



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 23, 2024 – 02:47 AM EDT

PDB ID : 1XDH
Title : Structure of plasmepsin II in complex with pepstatin A
Authors : Prade, L.
Deposited on : 2004-09-06
Resolution : 1.70 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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 : 4.02b-467
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 1.20.1
EDS : 3.0
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.003 (Gargrove)
Density-Fitness : 1.0.11
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

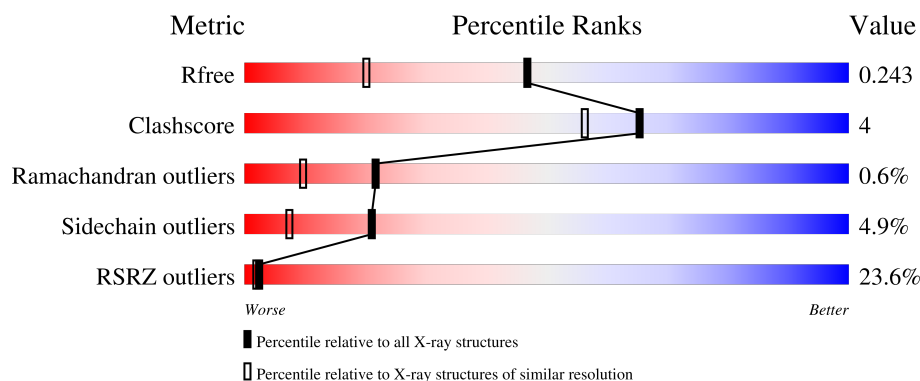
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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}	164625	5161 (1.70-1.70)
Clashscore	180529	5671 (1.70-1.70)
Ramachandran outliers	177936	5594 (1.70-1.70)
Sidechain outliers	177891	5594 (1.70-1.70)
RSRZ outliers	164620	5159 (1.70-1.70)

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	331	<div> <div>15%</div> <div>92%</div> <div>6%</div> <div>..</div> </div>
1	B	331	<div> <div>33%</div> <div>85%</div> <div>11%</div> <div>..</div> </div>
2	C	6	<div> <div>67%</div> <div>17%</div> <div>17%</div> </div>
2	D	6	<div> <div>33%</div> <div>50%</div> <div>17%</div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6046 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 Plasmepsin 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	329	Total	C	N	O	S	0	0	0
			2607	1689	404	503	11			
1	B	329	Total	C	N	O	S	0	0	0
			2607	1689	404	503	11			

- Molecule 2 is a protein called Pepstatin.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	6	Total	C	N	O	0	0	0
			48	34	5	9			
2	D	6	Total	C	N	O	0	0	0
			48	34	5	9			

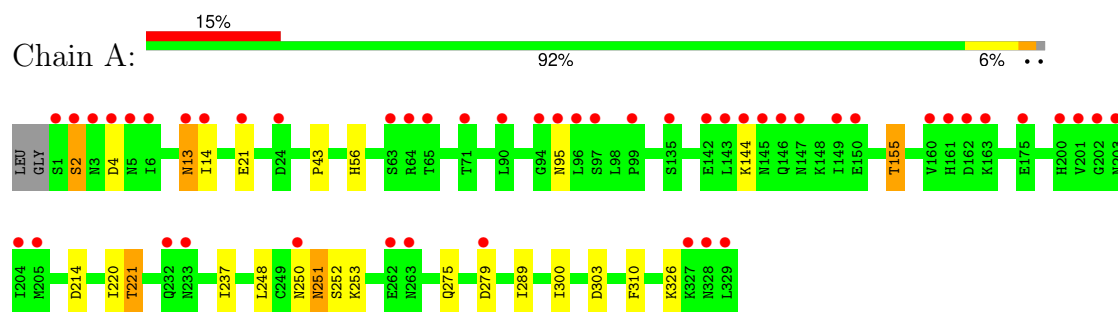
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	413	Total	O	0	0
			413	413		
3	B	317	Total	O	0	0
			317	317		
3	C	1	Total	O	0	0
			1	1		
3	D	5	Total	O	0	0
			5	5		

