



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 13, 2025 – 07:16 pm BST

PDB ID : 9S6B / pdb_00009s6b
Title : Aeropyrum pernix acylaminoacyl peptidase co-crystallized with meropenem.
Authors : Harmat, V.; Takacs, L.; Kiss-Szeman, A.; Banoczi, Z.; Jakli, I.; Hosogi, N.;
Traore, D.A.K.; Perczel, A.; Menyhard, D.K.
Deposited on : 2025-07-31
Resolution : 2.30 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
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
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) : 2.46

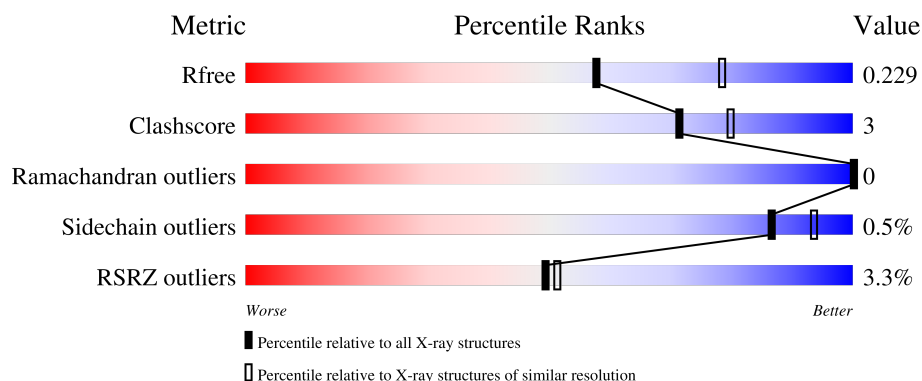
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	5963 (2.30-2.30)
Clashscore	180529	6698 (2.30-2.30)
Ramachandran outliers	177936	6640 (2.30-2.30)
Sidechain outliers	177891	6640 (2.30-2.30)
RSRZ outliers	164620	5963 (2.30-2.30)

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	582	<div> <div>%</div> <div> <div></div> <div>93%</div> <div>6%</div> <div>.</div> </div> </div>
1	B	582	<div> <div>3%</div> <div> <div></div> <div>89%</div> <div>9%</div> <div>.</div> </div> </div>
1	C	582	<div> <div>4%</div> <div> <div></div> <div>90%</div> <div>7%</div> <div>.</div> </div> </div>
1	D	582	<div> <div>4%</div> <div> <div></div> <div>88%</div> <div>10%</div> <div>.</div> </div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 16990 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.

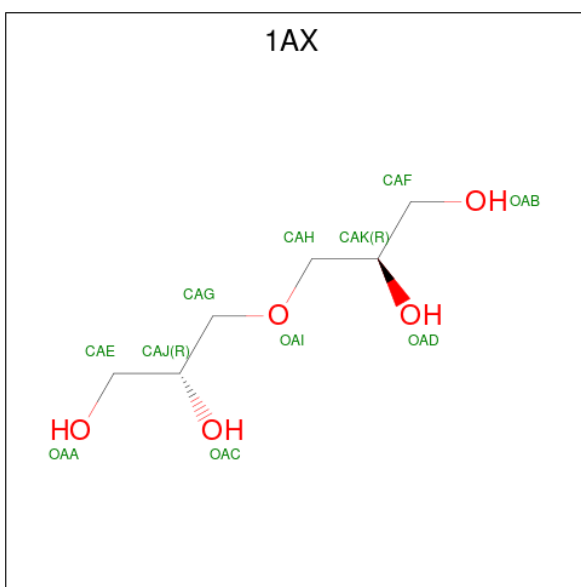
- Molecule 1 is a protein called Acylamino-acid-releasing enzyme.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	577	Total	C	N	O	S	0	3	0
			4294	2729	738	815	12			
1	B	569	Total	C	N	O	S	0	4	0
			4139	2637	707	783	12			
1	C	565	Total	C	N	O	S	0	1	0
			4093	2590	706	785	12			
1	D	571	Total	C	N	O	S	0	3	0
			4190	2681	710	787	12			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	524	ALA	ASP	engineered mutation	UNP Q9YBQ2
B	524	ALA	ASP	engineered mutation	UNP Q9YBQ2
C	524	ALA	ASP	engineered mutation	UNP Q9YBQ2
D	524	ALA	ASP	engineered mutation	UNP Q9YBQ2

