



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 02:39 PM UTC

PDB ID : 3OMH / pdb_00003omh
Title : Crystal structure of PTPN22 in complex with SKAP-HOM pTyr75 peptide
Authors : Yu, X.; Sun, J.-P.; Zhang, S.; Zhang, Z.-Y.
Deposited on : 2010-08-26
Resolution : 2.90 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

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>.

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	:	2022.3.0, CSD as543be (2022)
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

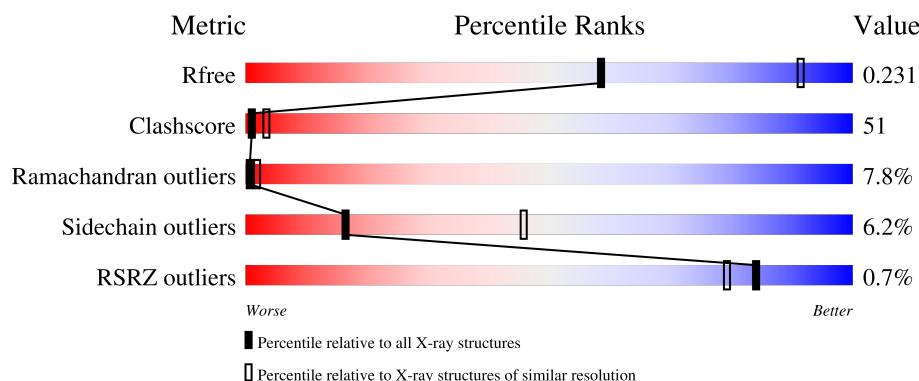
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

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 ≥ 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	313	
1	B	313	
1	C	313	
1	D	313	
2	E	9	

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Mol	Chain	Length	Quality of chain
2	F	9	
2	G	9	
2	H	9	

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
2	PTR	H	394	-	-	X	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 10155 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 Tyrosine-protein phosphatase non-receptor type 22.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	294	Total	C	N	O	S	0	0	0
			2432	1562	399	455	16			
1	B	291	Total	C	N	O	S	0	0	0
			2407	1547	394	450	16			
1	C	294	Total	C	N	O	S	0	0	0
			2432	1562	399	455	16			
1	D	294	Total	C	N	O	S	0	0	0
			2432	1562	399	455	16			