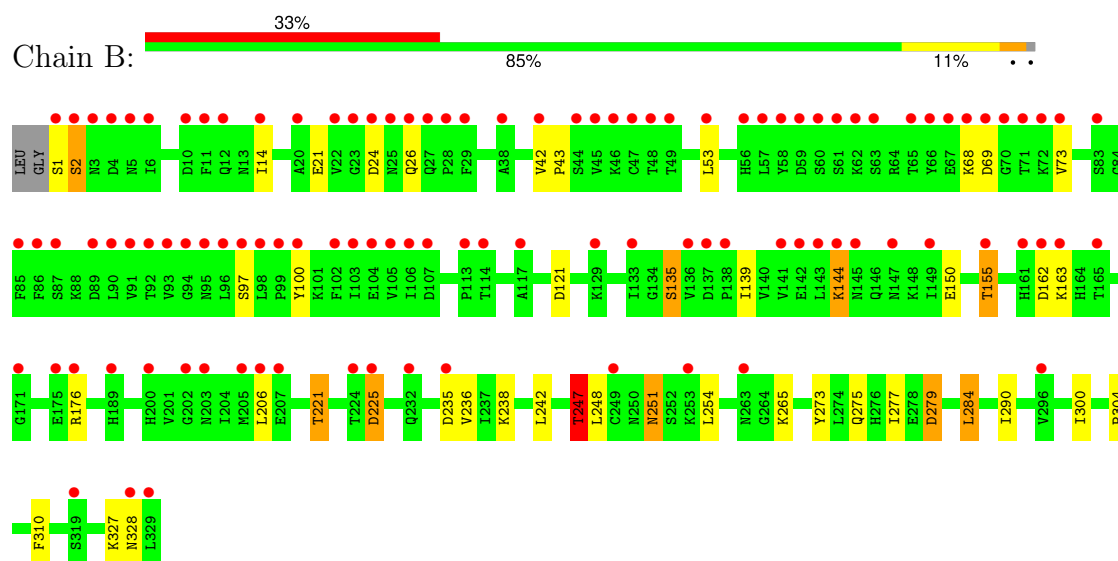
3 Residue-property plots [i](#)

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.

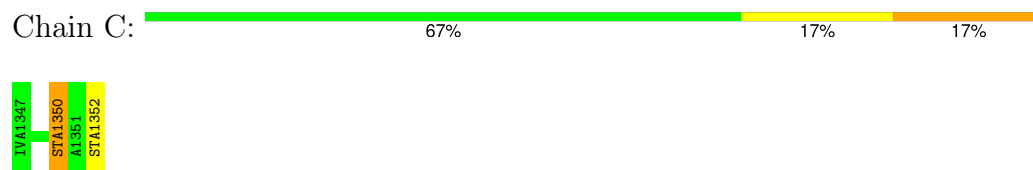
• Molecule 1: Plasmepsin 2



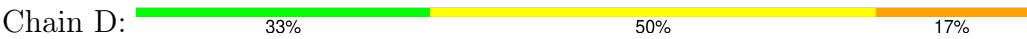
• Molecule 1: Plasmepsin 2



• Molecule 2: Pepstatin



• Molecule 2: Pepstatin



IYA1347
V1348
V1349
STA1350
A1351
STA1352

4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	141.11Å 141.11Å 97.10Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	119.52 – 1.70 119.52 – 1.70	Depositor EDS
% Data completeness (in resolution range)	98.8 (119.52-1.70) 98.8 (119.52-1.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.47 (at 1.70Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.214 , 0.237 0.221 , 0.243	Depositor DCC
R_{free} test set	6068 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	22.6	Xtriage
Anisotropy	0.027	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 41.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.023 for -h,-k,l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6046	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.56% of the height of the origin peak. No significant pseudotranslation is detected.*

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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: STA, IVA

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	0.40	0/2674	0.75	3/3638 (0.1%)
1	B	0.37	0/2674	0.77	9/3638 (0.2%)
2	C	0.62	0/17	0.81	0/21
2	D	0.84	0/17	0.93	0/21
All	All	0.39	0/5382	0.76	12/7318 (0.2%)

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	B	2	0
2	C	0	2
2	D	0	2
All	All	2	4

There are no bond length outliers.

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	279	ASP	CB-CG-OD2	7.48	125.03	118.30
1	B	221	THR	CA-CB-CG2	6.43	121.41	112.40
1	B	247	THR	CA-CB-CG2	5.91	120.68	112.40
1	A	279	ASP	CB-CG-OD2	5.82	123.53	118.30
1	B	225	ASP	CB-CG-OD2	5.53	123.28	118.30
1	B	121	ASP	CB-CG-OD2	5.46	123.22	118.30
1	B	162	ASP	CB-CG-OD2	5.28	123.05	118.30
1	B	24	ASP	CB-CG-OD2	5.14	122.93	118.30
1	A	303	ASP	CB-CG-OD2	5.13	122.92	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	214	ASP	CB-CG-OD2	5.10	122.89	118.30
1	B	69	ASP	CB-CG-OD2	5.07	122.86	118.30
1	B	235	ASP	CB-CG-OD2	5.04	122.84	118.30