- Molecule 2 is (2R,2'R)-3,3'-oxydipropene-1,2-diol (CCD ID: 1AX) (formula: C₆H₁₄O₅).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total C O 7 4 3	0	0
2	C	1	Total C O 9 6 3	0	0
2	D	1	Total C O 7 3 4	0	0

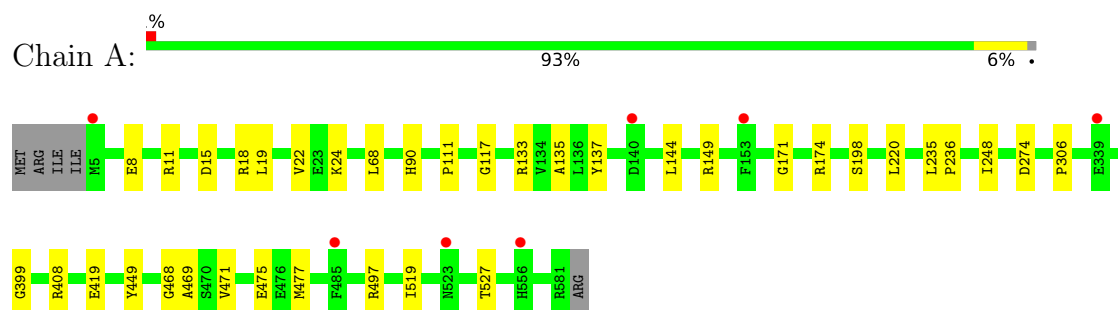
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	73	Total O 73 73	0	0
3	B	42	Total O 42 42	0	0
3	C	75	Total O 75 75	0	0
3	D	61	Total O 61 61	0	0

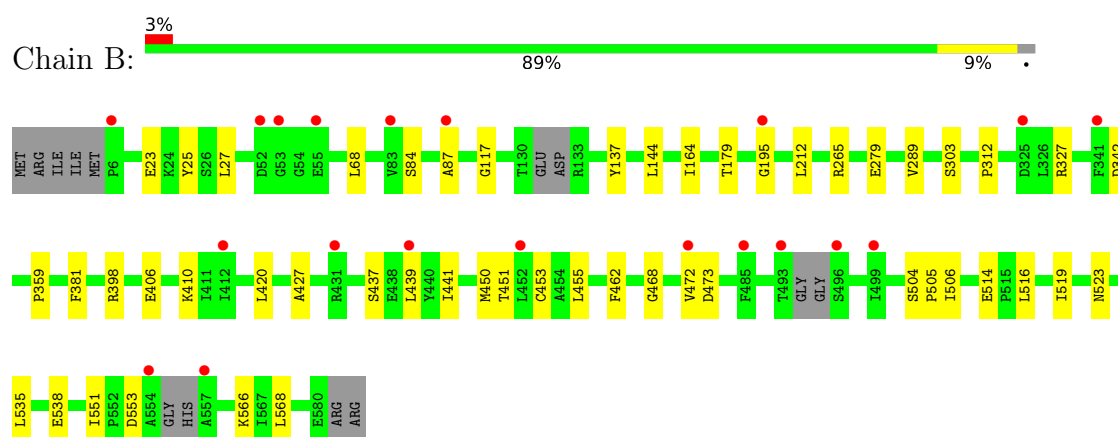
3 Residue-property plots [i](#)

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.

