



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 02:46 PM UTC

PDB ID : 3BX1 / pdb_00003bx1
Title : Complex between the Barley alpha-Amylase/Subtilisin Inhibitor and the subtilisin Savinase
Authors : Micheelsen, P.O.; Vevodova, J.; Wilson, K.; Skjot, M.
Deposited on : 2008-01-11
Resolution : 1.85 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	:	4-5-2 with Phenix2.0
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

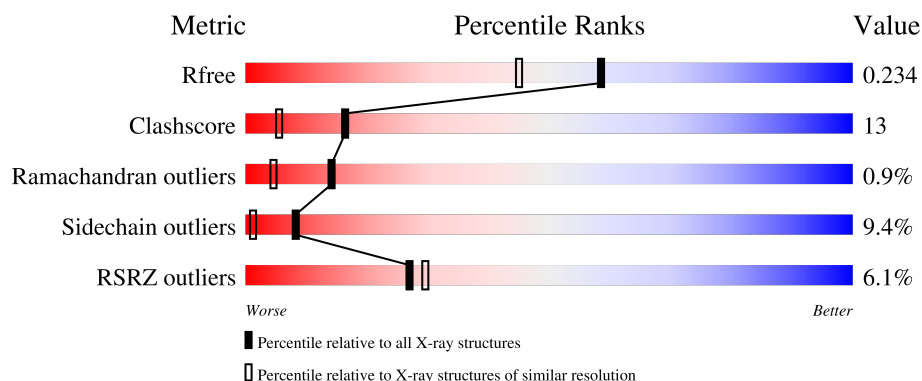
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.85 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	3428 (1.86-1.86)
Clashscore	190562	3579 (1.86-1.86)
Ramachandran outliers	187476	3553 (1.86-1.86)
Sidechain outliers	187428	3553 (1.86-1.86)
RSRZ outliers	180081	3429 (1.86-1.86)

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	269	90% 9% .
1	B	269	3% 87% 11% .
2	C	181	11% 68% 20% 8% .
2	D	181	14% 66% 19% 8% 7%

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
4	CL	B	282	-	-	X	-

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 7228 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 Subtilisin Savinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	269	Total	C	N	O	S	1	6	0
			1903	1165	349	386	3			
1	B	269	Total	C	N	O	S	1	3	0
			1889	1156	347	383	3			

- Molecule 2 is a protein called Alpha-amylase/subtilisin inhibitor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	181	Total	C	N	O	S	0	1	0
			1407	887	255	259	6			
2	C	181	Total	C	N	O	S	0	3	0
			1421	897	259	259	6			

- Molecule 3 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Ca	0	0
			1	1		
3	B	1	Total	Ca	0	0
			1	1		
3	D	1	Total	Ca	0	0
			1	1		
3	C	1	Total	Ca	0	0
			1	1		

- Molecule 4 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	11	Total	Cl	0	0
			11	11		
4	B	6	Total	Cl	0	0
			6	6		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	D	3	Total 3	Cl 3	0	0
4	C	4	Total 4	Cl 4	0	0

- Molecule 5 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	3	Total 3	Na 3	0	0
5	B	2	Total 2	Na 2	0	0
5	C	1	Total 1	Na 1	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	211	Total 211	O 211	0	0
6	B	127	Total 127	O 127	0	0
6	D	96	Total 96	O 96	0	0
6	C	140	Total 140	O 140	0	0

3 Residue-property plots

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.

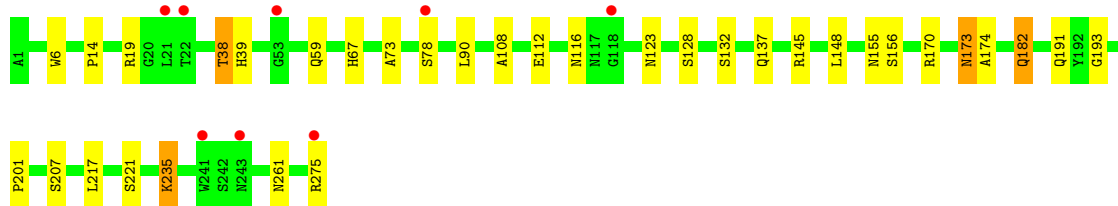
• Molecule 1: Subtilisin Savinase

Chain A: 