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	B	221	THR	CB
1	B	247	THR	CB

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	C	1350	STA	Mainchain,Peptide
2	D	1350	STA	Mainchain,Peptide

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	2607	0	2536	16	0
1	B	2607	0	2536	23	0
2	C	48	0	60	0	0
2	D	48	0	60	3	0
3	A	413	0	0	6	0
3	B	317	0	0	5	0
3	C	1	0	0	0	0
3	D	5	0	0	0	0
All	All	6046	0	5192	39	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.

All (39) 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:A:221:THR:HB	1:A:300:ILE:HB	1.72	0.71
1:A:155:THR:HG22	3:A:1348:HOH:O	1.92	0.69
1:A:155:THR:HG21	3:A:1354:HOH:O	1.93	0.69
1:B:155:THR:HG21	3:B:1352:HOH:O	1.92	0.68
1:B:221:THR:HG23	3:B:1364:HOH:O	1.92	0.68
1:B:155:THR:HG22	3:B:1353:HOH:O	1.97	0.64
1:B:155:THR:HG23	1:B:310:PHE:CE1	2.33	0.63
1:B:273:TYR:HA	1:B:304:PRO:HB3	1.81	0.61
1:B:236:VAL:HG12	1:B:247:THR:HG23	1.83	0.59
1:B:290:ILE:HG23	3:B:1642:HOH:O	2.03	0.58
1:B:247:THR:HG21	1:B:254:LEU:HD21	1.87	0.57
1:B:14:ILE:HD11	1:B:275:GLN:HB2	1.87	0.56
1:A:251:ASN:HD22	1:A:251:ASN:C	2.08	0.55
1:A:221:THR:CG2	3:A:1349:HOH:O	2.55	0.55
1:A:251:ASN:ND2	1:A:253:LYS:H	2.05	0.54
1:A:155:THR:HG23	1:A:310:PHE:CE1	2.44	0.52
1:B:265:LYS:HG3	3:B:1625:HOH:O	2.12	0.49
1:A:221:THR:HG22	3:A:1349:HOH:O	2.11	0.49
1:A:251:ASN:HD22	1:A:253:LYS:H	1.63	0.46
1:B:290:ILE:HG13	2:D:1347:IVA:HG11	1.97	0.46
1:B:238:LYS:HE3	1:B:242:LEU:O	2.16	0.45
2:D:1348:VAL:HG12	2:D:1350:STA:HG	1.99	0.45
1:B:251:ASN:C	1:B:251:ASN:HD22	2.19	0.45
1:B:290:ILE:HD11	2:D:1347:IVA:HG11	1.99	0.44
1:A:14:ILE:HD11	1:A:275:GLN:HG3	2.00	0.44
1:A:43:PRO:HG2	1:A:56:HIS:O	2.17	0.44
1:B:155:THR:HG23	1:B:310:PHE:CZ	2.53	0.43
1:B:221:THR:HG22	1:B:300:ILE:H	1.83	0.43
1:B:1:SER:O	1:B:2:SER:CB	2.67	0.43
1:A:251:ASN:HD22	1:A:252:SER:N	2.18	0.42
1:B:221:THR:HB	1:B:300:ILE:HB	1.99	0.42
1:B:144:LYS:NZ	1:B:150:GLU:O	2.41	0.42
1:A:220:ILE:O	1:A:289:ILE:HA	2.18	0.42
1:A:237:ILE:CD1	1:B:279:ASP:O	2.68	0.42
1:A:250:ASN:HB3	3:A:1490:HOH:O	2.20	0.41
1:B:100:TYR:CZ	1:B:139:ILE:HG13	2.56	0.41
1:B:277:ILE:HG13	1:B:284:LEU:HB3	2.03	0.41
1:B:42:VAL:HG13	1:B:43:PRO:HD2	2.03	0.40
1:A:13:ASN:ND2	3:A:1551:HOH:O	2.53	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	327/331 (99%)	311 (95%)	15 (5%)	1 (0%)	37	23
1	B	327/331 (99%)	315 (96%)	9 (3%)	3 (1%)	14	4
2	C	3/6 (50%)	3 (100%)	0	0	100	100
2	D	3/6 (50%)	3 (100%)	0	0	100	100
All	All	660/674 (98%)	632 (96%)	24 (4%)	4 (1%)	22	10