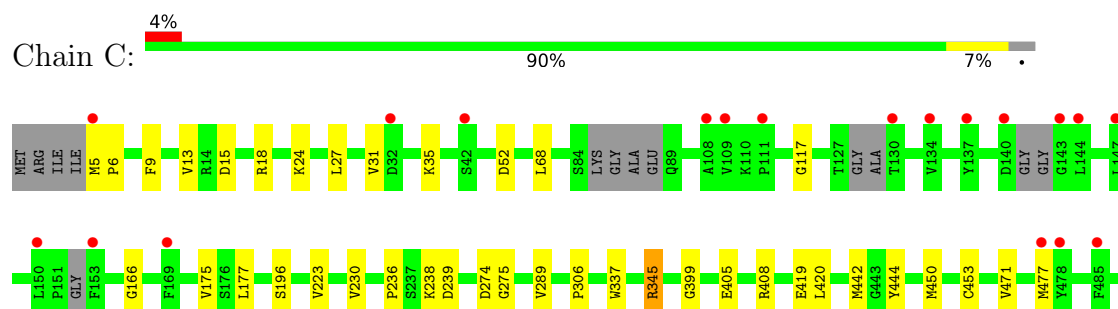
- Molecule 1: Acylamino-acid-releasing enzyme

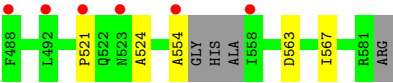


- Molecule 1: Acylamino-acid-releasing enzyme

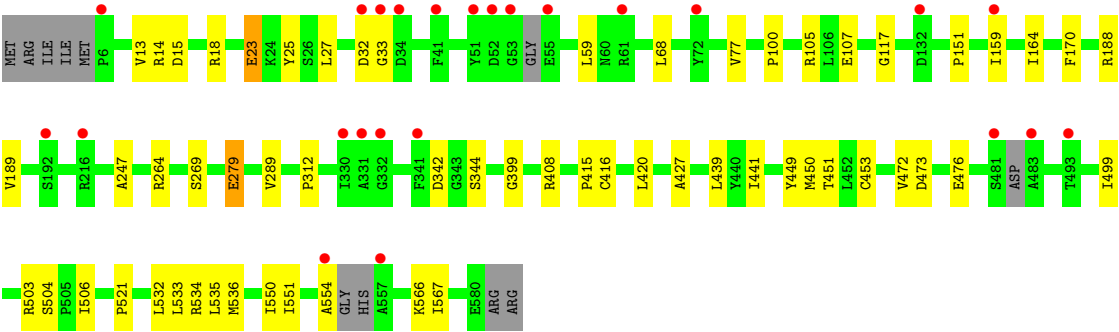
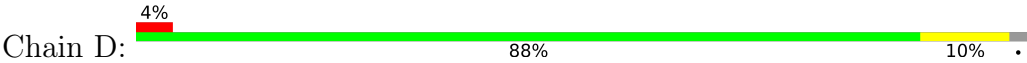


- Molecule 1: Acylamino-acid-releasing enzyme





● Molecule 1: Acylamino-acid-releasing enzyme



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	71.04Å 98.28Å 98.90Å 105.51° 103.19° 100.39°	Depositor
Resolution (Å)	39.22 – 2.30 39.22 – 2.30	Depositor EDS
% Data completeness (in resolution range)	98.2 (39.22-2.30) 98.2 (39.22-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.30 (at 2.29Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.197 , 0.229 0.197 , 0.229	Depositor DCC
R_{free} test set	2101 reflections (1.95%)	wwPDB-VP
Wilson B-factor (Å ²)	54.9	Xtriage
Anisotropy	0.206	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 49.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	0.000 for -h,-l,-k	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	16990	wwPDB-VP
Average B, all atoms (Å ²)	69.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.62% 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: 1AX