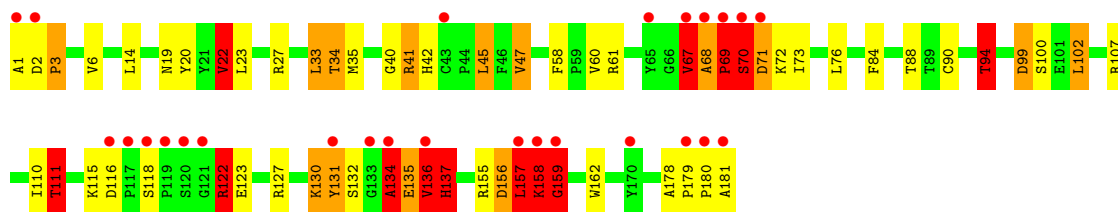
• Molecule 1: Subtilisin Savinase

Chain B: 



• Molecule 2: Alpha-amylase/subtilisin inhibitor

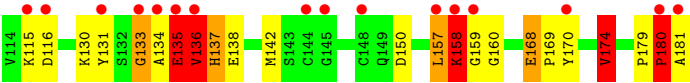
Chain D: 



• Molecule 2: Alpha-amylase/subtilisin inhibitor

Chain C: 





4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	100.64Å 100.64Å 216.24Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	35.11 – 1.85 35.11 – 1.85	Depositor EDS
% Data completeness (in resolution range)	87.3 (35.11-1.85) 87.6 (35.11-1.85)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.31 (at 1.84Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.202 , 0.239 0.200 , 0.234	Depositor DCC
R_{free} test set	4208 reflections (4.39%)	wwPDB-VP
Wilson B-factor (Å ²)	29.0	Xtriage
Anisotropy	0.409	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 42.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7228	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.71% 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

5.1 Standard geometry

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

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	1.08	0/1955	1.06	2/2669 (0.1%)
1	B	0.90	0/1932	1.07	5/2638 (0.2%)
2	C	1.06	2/1474 (0.1%)	1.32	12/2005 (0.6%)
2	D	1.06	2/1454 (0.1%)	1.27	14/1980 (0.7%)
All	All	1.02	4/6815 (0.1%)	1.17	33/9292 (0.4%)

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	A	0	1
1	B	0	1
2	C	0	6
2	D	0	9
All	All	0	17

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	69	PRO	N-CA	8.78	1.58	1.47
2	D	134	ALA	CA-CB	-6.41	1.44	1.53
2	C	158	LYS	N-CA	5.67	1.53	1.46
2	C	137	HIS	CA-C	5.09	1.59	1.52

All (33) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	137	HIS	N-CA-C	-15.70	91.60	110.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	174	ALA	N-CA-C	9.40	130.81	110.80
2	C	135	GLU	N-CA-C	-8.54	98.81	110.68
1	A	174	ALA	N-CA-C	8.29	122.93	109.76
2	D	159	GLY	N-CA-C	8.04	132.23	113.18
2	C	39	HIS	N-CA-C	7.44	126.66	110.80
2	C	137	HIS	N-CA-C	-7.33	95.09	107.99
2	C	136	VAL	N-CA-CB	-6.84	99.95	111.23
2	C	136	VAL	N-CA-C	-6.73	95.33	109.34
2	D	157	LEU	N-CA-C	6.71	119.96	109.96
2	C	22	VAL	CB-CA-C	6.71	120.25	111.53
2	C	111	THR	N-CA-CB	-6.66	100.77	110.70
2	D	94	THR	N-CA-C	-6.58	104.49	113.30
2	D	111	THR	N-CA-CB	-6.39	101.18	110.70
2	C	158	LYS	N-CA-C	6.29	124.20	110.80
2	D	47	VAL	N-CA-CB	5.87	116.92	110.53
1	B	39	HIS	CA-C-N	-5.83	114.10	119.82
1	B	39	HIS	C-N-CA	-5.83	114.10	119.82
2	C	34	THR	CB-CA-C	-5.64	100.35	114.11
2	D	99	ASP	CB-CA-C	5.57	119.79	109.54
2	D	122	ARG	N-CA-C	5.56	118.00	110.88
2	D	70	SER	N-CA-C	5.56	122.64	110.80
2	D	67	VAL	N-CA-C	5.54	120.86	109.34
2	C	107	ARG	NE-CZ-NH1	5.50	127.00	121.50
2	C	70	SER	N-CA-C	5.48	118.18	111.82
1	B	73	ALA	N-CA-C	5.47	119.04	111.71
2	D	22	VAL	CB-CA-C	5.44	119.27	111.81
1	A	173	ASN	CB-CA-C	-5.21	101.75	110.56
2	D	136	VAL	CA-C-N	-5.21	113.96	123.34
2	D	136	VAL	C-N-CA	-5.21	113.96	123.34
2	C	174	VAL	N-CA-CB	-5.21	102.19	111.92
1	B	173	ASN	CB-CA-C	-5.13	101.51	110.17
2	D	3	PRO	N-CA-C	5.00	115.27	110.47