There are 80 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-18	HIS	-	expression tag	UNP Q9Y2R2
A	-17	HIS	-	expression tag	UNP Q9Y2R2
A	-16	HIS	-	expression tag	UNP Q9Y2R2
A	-15	HIS	-	expression tag	UNP Q9Y2R2
A	-14	HIS	-	expression tag	UNP Q9Y2R2
A	-13	HIS	-	expression tag	UNP Q9Y2R2
A	-12	SER	-	expression tag	UNP Q9Y2R2
A	-11	SER	-	expression tag	UNP Q9Y2R2
A	-10	GLY	-	expression tag	UNP Q9Y2R2
A	-9	LEU	-	expression tag	UNP Q9Y2R2
A	-8	VAL	-	expression tag	UNP Q9Y2R2
A	-7	PRO	-	expression tag	UNP Q9Y2R2
A	-6	ARG	-	expression tag	UNP Q9Y2R2
A	-5	GLY	-	expression tag	UNP Q9Y2R2
A	-4	SER	-	expression tag	UNP Q9Y2R2
A	-3	HIS	-	expression tag	UNP Q9Y2R2
A	-2	MET	-	expression tag	UNP Q9Y2R2
A	-1	ALA	-	expression tag	UNP Q9Y2R2
A	0	SER	-	expression tag	UNP Q9Y2R2
A	227	SER	CYS	engineered mutation	UNP Q9Y2R2
B	-18	HIS	-	expression tag	UNP Q9Y2R2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-17	HIS	-	expression tag	UNP Q9Y2R2
B	-16	HIS	-	expression tag	UNP Q9Y2R2
B	-15	HIS	-	expression tag	UNP Q9Y2R2
B	-14	HIS	-	expression tag	UNP Q9Y2R2
B	-13	HIS	-	expression tag	UNP Q9Y2R2
B	-12	SER	-	expression tag	UNP Q9Y2R2
B	-11	SER	-	expression tag	UNP Q9Y2R2
B	-10	GLY	-	expression tag	UNP Q9Y2R2
B	-9	LEU	-	expression tag	UNP Q9Y2R2
B	-8	VAL	-	expression tag	UNP Q9Y2R2
B	-7	PRO	-	expression tag	UNP Q9Y2R2
B	-6	ARG	-	expression tag	UNP Q9Y2R2
B	-5	GLY	-	expression tag	UNP Q9Y2R2
B	-4	SER	-	expression tag	UNP Q9Y2R2
B	-3	HIS	-	expression tag	UNP Q9Y2R2
B	-2	MET	-	expression tag	UNP Q9Y2R2
B	-1	ALA	-	expression tag	UNP Q9Y2R2
B	0	SER	-	expression tag	UNP Q9Y2R2
B	227	SER	CYS	engineered mutation	UNP Q9Y2R2
C	-18	HIS	-	expression tag	UNP Q9Y2R2
C	-17	HIS	-	expression tag	UNP Q9Y2R2
C	-16	HIS	-	expression tag	UNP Q9Y2R2
C	-15	HIS	-	expression tag	UNP Q9Y2R2
C	-14	HIS	-	expression tag	UNP Q9Y2R2
C	-13	HIS	-	expression tag	UNP Q9Y2R2
C	-12	SER	-	expression tag	UNP Q9Y2R2
C	-11	SER	-	expression tag	UNP Q9Y2R2
C	-10	GLY	-	expression tag	UNP Q9Y2R2
C	-9	LEU	-	expression tag	UNP Q9Y2R2
C	-8	VAL	-	expression tag	UNP Q9Y2R2
C	-7	PRO	-	expression tag	UNP Q9Y2R2
C	-6	ARG	-	expression tag	UNP Q9Y2R2
C	-5	GLY	-	expression tag	UNP Q9Y2R2
C	-4	SER	-	expression tag	UNP Q9Y2R2
C	-3	HIS	-	expression tag	UNP Q9Y2R2
C	-2	MET	-	expression tag	UNP Q9Y2R2
C	-1	ALA	-	expression tag	UNP Q9Y2R2
C	0	SER	-	expression tag	UNP Q9Y2R2
C	227	SER	CYS	engineered mutation	UNP Q9Y2R2
D	-18	HIS	-	expression tag	UNP Q9Y2R2
D	-17	HIS	-	expression tag	UNP Q9Y2R2
D	-16	HIS	-	expression tag	UNP Q9Y2R2

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-15	HIS	-	expression tag	UNP Q9Y2R2
D	-14	HIS	-	expression tag	UNP Q9Y2R2
D	-13	HIS	-	expression tag	UNP Q9Y2R2
D	-12	SER	-	expression tag	UNP Q9Y2R2
D	-11	SER	-	expression tag	UNP Q9Y2R2
D	-10	GLY	-	expression tag	UNP Q9Y2R2
D	-9	LEU	-	expression tag	UNP Q9Y2R2
D	-8	VAL	-	expression tag	UNP Q9Y2R2
D	-7	PRO	-	expression tag	UNP Q9Y2R2
D	-6	ARG	-	expression tag	UNP Q9Y2R2
D	-5	GLY	-	expression tag	UNP Q9Y2R2
D	-4	SER	-	expression tag	UNP Q9Y2R2
D	-3	HIS	-	expression tag	UNP Q9Y2R2
D	-2	MET	-	expression tag	UNP Q9Y2R2
D	-1	ALA	-	expression tag	UNP Q9Y2R2
D	0	SER	-	expression tag	UNP Q9Y2R2
D	227	SER	CYS	engineered mutation	UNP Q9Y2R2

- Molecule 2 is a protein called Src kinase-associated phosphoprotein 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	9	Total	C	N	O	P	0	0	0
			81	47	9	24	1			
2	F	9	Total	C	N	O	P	0	0	0
			81	47	9	24	1			
2	G	9	Total	C	N	O	P	0	0	0
			81	47	9	24	1			
2	H	8	Total	C	N	O	P	0	0	0
			69	38	8	22	1			

- Molecule 3 is water.

