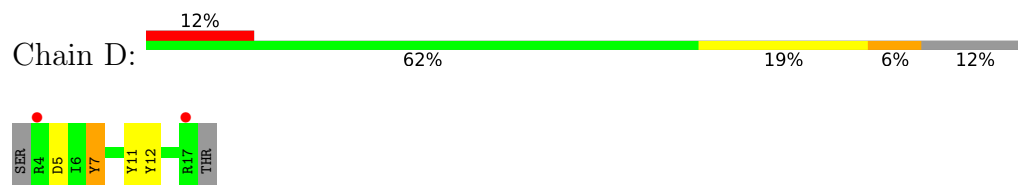
- Molecule 1: 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1



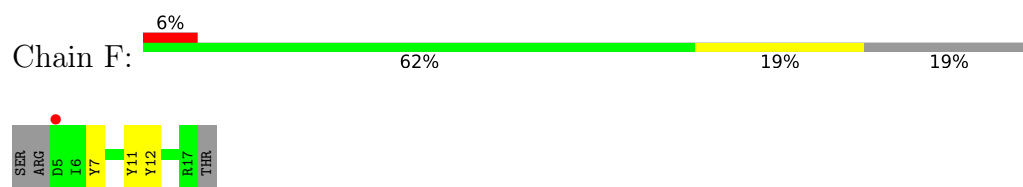
- Molecule 2: High affinity nerve growth factor receptor



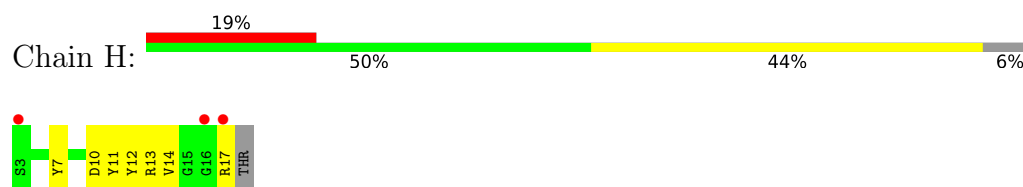
- Molecule 2: High affinity nerve growth factor receptor



- Molecule 2: High affinity nerve growth factor receptor



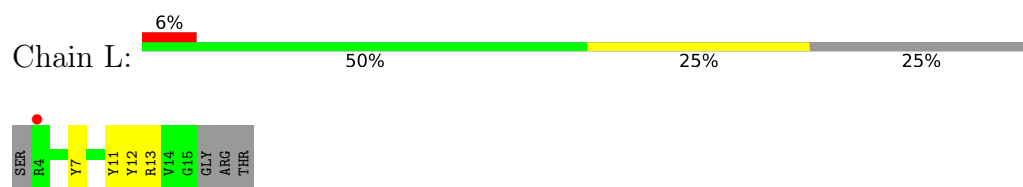
- Molecule 2: High affinity nerve growth factor receptor



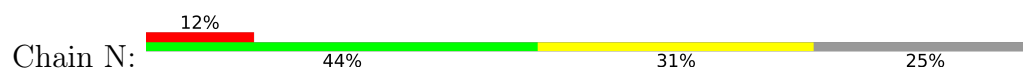
- Molecule 2: High affinity nerve growth factor receptor



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- Molecule 2: High affinity nerve growth factor receptor

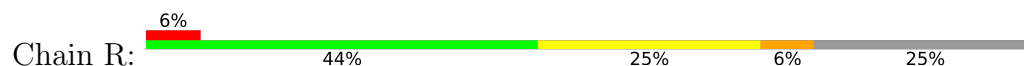




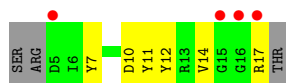
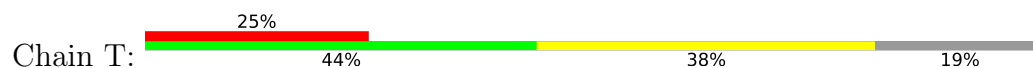
- Molecule 2: High affinity nerve growth factor receptor



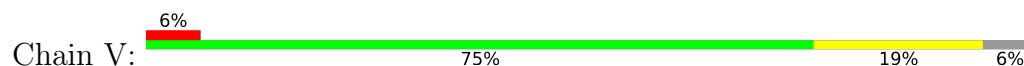
- Molecule 2: High affinity nerve growth factor receptor