There are no chirality outliers.

All (17) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	173	ASN	Peptide
1	B	173	ASN	Peptide
2	C	133	GLY	Peptide
2	C	135	GLU	Peptide
2	C	136	VAL	Peptide

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Mol	Chain	Res	Type	Group
2	C	157	LEU	Peptide
2	C	180	PRO	Peptide
2	C	38	GLY	Peptide
2	D	134	ALA	Peptide
2	D	135	GLU	Peptide
2	D	136	VAL	Peptide
2	D	156	ASP	Peptide
2	D	158	LYS	Peptide
2	D	67	VAL	Peptide
2	D	68	ALA	Peptide
2	D	69	PRO	Peptide
2	D	70	SER	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	1903	0	1870	25	0
1	B	1889	0	1851	19	0
2	C	1421	0	1369	55	1
2	D	1407	0	1344	75	1
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	11	0	0	0	0
4	B	6	0	0	4	0
4	C	4	0	0	0	0
4	D	3	0	0	0	0
5	A	3	0	0	0	0
5	B	2	0	0	0	0
5	C	1	0	0	0	0
6	A	211	0	0	4	0
6	B	127	0	0	0	0
6	C	140	0	0	10	0
6	D	96	0	0	4	0
All	All	7228	0	6434	170	1

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 13.