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	0.12	0/4395	0.31	0/5976
1	B	0.13	0/4236	0.32	0/5769
1	C	0.12	0/4179	0.30	0/5690
1	D	0.13	0/4290	0.32	0/5839
All	All	0.12	0/17100	0.31	0/23274

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 [i](#)

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	4294	0	4197	20	0
1	B	4139	0	3922	26	0
1	C	4093	0	3868	24	0
1	D	4190	0	4029	36	0
2	B	7	0	7	0	0
2	C	9	0	10	0	0
2	D	7	0	7	0	0
3	A	73	0	0	0	0
3	B	42	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	75	0	0	0	0
3	D	61	0	0	0	0
All	All	16990	0	16040	105	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 3.

All (105) 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:472:VAL:HG12	1:D:506:ILE:HB	1.69	0.74
1:D:536:MET:HE1	1:D:550:ILE:HD11	1.78	0.66
1:A:8:GLU:HG3	1:A:11:ARG:HB3	1.78	0.66
1:D:23:GLU:HG2	1:D:25:TYR:CZ	2.31	0.65
1:D:105:ARG:HD3	1:D:107:GLU:HG3	1.83	0.61
1:D:32:ASP:OD1	1:D:33:GLY:N	2.34	0.61
1:D:521:PRO:HB3	1:D:554:ALA:HB3	1.82	0.60
1:D:554:ALA:HB1	1:D:567:ILE:HD11	1.83	0.60
1:C:24:LYS:HG2	1:C:306:PRO:HD2	1.84	0.59
1:C:420:LEU:HA	1:C:450:MET:HE1	1.84	0.58
1:D:551:ILE:HG21	1:D:566:LYS:HG2	1.85	0.58
1:B:472:VAL:HG12	1:B:506:ILE:HB	1.86	0.57
1:A:449:TYR:HB2	1:A:471:VAL:HB	1.86	0.57
1:D:420:LEU:HA	1:D:450:MET:HE1	1.88	0.56
1:C:521:PRO:HB2	1:C:524:ALA:HB2	1.87	0.55
1:B:453:CYS:HB2	1:B:505:PRO:HG3	1.88	0.54
1:D:264[B]:ARG:HA	1:D:269:SER:HA	1.88	0.54
1:D:264[A]:ARG:HA	1:D:269:SER:HA	1.88	0.54
1:A:171:GLY:O	1:A:174:ARG:HG2	2.08	0.53
1:A:471:VAL:HG22	1:A:477:MET:HE1	1.89	0.53
1:B:427:ALA:HB1	1:B:439:LEU:HD13	1.91	0.53
1:A:24:LYS:HG2	1:A:306:PRO:HD2	1.92	0.52
1:D:499:ILE:O	1:D:503:ARG:HG2	2.11	0.51
1:B:420:LEU:HA	1:B:450:MET:HE1	1.93	0.51
1:C:337:TRP:HB3	1:C:345:ARG:HG3	1.92	0.51
1:A:137:TYR:HB3	1:A:144:LEU:HD11	1.92	0.51
1:B:279:GLU:HB3	1:B:312:PRO:HB2	1.93	0.51
1:C:15:ASP:OD1	1:C:18:ARG:NH2	2.43	0.51
1:D:27:LEU:HD21	1:D:289:VAL:HG22	1.93	0.51
1:B:441:ILE:HG23	1:B:451:THR:HG23	1.93	0.50
1:A:15:ASP:OD1	1:A:18:ARG:NH2	2.43	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:196:SER:OG	1:C:405:GLU:OE2	2.25	0.50
1:D:415:PRO:HG2	1:D:503:ARG:HG3	1.92	0.50
1:C:27:LEU:HD21	1:C:289:VAL:HG22	1.93	0.50
1:B:84:SER:HB2	1:B:87:ALA:HB2	1.94	0.50