- Molecule 2: High affinity nerve growth factor receptor



- Molecule 2: High affinity nerve growth factor receptor



- Molecule 2: High affinity nerve growth factor receptor



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	157.69Å 157.69Å 158.20Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	70.70 – 2.40 70.70 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.9 (70.70-2.40) 100.0 (70.70-2.40)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.41 (at 2.40Å)	Xtriage
Refinement program	PHENIX 1.21.2_5419	Depositor
R, $R_{free}$	0.215 , 0.259 0.215 , 0.258	Depositor DCC
$R_{free}$ test set	3909 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	46.6	Xtriage
Anisotropy	0.083	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 50.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.000 for -h,l,k 0.000 for -l,-k,-h	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	11376	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 52.11 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 5.0972e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CL, PTR, PO4

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.09	0/817	0.29	0/1096
1	C	0.08	0/826	0.25	0/1106
1	E	0.09	0/809	0.29	0/1085
1	G	0.09	0/821	0.26	0/1101
1	I	0.08	0/786	0.24	0/1053
1	K	0.09	0/819	0.26	0/1100
1	M	0.09	0/809	0.28	0/1084
1	O	0.08	0/810	0.26	0/1087
1	Q	0.08	0/792	0.26	0/1061
1	S	0.08	0/815	0.26	0/1093
1	U	0.10	0/819	0.29	0/1098
1	W	0.07	0/811	0.26	0/1087
2	B	0.09	0/71	0.30	0/90
2	D	0.11	0/76	0.27	0/97
2	F	0.09	0/71	0.22	0/90
2	H	0.12	0/87	0.24	0/111
2	J	0.08	0/71	0.26	0/90
2	L	0.11	0/61	0.32	0/78
2	N	0.07	0/60	0.21	0/76
2	P	0.11	0/76	0.25	0/97
2	R	0.10	0/60	0.25	0/76
2	T	0.17	0/71	0.55	0/90
2	V	0.09	0/83	0.29	0/107
2	X	0.11	0/61	0.26	0/78
All	All	0.09	0/10582	0.27	0/14131

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	794	0	790	7	0
1	C	800	0	803	5	0
1	E	786	0	779	5	0
1	G	798	0	793	11	0
1	I	765	0	767	5	0
1	K	796	0	788	9	0
1	M	789	0	785	6	0
1	O	790	0	782	8	0
1	Q	773	0	771	4	0
1	S	795	0	789	8	0
1	U	799	0	792	7	0
1	W	788	0	786	6	0
2	B	122	0	92	2	0
2	D	127	0	94	1	0
2	F	135	0	99	0	0
2	H	138	0	107	2	0
2	J	135	0	99	1	0
2	L	112	0	78	1	0
2	N	111	0	79	2	0
2	P	127	0	94	1	0
2	R	124	0	86	2	0
2	T	122	0	92	1	0
2	V	134	0	101	0	0
2	X	112	0	78	1	0
3	A	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	E	1	0	0	0	0
3	G	3	0	0	2	0
3	L	1	0	0	0	0
3	M	1	0	0	0	0
3	O	1	0	0	0	0
3	Q	1	0	0	1	0
3	U	2	0	0	0	0
4	C	5	0	0	0	0
4	E	10	0	0	0	0
4	G	10	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	I	5	0	0	0	0
4	M	5	0	0	0	0
4	Q	5	0	0	0	0
5	A	34	0	0	3	0
5	B	7	0	0	0	0
5	C	24	0	0	0	0
5	D	10	0	0	0	0
5	E	31	0	0	0	0
5	F	7	0	0	0	0
5	G	21	0	0	1	0
5	H	7	0	0	0	0
5	I	8	0	0	1	0
5	J	7	0	0	0	0
5	K	15	0	0	0	0
5	L	6	0	0	0	0
5	M	22	0	0	0	0
5	N	7	0	0	0	0
5	O	23	0	0	2	0
5	P	6	0	0	0	0
5	Q	17	0	0	0	0
5	R	4	0	0	0	0
5	S	16	0	0	1	0
5	T	9	0	0	0	0
5	U	44	0	0	1	0
5	V	10	0	0	0	0
5	W	9	0	0	1	0
5	X	7	0	0	0	0
All	All	11376	0	10524	83	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