All (170) 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:D:135:GLU:HB3	2:D:136:VAL:CG1	1.58	1.32
1:A:116:ASN:ND2	1:A:145:ARG:HH22	1.32	1.26
2:D:136:VAL:CG2	2:D:137:HIS:N	1.96	1.24
1:B:116:ASN:ND2	1:B:145:ARG:HH12	1.39	1.21
2:D:136:VAL:HG22	2:D:137:HIS:N	1.40	1.16
2:D:135:GLU:HB3	2:D:136:VAL:HG13	1.24	1.14
2:D:136:VAL:CG2	2:D:137:HIS:H	1.57	1.12
1:A:116:ASN:ND2	1:A:145:ARG:NH2	2.01	1.08
2:C:88[A]:THR:HG22	2:C:90:CYS:H	1.15	1.08
2:D:19:ASN:ND2	2:D:61:ARG:NH1	2.02	1.07
2:D:135:GLU:HB3	2:D:136:VAL:HG12	1.36	1.05
2:D:19:ASN:ND2	2:D:61:ARG:HH12	1.55	1.01
1:A:182:GLN:HE21	1:A:182:GLN:H	1.07	0.96
2:D:88[A]:THR:HG22	2:D:90:CYS:H	1.29	0.96
2:D:2:ASP:HB2	2:D:3:PRO:HD3	1.45	0.95
2:D:180:PRO:HA	2:D:181:ALA:HB3	1.48	0.94
2:D:158:LYS:N	2:D:159:GLY:O	1.99	0.94
1:B:182:GLN:HE21	1:B:182:GLN:H	1.14	0.92
1:A:116:ASN:HD22	1:A:145:ARG:NH2	1.65	0.91
1:B:116:ASN:ND2	1:B:145:ARG:NH1	2.19	0.91
2:D:135:GLU:CB	2:D:136:VAL:HG13	2.02	0.90
1:B:116:ASN:HD21	1:B:145:ARG:HH12	1.19	0.87
2:D:68:ALA:HB1	2:D:69:PRO:O	1.77	0.85
2:C:88[A]:THR:HG22	2:C:90:CYS:N	1.90	0.84
1:A:2:GLN:HE22	1:A:76:ASN:ND2	1.76	0.83
2:C:19:ASN:ND2	2:C:61:ARG:HD2	1.92	0.83
2:C:136:VAL:HG23	6:C:327:HOH:O	1.77	0.83
2:D:122:ARG:HB3	2:D:122:ARG:HH11	1.46	0.80
2:C:113:PRO:HD3	6:C:307:HOH:O	1.79	0.80
1:A:2:GLN:HE22	1:A:76:ASN:HD22	1.27	0.80
2:D:136:VAL:HG22	2:D:137:HIS:H	0.70	0.80
2:D:131:TYR:CE2	2:D:134:ALA:HB3	2.18	0.79
2:D:71:ASP:HB2	2:D:73:ILE:HG12	1.63	0.78
2:C:15:ARG:HD3	2:C:73:ILE:HD13	1.66	0.78
2:C:131:TYR:CZ	2:C:133:GLY:HA3	2.20	0.77
2:C:19:ASN:HD21	2:C:61:ARG:HD2	1.47	0.77
2:D:131:TYR:CE2	2:D:134:ALA:CB	2.68	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:122:ARG:HB3	2:D:122:ARG:NH1	2.00	0.77
1:B:156:SER:H	1:B:191:GLN:HE21	1.33	0.76
1:A:156:SER:H	1:A:191:GLN:HE21	1.34	0.76
1:A:116:ASN:HD22	1:A:145:ARG:HH22	0.82	0.76
2:D:131:TYR:CZ	2:D:134:ALA:CB	2.68	0.76
1:B:116:ASN:HD22	1:B:145:ARG:HH12	1.31	0.75
2:D:2:ASP:HB2	2:D:3:PRO:CD	2.14	0.75
2:D:136:VAL:HG23	2:D:137:HIS:N	1.97	0.75
2:D:22:VAL:HG22	2:D:33:LEU:HD22	1.67	0.74
2:C:22:VAL:HG22	2:C:33:LEU:HD22	1.69	0.74
2:D:88[A]:THR:HG22	2:D:90:CYS:N	2.03	0.73
2:C:46:PHE:CD2	2:C:110:ILE:HG22	2.23	0.73
2:D:19:ASN:HD21	2:D:61:ARG:NH1	1.82	0.73
1:A:45:ARG:NH1	6:A:497:HOH:O	2.01	0.72
2:C:97:HIS:HD2	6:C:206:HOH:O	1.72	0.72
1:B:108:ALA:O	1:B:112:GLU:HG2	1.92	0.70
2:D:84:PHE:O	2:D:94:THR:HG21	1.91	0.70
2:D:180:PRO:CA	2:D:181:ALA:HB3	2.19	0.70
2:D:19:ASN:HD22	2:D:61:ARG:NH1	1.88	0.69