1:B:68:LEU:HD22	1:B:117:GLY:HA3	1.92	0.49
1:D:151:PRO:HG2	1:D:170:PHE:CG	2.47	0.49
1:A:133:ARG:HB2	1:A:149:ARG:HE	1.78	0.49
1:B:137:TYR:HB3	1:B:144:LEU:HD11	1.94	0.49
1:D:188:ARG:NH1	1:D:189:VAL:O	2.45	0.49
1:B:473:ASP:HA	1:B:504:SER:HB3	1.95	0.48
1:C:471:VAL:HG22	1:C:477:MET:HE1	1.94	0.48
1:A:135:ALA:HB3	1:A:137:TYR:CZ	2.49	0.48
1:B:381:PHE:CD2	1:B:568:LEU:HD13	2.49	0.48
1:B:27:LEU:HD21	1:B:289:VAL:HG22	1.96	0.47
1:C:175:VAL:HB	1:C:196:SER:HB3	1.96	0.47
1:C:68:LEU:HD22	1:C:117:GLY:HA3	1.97	0.47
1:D:473:ASP:HA	1:D:504:SER:HB3	1.95	0.47
1:C:13:VAL:HG21	1:D:13:VAL:HG21	1.97	0.47
1:A:220:LEU:HD12	1:A:235:LEU:HD11	1.97	0.47
1:C:420:LEU:HD22	1:C:453:CYS:SG	2.54	0.47
1:D:279:GLU:HB3	1:D:312:PRO:HB2	1.97	0.47
1:A:68:LEU:HD22	1:A:117:GLY:HA3	1.95	0.46
1:B:342:ASP:OD2	1:B:398:ARG:NH2	2.42	0.46
1:D:441:ILE:HG23	1:D:451:THR:HG23	1.98	0.46
1:B:359:PRO:HB2	1:B:437:SER:HB3	1.98	0.45
1:D:399:GLY:HA2	1:D:408:ARG:O	2.16	0.45
1:D:247:ALA:HB3	1:D:264[A]:ARG:HG2	1.97	0.45
1:D:427:ALA:HB1	1:D:439:LEU:HD13	1.98	0.45
1:D:159:ILE:HG12	1:D:164:ILE:HG12	1.99	0.45
1:C:31:VAL:HG23	1:C:35:LYS:HB2	1.99	0.44
1:C:521:PRO:HB3	1:C:554:ALA:O	2.17	0.44
1:B:462:PHE:O	1:B:514:GLU:HG2	2.18	0.44
1:B:468:GLY:HA2	1:B:519:ILE:O	2.17	0.44
1:C:236:PRO:HG2	1:C:274:ASP:HB3	1.99	0.44
1:C:9:PHE:O	1:C:13:VAL:HG23	2.17	0.44
1:D:59:LEU:HD13	1:D:77:VAL:HG21	1.99	0.44
1:B:551:ILE:HG21	1:B:566:LYS:HG2	2.00	0.44
1:B:472:VAL:HG11	1:B:535:LEU:HB2	2.00	0.44
1:C:239:ASP:HB2	1:C:275:GLY:O	2.17	0.44
1:D:15:ASP:OD1	1:D:18:ARG:NH1	2.51	0.44
1:D:416:CYS:HB2	1:D:449:TYR:OH	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:223:VAL:HG22	1:C:230:VAL:HG22	2.00	0.43
1:C:399:GLY:HA2	1:C:408:ARG:O	2.19	0.43
1:D:68:LEU:HD22	1:D:117:GLY:HA3	2.01	0.43
1:A:198:SER:OG	1:A:248:ILE:O	2.34	0.43
1:D:420:LEU:HD22	1:D:453:CYS:SG	2.59	0.43
1:A:469:ALA:O	1:A:527:THR:HG21	2.18	0.42
1:D:476:GLU:OE1	1:D:534:ARG:NH2	2.48	0.42
1:A:475:GLU:OE1	1:A:497:ARG:NH1	2.49	0.42
1:C:563:ASP:O	1:C:567:ILE:HG23	2.19	0.42
1:D:342:ASP:OD1	1:D:344:SER:OG	2.37	0.42
1:D:533:LEU:HD23	1:D:536:MET:HE3	2.00	0.42
1:A:399:GLY:HA2	1:A:408:ARG:O	2.19	0.42
1:B:455:LEU:HD12	1:B:516:LEU:HD13	2.01	0.42
1:D:14:ARG:O	1:D:18:ARG:HG3	2.19	0.42