The worst 5 of 83 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:11:PTR:HE1	1:C:96:PRO:HG3	1.64	0.79
1:W:67:LEU:HG	2:X:14:VAL:HG11	1.65	0.79
1:G:41:ASN:HB3	1:G:60:GLN:HB3	1.66	0.78
1:I:50:GLU:OE2	5:I:201:HOH:O	2.11	0.69
1:A:48:ARG:NH1	5:A:202:HOH:O	2.28	0.67

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	94/96 (98%)	91 (97%)	3 (3%)	0	100	100
1	C	94/96 (98%)	90 (96%)	4 (4%)	0	100	100
1	E	93/96 (97%)	91 (98%)	2 (2%)	0	100	100
1	G	95/96 (99%)	93 (98%)	2 (2%)	0	100	100
1	I	90/96 (94%)	88 (98%)	2 (2%)	0	100	100
1	K	94/96 (98%)	92 (98%)	2 (2%)	0	100	100
1	M	92/96 (96%)	90 (98%)	2 (2%)	0	100	100
1	O	93/96 (97%)	91 (98%)	2 (2%)	0	100	100
1	Q	90/96 (94%)	88 (98%)	2 (2%)	0	100	100
1	S	93/96 (97%)	90 (97%)	3 (3%)	0	100	100
1	U	94/96 (98%)	92 (98%)	2 (2%)	0	100	100
1	W	93/96 (97%)	91 (98%)	2 (2%)	0	100	100
2	B	8/16 (50%)	8 (100%)	0	0	100	100
2	D	9/16 (56%)	8 (89%)	1 (11%)	0	100	100
2	F	8/16 (50%)	8 (100%)	0	0	100	100
2	H	10/16 (62%)	10 (100%)	0	0	100	100
2	J	8/16 (50%)	8 (100%)	0	0	100	100
2	L	7/16 (44%)	7 (100%)	0	0	100	100
2	N	7/16 (44%)	7 (100%)	0	0	100	100
2	P	9/16 (56%)	9 (100%)	0	0	100	100
2	R	7/16 (44%)	7 (100%)	0	0	100	100
2	T	8/16 (50%)	7 (88%)	1 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	V	10/16 (62%)	9 (90%)	1 (10%)	0	100	100
2	X	7/16 (44%)	7 (100%)	0	0	100	100
All	All	1213/1344 (90%)	1182 (97%)	31 (3%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	85/85 (100%)	85 (100%)	0	100	100
1	C	86/85 (101%)	85 (99%)	1 (1%)	63	81
1	E	84/85 (99%)	84 (100%)	0	100	100
1	G	85/85 (100%)	85 (100%)	0	100	100
1	I	82/85 (96%)	81 (99%)	1 (1%)	63	81
1	K	84/85 (99%)	83 (99%)	1 (1%)	63	81
1	M	84/85 (99%)	83 (99%)	1 (1%)	63	81
1	O	83/85 (98%)	81 (98%)	2 (2%)	43	65
1	Q	82/85 (96%)	82 (100%)	0	100	100
1	S	85/85 (100%)	85 (100%)	0	100	100
1	U	85/85 (100%)	85 (100%)	0	100	100
1	W	84/85 (99%)	83 (99%)	1 (1%)	63	81
2	B	8/11 (73%)	8 (100%)	0	100	100
2	D	8/11 (73%)	8 (100%)	0	100	100
2	F	8/11 (73%)	8 (100%)	0	100	100
2	H	9/11 (82%)	8 (89%)	1 (11%)	6	9
2	J	8/11 (73%)	8 (100%)	0	100	100
2	L	7/11 (64%)	7 (100%)	0	100	100
2	N	7/11 (64%)	7 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	P	8/11 (73%)	8 (100%)	0	100	100
2	R	7/11 (64%)	7 (100%)	0	100	100
2	T	8/11 (73%)	7 (88%)	1 (12%)	4	6
2	V	9/11 (82%)	9 (100%)	0	100	100
2	X	7/11 (64%)	6 (86%)	1 (14%)	3	4
All	All	1103/1152 (96%)	1093 (99%)	10 (1%)	70	85

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	T	17	ARG
1	W	26	VAL
2	X	14	VAL
1	K	26	VAL
1	M	26	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
1	O	69	ASN
1	U	38	ASN
1	W	38	ASN
1	G	59	GLN
1	G	69	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