1:A:104:VAL:HG23	2:C:85:ARG:HD3	1.75	0.68
1:A:182:GLN:HE21	1:A:182:GLN:N	1.86	0.68
2:D:157:LEU:HD12	2:D:157:LEU:H	1.60	0.67
2:C:85:ARG:HH22	2:C:181:ALA:HB1	1.59	0.66
2:D:19:ASN:HD21	2:D:61:ARG:HH12	1.38	0.65
1:B:38:THR:H	1:B:59:GLN:HE22	1.43	0.65
2:C:15:ARG:HG2	2:C:15:ARG:HH11	1.60	0.65
2:C:136:VAL:HG22	2:C:137:HIS:H	1.61	0.64
2:C:131:TYR:CE2	2:C:133:GLY:HA3	2.32	0.64
2:D:136:VAL:HG23	2:D:137:HIS:HB2	1.80	0.63
1:B:182:GLN:HE21	1:B:182:GLN:N	1.92	0.63
2:D:158:LYS:H	2:D:159:GLY:C	2.04	0.62
1:A:182:GLN:H	1:A:182:GLN:NE2	1.90	0.61
2:D:179:PRO:O	2:D:181:ALA:CB	2.48	0.61
2:D:84:PHE:O	2:D:94:THR:CG2	2.49	0.61
1:B:116:ASN:HD22	1:B:145:ARG:NH1	1.94	0.61
2:C:19:ASN:ND2	2:C:61:ARG:CD	2.62	0.60
1:B:221:SER:HB2	4:B:282:CL:CL	2.38	0.60
2:C:168:GLU:HA	2:C:169:PRO:C	2.27	0.60
2:D:2:ASP:CB	2:D:3:PRO:CD	2.80	0.59
1:A:38:THR:HG22	6:A:476:HOH:O	2.02	0.59
2:D:179:PRO:O	2:D:181:ALA:HB3	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:235:LYS:O	1:B:235:LYS:HD2	2.03	0.58
2:D:131:TYR:CZ	2:D:134:ALA:HB3	2.38	0.57
2:D:41:ARG:HG2	2:D:41:ARG:HH11	1.70	0.57
2:C:4:PRO:HG2	2:C:76:LEU:HD12	1.86	0.57
2:C:168:GLU:HB2	2:C:170:TYR:CE1	2.40	0.57
2:D:180:PRO:HA	2:D:181:ALA:CB	2.18	0.56
2:D:41:ARG:HA	6:D:224:HOH:O	2.06	0.56
2:D:88[A]:THR:CG2	2:D:90:CYS:H	2.10	0.55
2:D:6:VAL:HG22	2:D:76:LEU:HD23	1.89	0.55
2:C:12:HIS:HD2	6:C:228:HOH:O	1.90	0.55
2:D:41:ARG:HG2	2:D:41:ARG:NH1	2.22	0.54
6:A:473:HOH:O	2:D:157:LEU:HD11	2.07	0.54
2:D:42:HIS:O	2:D:45:LEU:HD13	2.08	0.54
2:C:113:PRO:CD	6:C:307:HOH:O	2.45	0.53
2:D:45:LEU:O	2:D:111:THR:HB	2.08	0.53
2:C:45:LEU:O	2:C:111:THR:HB	2.09	0.52
1:A:22:THR:HG23	6:A:466:HOH:O	2.09	0.52
2:D:99:ASP:OD1	2:D:107:ARG:HA	2.10	0.52
2:D:19:ASN:HB2	2:D:178:ALA:HB3	1.92	0.52
2:C:97:HIS:HE1	6:C:257:HOH:O	1.93	0.51
2:D:131:TYR:CE2	2:D:134:ALA:HB1	2.43	0.51
1:A:77:ASN:HD22	1:A:77:ASN:C	2.19	0.50
2:C:142:MET:HG2	2:C:150:ASP:OD1	2.10	0.50
1:B:67:HIS:CD2	1:B:207:SER:HB3	2.46	0.50
2:C:134:ALA:HB1	2:C:138:GLU:H	1.77	0.50
2:D:71:ASP:O	2:D:72:LYS:HB2	2.10	0.50
2:C:39:HIS:CD2	6:C:312:HOH:O	2.65	0.49
2:C:131:TYR:C	2:C:133:GLY:H	2.19	0.49
2:C:39:HIS:HD2	6:C:312:HOH:O	1.96	0.49
1:A:107:ILE:HD11	2:C:87:TYR:HB2	1.94	0.49
1:A:156:SER:H	1:A:191:GLN:NE2	2.05	0.49
2:C:38:GLY:HA3	2:C:41:ARG:O	2.13	0.49
2:D:179:PRO:O	2:D:181:ALA:HB2	2.13	0.48
2:D:136:VAL:HG23	2:D:137:HIS:CB	2.43	0.48
2:C:15:ARG:HH11	2:C:15:ARG:CG	2.24	0.48
2:D:156:ASP:H	2:D:162:TRP:CD1	2.32	0.48