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	2	SER
1	B	2	SER
1	B	26	GLN
1	B	135	SER

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	294/295 (100%)	283 (96%)	11 (4%)	29	13
1	B	294/295 (100%)	276 (94%)	18 (6%)	15	4
2	C	2/2 (100%)	2 (100%)	0	100	100
2	D	2/2 (100%)	2 (100%)	0	100	100
All	All	592/594 (100%)	563 (95%)	29 (5%)	21	7

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	SER
1	A	4	ASP
1	A	13	ASN
1	A	21	GLU
1	A	95	ASN
1	A	144	LYS
1	A	155	THR
1	A	221	THR
1	A	248	LEU
1	A	251	ASN
1	A	326	LYS
1	B	21	GLU
1	B	53	LEU
1	B	68	LYS
1	B	73	VAL
1	B	97	SER
1	B	135	SER
1	B	144	LYS
1	B	155	THR
1	B	163	LYS
1	B	176	ARG
1	B	206	LEU
1	B	225	ASP
1	B	247	THR
1	B	248	LEU
1	B	251	ASN
1	B	284	LEU
1	B	327	LYS
1	B	328	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	147	ASN
1	A	250	ASN
1	A	251	ASN
1	B	232	GLN
1	B	251	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	STA	D	1350	2	10,10,11	0.35	0	9,12,14	0.70	0
2	STA	C	1352	2	11,11,11	1.27	2 (18%)	11,14,14	1.10	1 (9%)
2	STA	C	1350	2	10,10,11	0.47	0	9,12,14	0.92	1 (11%)
2	STA	D	1352	2	11,11,11	1.33	2 (18%)	11,14,14	1.02	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	STA	D	1350	2	-	1/11/11/12	-
2	STA	C	1352	2	-	0/12/12/12	-
2	STA	C	1350	2	-	2/11/11/12	-
2	STA	D	1352	2	-	1/12/12/12	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	1352	STA	O-C	3.51	1.33	1.22
2	C	1352	STA	O-C	3.39	1.33	1.22
2	D	1352	STA	OXT-C	-2.54	1.22	1.30
2	C	1352	STA	OXT-C	-2.42	1.22	1.30

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	C	1352	STA	OXT-C-CM	2.24	120.97	114.00
2	C	1350	STA	CH-CM-C	-2.06	109.51	113.02

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	1350	STA	O-C-CM-CH
2	D	1350	STA	O-C-CM-CH
2	D	1352	STA	OXT-C-CM-CH
2	C	1350	STA	OH-CH-CM-C

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	1350	STA	1	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	329/331 (99%)	0.76	49 (14%) 7 6	12, 21, 35, 58	0
1	B	329/331 (99%)	1.45	108 (32%) 1 1	14, 28, 49, 62	0
2	C	3/6 (50%)	-0.41	0 100 100	13, 13, 15, 20	0
2	D	3/6 (50%)	0.43	0 100 100	20, 20, 23, 28	0
All	All	664/674 (98%)	1.09	157 (23%) 2 2	12, 24, 45, 62	0

All (157) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1	SER	7.3
1	B	26	GLN	6.1
1	B	1	SER	6.0
1	A	162	ASP	5.6
1	A	202	GLY	5.5
1	B	94	GLY	5.3
1	B	22	VAL	4.8
1	A	4	ASP	4.8
1	A	232	GLN	4.6
1	A	5	ASN	4.5
1	B	95	ASN	4.5
1	B	24	ASP	4.4
1	B	28	PRO	4.3
1	B	2	SER	4.3
1	B	14	ILE	4.3
1	B	73	VAL	4.3
1	B	4	ASP	4.2
1	B	70	GLY	4.2
1	B	328	ASN	4.1
1	B	141	VAL	4.1
1	B	47	CYS	4.1