39 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the

expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z  > 2$	Counts	RMSZ	# $ Z  > 2$
2	PTR	T	7	2	15,16,17	3.13	2 (13%)	19,22,24	1.09	1 (5%)
2	PTR	X	7	2	15,16,17	3.10	2 (13%)	19,22,24	1.10	1 (5%)
2	PTR	P	7	2	15,16,17	3.05	2 (13%)	19,22,24	1.09	1 (5%)
2	PTR	R	11	2	15,16,17	3.18	2 (13%)	19,22,24	1.28	3 (15%)
2	PTR	F	12[A]	-	15,16,17	3.12	2 (13%)	19,22,24	1.42	3 (15%)
2	PTR	J	12[A]	-	15,16,17	3.12	2 (13%)	19,22,24	1.14	1 (5%)
2	PTR	F	12[B]	-	15,16,17	3.12	2 (13%)	19,22,24	1.11	2 (10%)
2	PTR	B	11	2	15,16,17	3.08	2 (13%)	19,22,24	1.26	3 (15%)
2	PTR	D	11	2	15,16,17	3.07	2 (13%)	19,22,24	1.24	2 (10%)
2	PTR	X	12	2	15,16,17	3.14	2 (13%)	19,22,24	1.14	1 (5%)
2	PTR	L	12	2	15,16,17	3.13	2 (13%)	19,22,24	1.09	1 (5%)
2	PTR	J	12[B]	-	15,16,17	3.12	2 (13%)	19,22,24	1.15	1 (5%)
2	PTR	T	12	2	15,16,17	3.22	2 (13%)	19,22,24	1.12	2 (10%)
2	PTR	F	11	2	15,16,17	3.05	2 (13%)	19,22,24	1.18	2 (10%)
2	PTR	J	7	2	15,16,17	3.10	2 (13%)	19,22,24	1.09	1 (5%)
2	PTR	P	12	2	15,16,17	3.13	2 (13%)	19,22,24	1.11	1 (5%)
2	PTR	R	12[A]	-	15,16,17	3.12	2 (13%)	19,22,24	1.09	2 (10%)
2	PTR	V	11	2	15,16,17	3.11	2 (13%)	19,22,24	1.19	1 (5%)
2	PTR	H	12	2	15,16,17	3.18	2 (13%)	19,22,24	1.08	1 (5%)
2	PTR	N	11	2	15,16,17	3.10	2 (13%)	19,22,24	1.18	2 (10%)
2	PTR	R	12[B]	-	15,16,17	3.12	2 (13%)	19,22,24	1.22	2 (10%)
2	PTR	L	7	2	15,16,17	3.07	2 (13%)	19,22,24	1.08	1 (5%)
2	PTR	D	7	2	15,16,17	3.10	2 (13%)	19,22,24	1.11	1 (5%)
2	PTR	H	7	2	15,16,17	3.14	2 (13%)	19,22,24	1.06	1 (5%)
2	PTR	T	11	2	15,16,17	3.09	2 (13%)	19,22,24	1.17	1 (5%)
2	PTR	X	11	2	15,16,17	3.11	2 (13%)	19,22,24	1.18	2 (10%)
2	PTR	F	7	2	15,16,17	3.15	2 (13%)	19,22,24	1.14	1 (5%)
2	PTR	V	12	2	15,16,17	3.18	2 (13%)	19,22,24	1.22	3 (15%)
2	PTR	N	12	2	15,16,17	3.14	2 (13%)	19,22,24	1.10	1 (5%)
2	PTR	J	11	2	15,16,17	3.08	2 (13%)	19,22,24	1.24	2 (10%)
2	PTR	R	7	2	15,16,17	3.06	2 (13%)	19,22,24	1.10	1 (5%)