2:C:110:ILE:HD13	2:C:110:ILE:HG23	1.54	0.48
2:D:1:ALA:N	6:D:252:HOH:O	2.44	0.47
2:D:115:LYS:HA	2:D:115:LYS:HE2	1.96	0.47
2:D:130:LYS:NZ	2:D:134:ALA:O	2.41	0.47
2:C:136:VAL:HG22	2:C:137:HIS:N	2.27	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:179:PRO:O	2:C:180:PRO:C	2.57	0.47
2:D:69:PRO:HA	2:D:70:SER:C	2.39	0.47
2:D:135:GLU:OE1	2:D:136:VAL:HG12	2.15	0.47
1:A:150:VAL:HG12	1:A:224:THR:HG23	1.97	0.47
2:D:34:THR:HG22	2:D:58:PHE:CD2	2.50	0.47
2:D:111:THR:HG22	6:D:201:HOH:O	2.14	0.46
2:C:46:PHE:CD2	2:C:110:ILE:CG2	2.95	0.46
1:A:104:VAL:CG2	2:C:85:ARG:HD3	2.44	0.46
1:B:156:SER:H	1:B:191:GLN:NE2	2.09	0.46
2:C:158:LYS:HB2	2:C:160:GLY:N	2.31	0.46
1:B:14:PRO:HD2	4:B:280:CL:CL	2.54	0.45
2:C:168:GLU:HB2	2:C:170:TYR:CZ	2.51	0.45
2:D:135:GLU:O	2:D:136:VAL:C	2.60	0.45
2:D:179:PRO:HA	2:D:180:PRO:HD3	1.77	0.45
2:C:158:LYS:HB2	2:C:159:GLY:CA	2.47	0.45
2:D:131:TYR:CD2	2:D:134:ALA:HB3	2.52	0.44
2:D:135:GLU:CB	2:D:136:VAL:CG1	2.54	0.44
1:A:116:ASN:HD21	1:A:145:ARG:NH2	2.04	0.44
2:D:155:ARG:O	2:D:156:ASP:C	2.60	0.44
2:C:16:ALA:O	2:C:17:ASP:HB2	2.18	0.44
2:D:180:PRO:HA	2:D:181:ALA:C	2.43	0.44
2:C:131:TYR:HA	6:C:328:HOH:O	2.18	0.43
1:A:77:ASN:ND2	1:A:79:ILE:H	2.16	0.43
2:C:134:ALA:HB1	2:C:136:VAL:O	2.18	0.43
2:D:156:ASP:O	2:D:156:ASP:OD2	2.36	0.43
2:C:158:LYS:HB2	2:C:159:GLY:HA2	1.99	0.43
1:B:221:SER:CB	4:B:282:CL:CL	3.03	0.43
2:C:9:THR:CG2	2:C:174:VAL:HG13	2.48	0.43
2:C:47:VAL:HG13	2:C:109:VAL:HG12	1.99	0.43
1:A:154:GLY:HA2	2:C:91:LEU:HB3	2.01	0.43
1:B:6:TRP:CH2	1:B:201:PRO:HB3	2.53	0.43
2:C:88[A]:THR:CG2	2:C:90:CYS:H	2.06	0.42
2:D:156:ASP:HB2	2:D:157:LEU:C	2.44	0.42
2:D:67:VAL:HG13	2:D:68:ALA:N	2.34	0.42
2:D:131:TYR:HA	6:D:251:HOH:O	2.18	0.42
2:C:85:ARG:HD2	6:C:306:HOH:O	2.20	0.42
2:D:100:SER:OG	2:D:102:LEU:HD22	2.20	0.42
1:A:67:HIS:CD2	1:A:207:SER:HB3	2.54	0.41
2:D:14:LEU:HD22	2:D:20:TYR:CE1	2.55	0.41
1:A:251:LYS:HB3	1:A:265[A]:SER:OG	2.20	0.41
2:D:34:THR:HB	2:D:35:MET:H	1.48	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:132:SER:C	2:D:134:ALA:H	2.28	0.41
2:C:110:ILE:HG21	2:C:110:ILE:HD12	1.59	0.41
1:A:192:TYR:HB2	1:A:261:ASN:O	2.21	0.41
2:C:19:ASN:HD21	2:C:61:ARG:CD	2.21	0.41
2:C:15:ARG:HD3	2:C:73:ILE:CD1	2.45	0.41
2:C:102:LEU:N	2:C:102:LEU:HD12	2.36	0.41
2:C:131:TYR:C	2:C:133:GLY:N	2.79	0.41
1:B:155:ASN:ND2	4:B:282:CL:CL	2.78	0.40
1:B:193:GLY:HA2	1:B:261:ASN:ND2	2.37	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:131:TYR:OH	2:C:131:TYR:OH[3_545]	1.78	0.42