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Mol	Chain	Res	Type	RSRZ
1	B	65	THR	4.0
1	B	66	TYR	4.0
1	B	96	LEU	4.0
1	A	329	LEU	3.9
1	B	63	SER	3.9
1	B	27	GLN	3.9
1	A	3	ASN	3.9
1	A	95	ASN	3.9
1	B	48	THR	3.9
1	A	14	ILE	3.8
1	A	147	ASN	3.8
1	A	2	SER	3.8
1	B	97	SER	3.7
1	B	57	LEU	3.7
1	B	71	THR	3.7
1	B	45	VAL	3.7
1	B	49	THR	3.7
1	B	61	SER	3.6
1	B	23	GLY	3.6
1	A	175	GLU	3.6
1	A	201	VAL	3.6
1	B	87	SER	3.6
1	B	235	ASP	3.5
1	B	6	ILE	3.5
1	B	100	TYR	3.5
1	B	91	VAL	3.5
1	A	263	ASN	3.5
1	B	25	ASN	3.4
1	B	11	PHE	3.4
1	B	107	ASP	3.4
1	B	329	LEU	3.4
1	A	142	GLU	3.4
1	B	149	ILE	3.3
1	A	150	GLU	3.3
1	A	203	ASN	3.2
1	A	328	ASN	3.2
1	B	114	THR	3.2
1	B	98	LEU	3.2
1	B	5	ASN	3.1
1	B	85	PHE	3.1
1	B	103	ILE	3.1
1	A	163	LYS	3.1

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Mol	Chain	Res	Type	RSRZ
1	B	53	LEU	3.1
1	B	137	ASP	3.1
1	A	143	LEU	3.0
1	A	149	ILE	3.0
1	B	165	THR	3.0
1	A	144	LYS	3.0
1	B	145	ASN	3.0
1	A	205	MET	3.0
1	B	69	ASP	3.0
1	B	144	LYS	3.0
1	A	94	GLY	2.9
1	B	90	LEU	2.9
1	B	163	LYS	2.9
1	B	117	ALA	2.9
1	B	205	MET	2.9
1	B	224	THR	2.8
1	A	13	ASN	2.8
1	A	90	LEU	2.8
1	A	161	HIS	2.8
1	B	56	HIS	2.8
1	B	60	SER	2.8
1	B	175	GLU	2.8
1	B	225	ASP	2.7
1	B	83	SER	2.7
1	B	99	PRO	2.7
1	B	102	PHE	2.7
1	B	12	GLN	2.7
1	B	162	ASP	2.7
1	A	233	ASN	2.7
1	A	262	GLU	2.7
1	A	24	ASP	2.7
1	B	10	ASP	2.7
1	A	64	ARG	2.7
1	B	106	ILE	2.6
1	A	250	ASN	2.6
1	B	20	ALA	2.6
1	B	200	HIS	2.6
1	B	29	PHE	2.5
1	B	143	LEU	2.5
1	B	203	ASN	2.5
1	B	147	ASN	2.5
1	B	46	LYS	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	207	GLU	2.5
1	A	97	SER	2.5
1	A	96	LEU	2.5
1	A	327	LYS	2.5
1	A	99	PRO	2.5
1	B	89	ASP	2.5
1	B	3	ASN	2.5
1	B	104	GLU	2.5
1	A	279	ASP	2.4
1	B	93	VAL	2.4
1	A	21	GLU	2.4
1	B	249	CYS	2.4
1	B	142	GLU	2.4
1	B	113	PRO	2.3
1	B	176	ARG	2.3
1	B	38	ALA	2.3
1	B	72	LYS	2.3
1	B	129	LYS	2.3
1	B	155	THR	2.3
1	A	200	HIS	2.3
1	A	204	ILE	2.3
1	A	160	VAL	2.3
1	B	161	HIS	2.3
1	B	67	GLU	2.3
1	B	133	ILE	2.3
1	B	68	LYS	2.3
1	B	44	SER	2.3
1	A	6	ILE	2.2
1	A	71	THR	2.2
1	A	135	SER	2.2
1	B	202	GLY	2.2
1	B	58	TYR	2.2
1	B	206	LEU	2.2
1	B	171	GLY	2.2
1	B	92	THR	2.2
1	B	189	HIS	2.2
1	B	253	LYS	2.1
1	B	86	PHE	2.1
1	A	146	GLN	2.1
1	B	59	ASP	2.1
1	B	263	ASN	2.1
1	A	65	THR	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	42	VAL	2.1
1	B	62	LYS	2.1
1	B	138	PRO	2.1
1	B	105	VAL	2.1
1	A	63	SER	2.0
1	A	145	ASN	2.0
1	B	136	VAL	2.0
1	B	296	VAL	2.0
1	B	232	GLN	2.0
1	B	319	SER	2.0

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, 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(\AA^2)	Q<0.9
2	STA	D	1352	12/12	0.84	0.17	32,37,40,41	0
2	STA	C	1352	12/12	0.85	0.17	25,33,39,39	0
2	STA	D	1350	11/12	0.95	0.07	19,20,21,23	0
2	STA	C	1350	11/12	0.97	0.06	12,13,15,15	0

6.3 Carbohydrates [i](#)

There are no monosaccharides 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.