2	PTR	N	7	2	15,16,17	3.10	2 (13%)	19,22,24	1.08	1 (5%)
2	PTR	D	12	2	15,16,17	3.11	2 (13%)	19,22,24	1.11	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	PTR	L	11	2	15,16,17	3.06	2 (13%)	19,22,24	1.23	2 (10%)
2	PTR	P	11	2	15,16,17	3.09	2 (13%)	19,22,24	1.25	2 (10%)
2	PTR	B	7	2	15,16,17	3.10	2 (13%)	19,22,24	1.01	0
2	PTR	V	7	2	15,16,17	3.09	2 (13%)	19,22,24	1.11	1 (5%)
2	PTR	B	12	2	15,16,17	3.12	2 (13%)	19,22,24	1.10	1 (5%)
2	PTR	H	11	2	15,16,17	3.11	2 (13%)	19,22,24	1.15	1 (5%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	PTR	T	7	2	-	1/10/11/13	0/1/1/1
2	PTR	X	7	2	-	0/10/11/13	0/1/1/1
2	PTR	P	7	2	-	1/10/11/13	0/1/1/1
2	PTR	R	11	2	-	3/10/11/13	0/1/1/1
2	PTR	F	12[A]	-	-	4/10/11/13	0/1/1/1
2	PTR	J	12[A]	-	-	4/10/11/13	0/1/1/1
2	PTR	F	12[B]	-	-	4/10/11/13	0/1/1/1
2	PTR	B	11	2	-	2/10/11/13	0/1/1/1
2	PTR	D	11	2	-	3/10/11/13	0/1/1/1
2	PTR	X	12	2	-	5/10/11/13	0/1/1/1
2	PTR	L	12	2	-	4/10/11/13	0/1/1/1
2	PTR	J	12[B]	-	-	2/10/11/13	0/1/1/1
2	PTR	T	12	2	-	4/10/11/13	0/1/1/1
2	PTR	F	11	2	-	2/10/11/13	0/1/1/1
2	PTR	J	7	2	-	0/10/11/13	0/1/1/1
2	PTR	P	12	2	-	4/10/11/13	0/1/1/1
2	PTR	R	12[A]	-	-	4/10/11/13	0/1/1/1
2	PTR	V	11	2	-	2/10/11/13	0/1/1/1
2	PTR	H	12	2	-	6/10/11/13	0/1/1/1
2	PTR	N	11	2	-	2/10/11/13	0/1/1/1
2	PTR	R	12[B]	-	-	0/10/11/13	0/1/1/1
2	PTR	L	7	2	-	1/10/11/13	0/1/1/1
2	PTR	D	7	2	-	1/10/11/13	0/1/1/1
2	PTR	H	7	2	-	1/10/11/13	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	PTR	T	11	2	-	2/10/11/13	0/1/1/1
2	PTR	X	11	2	-	2/10/11/13	0/1/1/1
2	PTR	F	7	2	-	0/10/11/13	0/1/1/1
2	PTR	V	12	2	-	2/10/11/13	0/1/1/1
2	PTR	N	12	2	-	1/10/11/13	0/1/1/1
2	PTR	J	11	2	-	2/10/11/13	0/1/1/1
2	PTR	R	7	2	-	2/10/11/13	0/1/1/1
2	PTR	N	7	2	-	0/10/11/13	0/1/1/1
2	PTR	D	12	2	-	4/10/11/13	0/1/1/1
2	PTR	L	11	2	-	2/10/11/13	0/1/1/1
2	PTR	P	11	2	-	2/10/11/13	0/1/1/1
2	PTR	B	7	2	-	1/10/11/13	0/1/1/1
2	PTR	V	7	2	-	2/10/11/13	0/1/1/1
2	PTR	B	12	2	-	4/10/11/13	0/1/1/1
2	PTR	H	11	2	-	0/10/11/13	0/1/1/1