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	273/269 (102%)	266 (97%)	7 (3%)	0	100	100
1	B	270/269 (100%)	263 (97%)	7 (3%)	0	100	100
2	C	182/181 (101%)	169 (93%)	10 (6%)	3 (2%)	7	2
2	D	180/181 (99%)	166 (92%)	9 (5%)	5 (3%)	4	0
All	All	905/900 (101%)	864 (96%)	33 (4%)	8 (1%)	14	4

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	159	GLY

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Mol	Chain	Res	Type
2	C	136	VAL
2	C	158	LYS
2	D	69	PRO
2	D	136	VAL
2	D	70	SER
2	C	180	PRO
2	D	40	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	200/194 (103%)	196 (98%)	4 (2%)	48	36
1	B	197/194 (102%)	183 (93%)	14 (7%)	13	3
2	C	150/147 (102%)	129 (86%)	21 (14%)	3	0
2	D	148/147 (101%)	122 (82%)	26 (18%)	2	0
All	All	695/682 (102%)	630 (91%)	65 (9%)	8	1

All (65) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	77	ASN
1	A	166	SER
1	A	182	GLN
1	A	217	LEU
1	B	19	ARG
1	B	38	THR
1	B	78	SER
1	B	90	LEU
1	B	123	ASN
1	B	128	SER
1	B	132	SER
1	B	137	GLN
1	B	148	LEU
1	B	170	ARG

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Mol	Chain	Res	Type
1	B	182	GLN
1	B	217	LEU
1	B	235	LYS
1	B	275	ARG
2	D	22	VAL
2	D	23	LEU
2	D	27	ARG
2	D	33	LEU
2	D	34	THR
2	D	41	ARG
2	D	45	LEU
2	D	47	VAL
2	D	60	VAL
2	D	70	SER
2	D	71	ASP
2	D	94	THR
2	D	102	LEU
2	D	110	ILE
2	D	111	THR
2	D	116	ASP
2	D	118	SER
2	D	122	ARG
2	D	123	GLU
2	D	127	ARG
2	D	130	LYS
2	D	131	TYR
2	D	136	VAL
2	D	137	HIS
2	D	157	LEU
2	D	158	LYS
2	C	15	ARG
2	C	22	VAL
2	C	23	LEU
2	C	33	LEU
2	C	34	THR
2	C	45	LEU
2	C	47	VAL
2	C	54	GLN
2	C	60	VAL
2	C	61	ARG
2	C	102	LEU
2	C	110	ILE

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Mol	Chain	Res	Type
2	C	111	THR
2	C	115[A]	LYS
2	C	115[B]	LYS
2	C	130	LYS
2	C	135	GLU
2	C	157	LEU
2	C	168	GLU
2	C	174	VAL
2	C	180	PRO

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (24) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	76	ASN
1	A	77	ASN
1	A	116	ASN
1	A	182	GLN
1	A	191	GLN
1	A	238	ASN
1	A	261	ASN
1	B	18	ASN
1	B	59	GLN
1	B	76	ASN
1	B	109	GLN
1	B	116	ASN
1	B	182	GLN
1	B	191	GLN
1	B	226	HIS
1	B	238	ASN
1	B	261	ASN
2	D	7	HIS
2	D	19	ASN
2	D	42	HIS
2	D	92	GLN
2	C	12	HIS
2	C	19	ASN
2	C	97	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 34 ligands modelled in this entry, 34 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

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, 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	269/269 (100%)	-0.05	1 (0%) 88 91	18, 28, 38, 45	7 (2%)
1	B	269/269 (100%)	0.47	8 (2%) 52 56	22, 34, 45, 50	5 (1%)
2	C	181/181 (100%)	0.66	20 (11%) 10 10	13, 31, 51, 58	10 (5%)
2	D	181/181 (100%)	0.91	26 (14%) 6 6	17, 35, 56, 65	5 (2%)
All	All	900/900 (100%)	0.44	55 (6%) 27 29	13, 32, 48, 65	27 (3%)

All (55) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	C	181	ALA	9.3
2	D	69	PRO	7.6
2	C	136	VAL	6.3
2	C	1	ALA	6.1
2	D	136	VAL	5.5
2	D	68	ALA	5.4
2	C	115[A]	LYS	5.4
2	D	157	LEU	5.0
2	C	131	TYR	5.0
2	D	1	ALA	4.8
2	D	180	PRO	4.7
2	C	157	LEU	4.5
2	D	118	SER	4.5
2	D	134	ALA	4.2
2	D	159	GLY	4.1
2	C	170	TYR	4.1
2	D	67	VAL	4.0
2	D	179	PRO	4.0
2	D	131	TYR	4.0
2	C	133	GLY	4.0
2	C	159	GLY	3.9