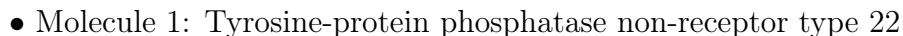
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	40	Total	O	0	0
			40	40		
3	B	34	Total	O	0	0
			34	34		
3	C	35	Total	O	0	0
			35	35		
3	D	26	Total	O	0	0
			26	26		
3	E	3	Total	O	0	0
			3	3		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	G	1	Total	O	0	0
			1	1		
3	H	1	Total	O	0	0
			1	1		

- Molecule 1: Tyrosine-protein phosphatase non-receptor type 22



[illegible]

Chain D:

Chain E:

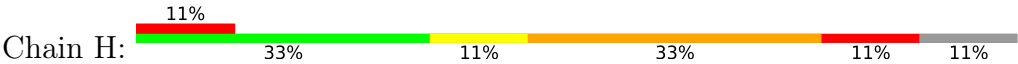
Chain F:



● Molecule 2: Src kinase-associated phosphoprotein 2



● Molecule 2: Src kinase-associated phosphoprotein 2



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	115.23Å 46.71Å 121.49Å 90.00° 101.43° 90.00°	Depositor
Resolution (Å)	36.75 – 2.90 36.75 – 2.90	Depositor EDS
% Data completeness (in resolution range)	(Not available) (36.75-2.90) 94.5 (36.75-2.90)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.45 (at 2.65Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.229 , 0.260 0.177 , 0.231	Depositor DCC
R_{free} test set	2441 reflections (7.32%)	wwPDB-VP
Wilson B-factor (Å ²)	44.9	Xtriage
Anisotropy	0.097	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 73.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	10155	wwPDB-VP
Average B, all atoms (Å ²)	32.0	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 40.70 % 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 2.6309e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

²Theoretical 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: PTR

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	0.45	1/2489 (0.0%)	0.96	11/3361 (0.3%)
1	B	0.41	0/2462	0.97	9/3321 (0.3%)
1	C	0.42	0/2489	0.99	13/3361 (0.4%)
1	D	0.42	0/2489	1.00	13/3361 (0.4%)
2	E	0.52	0/65	0.84	0/84
2	F	0.57	0/65	1.27	1/84 (1.2%)
2	G	0.55	0/65	1.09	0/84
2	H	0.56	0/52	1.11	1/68 (1.5%)
All	All	0.43	1/10176 (0.0%)	0.98	48/13724 (0.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	C	0	1
1	D	0	1
All	All	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	225	ILE	C-N	-6.80	1.24	1.33

The worst 5 of 48 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	198	VAL	N-CA-C	8.60	116.03	108.63
1	B	274	GLN	N-CA-C	8.09	120.88	111.02

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	110	LEU	N-CA-C	-7.40	103.71	112.89
1	A	214	CYS	N-CA-C	-7.37	103.85	112.92
1	C	84	TYR	N-CA-C	7.25	121.01	110.28

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	142	TYR	Sidechain
1	D	142	TYR	Sidechain

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	2432	0	2422	219	0
1	B	2407	0	2402	257	0
1	C	2432	0	2422	278	0
1	D	2432	0	2422	251	0
2	E	81	0	49	10	0
2	F	81	0	49	16	0
2	G	81	0	49	16	0
2	H	69	0	39	8	0
3	A	40	0	0	4	0
3	B	34	0	0	1	0
3	C	35	0	0	2	0
3	D	26	0	0	1	0
3	E	3	0	0	0	0
3	G	1	0	0	0	0
3	H	1	0	0	1	0
All	All	10155	0	9854	1013	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 51.

The worst 5 of 1013 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)
1:D:265:MET:HB3	1:D:272:LEU:HD23	1.26	1.15
1:C:168:ASP:HB3	1:C:192:ASN:HD22	1.14	1.10
1:B:168:ASP:HB3	1:B:192:ASN:HD22	1.18	1.05
1:C:142:TYR:HB3	1:C:143:TRP:HE3	1.22	1.04
1:C:142:TYR:HB3	1:C:143:TRP:CE3	1.93	1.02

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	292/313 (93%)	224 (77%)	46 (16%)	22 (8%)	1	2
1	B	287/313 (92%)	207 (72%)	60 (21%)	20 (7%)	1	2
1	C	292/313 (93%)	223 (76%)	48 (16%)	21 (7%)	1	2
1	D	292/313 (93%)	226 (77%)	48 (16%)	18 (6%)	1	3
2	E	6/9 (67%)	2 (33%)	0	4 (67%)	0	0
2	F	6/9 (67%)	2 (33%)	0	4 (67%)	0	0
2	G	6/9 (67%)	4 (67%)	0	2 (33%)	0	0
2	H	5/9 (56%)	3 (60%)	1 (20%)	1 (20%)	0	0
All	All	1186/1288 (92%)	891 (75%)	203 (17%)	92 (8%)	1	2