The worst 5 of 78 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	T	12	PTR	P-OH	11.98	1.78	1.59
2	R	11	PTR	P-OH	11.87	1.77	1.59
2	V	12	PTR	P-OH	11.80	1.77	1.59
2	H	12	PTR	P-OH	11.79	1.77	1.59
2	F	7	PTR	P-OH	11.71	1.77	1.59

The worst 5 of 57 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	12[A]	PTR	CG-CB-CA	3.43	121.04	114.10
2	P	11	PTR	CG-CB-CA	-2.82	108.38	114.10
2	J	11	PTR	CG-CB-CA	-2.66	108.71	114.10
2	D	11	PTR	CG-CB-CA	-2.63	108.78	114.10
2	H	11	PTR	O3P-P-O2P	2.50	117.18	107.64

There are no chirality outliers.

5 of 86 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	11	PTR	C-CA-CB-CG

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Mol	Chain	Res	Type	Atoms
2	F	11	PTR	C-CA-CB-CG
2	F	12[B]	PTR	C-CA-CB-CG
2	H	7	PTR	O-C-CA-CB
2	J	11	PTR	C-CA-CB-CG

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	11	PTR	1	0
2	D	7	PTR	1	0
2	R	7	PTR	1	0

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 21 ligands modelled in this entry, 13 are monoatomic - leaving 8 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
4	PO4	E	102	-	4,4,4	1.51	1 (25%)	6,6,6	0.45	0
4	PO4	C	101	-	4,4,4	1.57	1 (25%)	6,6,6	0.45	0
4	PO4	E	101	-	4,4,4	1.56	1 (25%)	6,6,6	0.48	0
4	PO4	Q	101	-	4,4,4	1.52	1 (25%)	6,6,6	0.44	0
4	PO4	G	102	-	4,4,4	1.53	1 (25%)	6,6,6	0.45	0
4	PO4	I	101	-	4,4,4	1.50	1 (25%)	6,6,6	0.49	0
4	PO4	G	101	-	4,4,4	1.52	1 (25%)	6,6,6	0.46	0
4	PO4	M	101	-	4,4,4	1.55	1 (25%)	6,6,6	0.47	0



The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	101	PO4	P-O1	2.69	1.57	1.50
4	M	101	PO4	P-O1	2.67	1.57	1.50
4	G	102	PO4	P-O1	2.66	1.57	1.50
4	E	101	PO4	P-O1	2.66	1.57	1.50
4	Q	101	PO4	P-O1	2.63	1.57	1.50

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	95/96 (98%)	0.30	5 (5%) 32 28	28, 41, 68, 98	1 (1%)
1	C	94/96 (97%)	0.61	10 (10%) 11 8	32, 50, 79, 113	2 (2%)
1	E	94/96 (97%)	0.48	6 (6%) 25 22	30, 46, 72, 115	1 (1%)
1	G	96/96 (100%)	0.82	15 (15%) 5 4	24, 50, 93, 120	1 (1%)
1	I	91/96 (94%)	1.21	19 (20%) 2 2	36, 59, 95, 116	1 (1%)
1	K	95/96 (98%)	0.42	4 (4%) 40 36	34, 47, 68, 98	1 (1%)
1	M	94/96 (97%)	0.48	7 (7%) 20 17	30, 47, 75, 110	0
1	O	95/96 (98%)	0.32	4 (4%) 40 36	29, 44, 76, 91	0
1	Q	92/96 (95%)	0.88	16 (17%) 4 3	38, 55, 88, 107	0
1	S	95/96 (98%)	0.72	10 (10%) 11 8	35, 54, 83, 108	0
1	U	96/96 (100%)	0.07	6 (6%) 26 22	27, 38, 65, 105	0
1	W	94/96 (97%)	0.95	13 (13%) 6 5	31, 57, 87, 113	1 (1%)
2	B	10/16 (62%)	0.57	1 (10%) 12 9	37, 42, 65, 66	0
2	D	11/16 (68%)	0.87	2 (18%) 3 3	41, 53, 72, 77	0
2	F	10/16 (62%)	1.02	1 (10%) 12 9	48, 55, 78, 85	0
2	H	12/16 (75%)	1.10	3 (25%) 2 1	36, 48, 84, 85	0
2	J	10/16 (62%)	1.10	2 (20%) 3 2	48, 57, 78, 87	0
2	L	9/16 (56%)	0.67	1 (11%) 10 7	41, 44, 66, 75	0
2	N	9/16 (56%)	0.63	2 (22%) 2 2	41, 45, 80, 92	0
2	P	11/16 (68%)	1.59	4 (36%) 1 1	39, 50, 101, 103	0
2	R	9/16 (56%)	1.05	1 (11%) 10 7	41, 47, 74, 99	0
2	T	10/16 (62%)	1.24	4 (40%) 1 0	45, 52, 90, 96	0
2	V	12/16 (75%)	0.59	1 (8%) 17 14	36, 45, 68, 85	0
2	X	9/16 (56%)	1.69	4 (44%) 0 0	42, 52, 82, 90	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
All	All	1253/1344 (93%)	0.64	141 (11%) 10 7	24, 50, 86, 120	8 (0%)

The worst 5 of 141 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	M	4	PRO	6.7
1	E	4	PRO	5.9
1	Q	6	PHE	5.4
1	C	4	PRO	5.0
1	U	6	PHE	4.9