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Mol	Chain	Res	Type	RSRZ
2	D	70	SER	3.8
2	C	38	GLY	3.7
2	C	135	GLU	3.7
2	C	2	ASP	3.6
2	D	133	GLY	3.5
2	D	120	SER	3.3
2	C	144	CYS	3.3
2	D	121	GLY	3.3
1	B	21	LEU	3.1
2	C	180	PRO	2.9
2	C	134	ALA	2.9
2	C	116	ASP	2.8
1	B	22	THR	2.8
2	D	119	PRO	2.7
1	B	241	TRP	2.6
1	A	256	SER	2.6
2	D	181	ALA	2.5
1	B	275	ARG	2.5
2	D	117	PRO	2.5
2	D	43	CYS	2.4
1	B	243	ASN	2.4
2	D	2	ASP	2.4
2	D	65	TYR	2.3
1	B	118	GLY	2.3
2	D	116	ASP	2.3
2	C	148	CYS	2.3
2	D	170	TYR	2.2
2	C	158	LYS	2.2
2	C	145	GLY	2.2
1	B	78	SER	2.1
2	D	158	LYS	2.1
2	D	71	ASP	2.1
2	C	3	PRO	2.0
1	B	53	GLY	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

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, 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
5	NA	C	187	1/1	0.79	0.21	58,58,58,58	0
4	CL	A	282	1/1	0.83	0.20	71,71,71,71	0
4	CL	C	183	1/1	0.85	0.19	69,69,69,69	0
4	CL	D	185	1/1	0.86	0.16	78,78,78,78	0
4	CL	A	287	1/1	0.90	0.14	75,75,75,75	0
4	CL	B	278	1/1	0.91	0.17	67,67,67,67	0
3	CA	C	182	1/1	0.91	0.16	70,70,70,70	0
4	CL	A	281	1/1	0.92	0.11	56,56,56,56	0
4	CL	D	184	1/1	0.93	0.15	74,74,74,74	0
3	CA	D	182	1/1	0.93	0.17	59,59,59,59	0
4	CL	B	280	1/1	0.94	0.09	58,58,58,58	0
4	CL	A	285	1/1	0.95	0.08	54,54,54,54	0
4	CL	A	279	1/1	0.95	0.13	53,53,53,53	0
4	CL	B	277	1/1	0.97	0.05	37,37,37,37	0
4	CL	A	286	1/1	0.97	0.05	36,36,36,36	0
3	CA	B	276	1/1	0.97	0.04	36,36,36,36	0
4	CL	C	185	1/1	0.97	0.10	41,41,41,41	0
4	CL	C	186	1/1	0.97	0.06	38,38,38,38	0
5	NA	A	290	1/1	0.97	0.04	27,27,27,27	0
4	CL	B	282	1/1	0.97	0.17	45,45,45,45	0
4	CL	B	279	1/1	0.98	0.13	40,40,40,40	0
5	NA	A	288	1/1	0.98	0.07	32,32,32,32	0
5	NA	A	289	1/1	0.98	0.06	23,23,23,23	0
4	CL	D	183	1/1	0.98	0.08	34,34,34,34	0
5	NA	B	284	1/1	0.98	0.05	36,36,36,36	0
4	CL	A	280	1/1	0.98	0.05	30,30,30,30	0
4	CL	B	281	1/1	0.99	0.04	31,31,31,31	0
3	CA	A	276	1/1	0.99	0.03	25,25,25,25	0
4	CL	A	283	1/1	0.99	0.02	27,27,27,27	0
4	CL	A	284	1/1	0.99	0.04	29,29,29,29	0
4	CL	A	277	1/1	0.99	0.07	40,40,40,40	0
5	NA	B	283	1/1	0.99	0.03	31,31,31,31	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	CL	A	278	1/1	0.99	0.12	38,38,38,38	0
4	CL	C	184	1/1	0.99	0.13	35,35,35,35	0

6.5 Other polymers [i](#)

There are no such residues in this entry.