5 of 92 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	47	THR
1	A	78	SER
1	A	179	ASN
1	A	200	SER
1	A	232	GLY

5.3.2 Protein sidechains ⓘ

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	271/287 (94%)	261 (96%)	10 (4%)	30	64
1	B	268/287 (93%)	248 (92%)	20 (8%)	12	37
1	C	271/287 (94%)	254 (94%)	17 (6%)	16	45
1	D	271/287 (94%)	258 (95%)	13 (5%)	23	55
2	E	7/7 (100%)	4 (57%)	3 (43%)	0	0
2	F	7/7 (100%)	6 (86%)	1 (14%)	3	11
2	G	7/7 (100%)	4 (57%)	3 (43%)	0	0
2	H	6/7 (86%)	4 (67%)	2 (33%)	0	0
All	All	1108/1176 (94%)	1039 (94%)	69 (6%)	16	46

5 of 69 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	215	TYR
1	D	294	MET
2	G	395	ASP
1	B	218	ASP
1	B	215	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 33 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	88	ASN
1	D	179	ASN
1	D	192	ASN
1	B	34	GLN
1	B	26	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

4 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	F	394	2	15,16,17	1.14	1 (6%)	17,22,24	0.63	0
2	PTR	E	394	2	15,16,17	1.19	1 (6%)	17,22,24	0.78	0
2	PTR	G	394	2	15,16,17	1.25	1 (6%)	17,22,24	0.64	0
2	PTR	H	394	2	15,16,17	1.25	1 (6%)	17,22,24	0.70	0

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	F	394	2	-	2/10/11/13	0/1/1/1
2	PTR	E	394	2	-	0/10/11/13	0/1/1/1
2	PTR	G	394	2	-	0/10/11/13	0/1/1/1
2	PTR	H	394	2	-	1/10/11/13	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	394	PTR	P-OH	3.44	1.66	1.59
2	G	394	PTR	P-OH	3.39	1.66	1.59
2	E	394	PTR	P-OH	3.09	1.65	1.59
2	F	394	PTR	P-OH	2.95	1.65	1.59

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	F	394	PTR	CZ-OH-P-O3P
2	F	394	PTR	CZ-OH-P-O1P
2	H	394	PTR	C-CA-CB-CG

There are no ring outliers.

4 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	F	394	PTR	3	0
2	E	394	PTR	2	0
2	G	394	PTR	4	0
2	H	394	PTR	6	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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, 95th 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 ²)	Q<0.9
1	A	294/313 (93%)	-0.41	0 100 100	7, 26, 50, 57	0
1	B	291/313 (92%)	-0.32	1 (0%) 90 87	11, 32, 55, 65	0
1	C	294/313 (93%)	-0.35	2 (0%) 84 79	6, 30, 53, 61	0
1	D	294/313 (93%)	-0.20	3 (1%) 79 73	8, 34, 59, 66	0
2	E	8/9 (88%)	0.07	0 100 100	27, 39, 48, 52	0
2	F	8/9 (88%)	0.74	1 (12%) 8 7	29, 38, 47, 52	0
2	G	8/9 (88%)	0.07	0 100 100	25, 35, 46, 48	0
2	H	7/9 (77%)	0.67	1 (14%) 6 5	27, 36, 46, 52	0
All	All	1204/1288 (93%)	-0.30	8 (0%) 84 79	6, 31, 55, 66	0

The worst 5 of 8 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	142	TYR	3.0
1	D	142	TYR	2.8
2	F	391	GLY	2.5
1	C	38	TYR	2.5
1	D	169	TYR	2.4

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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, 95th 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 ²)	Q<0.9
2	PTR	F	394	16/17	0.94	0.10	18,25,28,28	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	PTR	G	394	16/17	0.94	0.09	18,23,28,33	0
2	PTR	H	394	16/17	0.95	0.10	20,21,28,29	0
2	PTR	E	394	16/17	0.97	0.07	21,24,26,27	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.