## 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	PTR	F	12[A]	16/17	0.80	0.18	52,60,68,73	13
2	PTR	F	12[B]	16/17	0.80	0.18	52,56,59,60	13
2	PTR	H	12	16/17	0.87	0.19	45,63,90,117	0
2	PTR	P	12	16/17	0.87	0.17	44,60,89,91	0
2	PTR	R	12[A]	16/17	0.87	0.19	35,47,56,58	13
2	PTR	R	12[B]	16/17	0.87	0.19	44,59,74,74	13
2	PTR	J	7	16/17	0.88	0.16	57,64,78,84	0
2	PTR	H	11	16/17	0.88	0.13	42,47,59,59	0
2	PTR	J	12[B]	16/17	0.89	0.17	52,57,67,72	13
2	PTR	J	12[A]	16/17	0.89	0.17	38,53,58,62	13
2	PTR	X	7	16/17	0.89	0.15	49,59,70,81	0
2	PTR	N	12	16/17	0.90	0.12	39,58,115,129	0
2	PTR	L	11	16/17	0.91	0.13	36,49,75,78	0
2	PTR	D	11	16/17	0.91	0.12	37,57,79,82	0
2	PTR	J	11	16/17	0.92	0.13	47,59,68,74	0
2	PTR	P	11	16/17	0.92	0.11	36,52,61,65	0
2	PTR	D	12	16/17	0.92	0.12	39,55,62,66	0
2	PTR	B	12	16/17	0.93	0.10	38,51,58,59	0
2	PTR	F	11	16/17	0.93	0.11	41,50,64,70	0
2	PTR	R	11	16/17	0.93	0.13	41,49,69,74	0
2	PTR	D	7	16/17	0.93	0.10	44,55,63,64	0
2	PTR	L	12	16/17	0.93	0.11	40,54,62,71	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	PTR	T	12	16/17	0.93	0.11	41,59,70,70	0
2	PTR	B	11	16/17	0.93	0.12	32,50,68,81	0
2	PTR	X	12	16/17	0.93	0.11	40,51,62,62	0
2	PTR	V	12	16/17	0.94	0.11	34,52,59,70	0
2	PTR	T	11	16/17	0.94	0.09	38,56,69,70	0
2	PTR	R	7	16/17	0.94	0.12	41,51,63,68	0
2	PTR	V	11	16/17	0.95	0.09	29,45,60,70	0
2	PTR	X	11	16/17	0.95	0.12	45,51,72,72	0
2	PTR	T	7	16/17	0.95	0.10	52,60,67,69	0
2	PTR	N	7	16/17	0.96	0.08	37,45,53,58	0
2	PTR	L	7	16/17	0.96	0.09	38,44,49,52	0
2	PTR	P	7	16/17	0.97	0.07	28,35,45,47	0
2	PTR	H	7	16/17	0.97	0.07	31,39,49,50	0
2	PTR	F	7	16/17	0.97	0.08	39,47,56,56	0
2	PTR	N	11	16/17	0.97	0.07	35,42,49,55	0
2	PTR	B	7	16/17	0.97	0.08	32,37,41,44	0
2	PTR	V	7	16/17	0.98	0.07	33,38,43,46	0

### 6.3 Carbohydrates

There are no oligosaccharides in this entry.

### 6.4 Ligands

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
4	PO4	E	102	5/5	0.45	0.22	114,115,134,160	0
4	PO4	Q	101	5/5	0.73	0.20	100,116,124,165	0
4	PO4	E	101	5/5	0.74	0.16	54,82,114,130	0
4	PO4	M	101	5/5	0.75	0.13	69,88,111,130	0
3	CL	Q	102	1/1	0.77	0.28	101,101,101,101	0
4	PO4	G	102	5/5	0.77	0.12	92,101,113,144	0
3	CL	G	103	1/1	0.85	0.23	64,64,64,64	0
3	CL	L	101	1/1	0.91	0.16	71,71,71,71	0
4	PO4	G	101	5/5	0.91	0.20	57,64,66,75	0
3	CL	U	102	1/1	0.91	0.13	68,68,68,68	0
4	PO4	I	101	5/5	0.91	0.17	69,72,75,83	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
4	PO4	C	101	5/5	0.91	0.19	51,59,67,70	0
3	CL	O	101	1/1	0.91	0.16	88,88,88,88	0
3	CL	A	101	1/1	0.92	0.12	59,59,59,59	0
3	CL	D	101	1/1	0.93	0.14	64,64,64,64	0
3	CL	C	102	1/1	0.93	0.20	77,77,77,77	0
3	CL	G	104	1/1	0.93	0.10	68,68,68,68	0
3	CL	G	105	1/1	0.93	0.16	70,70,70,70	0
3	CL	U	101	1/1	0.94	0.13	65,65,65,65	0
3	CL	M	102	1/1	0.94	0.15	60,60,60,60	0
3	CL	E	103	1/1	0.95	0.12	52,52,52,52	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.