1:D:59:LEU:HD23	1:D:100:PRO:HB3	2.02	0.42
1:B:195:GLY:HA3	1:B:212:LEU:HD11	2.02	0.42
1:B:406:GLU:O	1:B:410:LYS:HG3	2.20	0.42
1:B:164:ILE:O	1:B:179:THR:HA	2.20	0.41
1:C:166:GLY:O	1:C:177:LEU:HD12	2.20	0.41
1:D:472:VAL:HG11	1:D:535:LEU:HB2	2.02	0.41
1:B:23:GLU:HG2	1:B:25:TYR:CZ	2.56	0.41
1:B:303:SER:O	1:B:327:ARG:NH2	2.50	0.41
1:C:35:LYS:HD3	1:C:52:ASP:HB2	2.01	0.41
1:A:236:PRO:HG2	1:A:274:ASP:HB3	2.02	0.41
1:D:532:LEU:HD23	1:D:536:MET:HE2	2.03	0.41
1:A:477:MET:HE2	1:A:527:THR:HA	2.02	0.41
1:C:5:MET:HA	1:C:6:PRO:HD3	1.92	0.41
1:A:19:LEU:O	1:A:22:VAL:HG12	2.21	0.41
1:A:468:GLY:HA2	1:A:519:ILE:O	2.21	0.41
1:B:523:ASN:ND2	1:B:553:ASP:OD1	2.51	0.41
1:B:342:ASP:CG	1:B:398:ARG:HH22	2.28	0.40
1:C:442:MET:HE3	1:C:444:TYR:HE1	1.87	0.40
1:A:90:HIS:O	1:A:111:PRO:HA	2.21	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	578/582 (99%)	566 (98%)	12 (2%)	0	100	100
1	B	565/582 (97%)	552 (98%)	13 (2%)	0	100	100
1	C	554/582 (95%)	542 (98%)	12 (2%)	0	100	100
1	D	566/582 (97%)	552 (98%)	14 (2%)	0	100	100
All	All	2263/2328 (97%)	2212 (98%)	51 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	438/468 (94%)	437 (100%)	1 (0%)	92	96
1	B	398/468 (85%)	396 (100%)	2 (0%)	86	93
1	C	401/468 (86%)	398 (99%)	3 (1%)	81	90
1	D	412/468 (88%)	410 (100%)	2 (0%)	86	93
All	All	1649/1872 (88%)	1641 (100%)	8 (0%)	86	93

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	419	GLU
1	B	265	ARG

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Mol	Chain	Res	Type
1	B	538	GLU
1	C	238	LYS
1	C	345	ARG
1	C	419	GLU
1	D	23	GLU
1	D	279	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	104	GLN
1	A	282	GLN
1	B	520	HIS
1	C	508	HIS
1	D	71	HIS
1	D	520	HIS

5.3.3 RNA [i](#)

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](#)

3 ligands 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	1AX	D	601	-	5,5,10	0.56	0	5,5,11	0.23	0
2	1AX	C	601	-	8,8,10	0.41	0	7,7,11	1.05	0
2	1AX	B	601	-	6,6,10	0.50	0	6,6,11	0.30	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	1AX	D	601	-	-	3/4/4/10	-
2	1AX	C	601	-	-	2/6/6/10	-
2	1AX	B	601	-	-	2/5/5/10	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	601	1AX	OAB-CAF-CAK-OAD
2	C	601	1AX	OAB-CAF-CAK-CAH
2	D	601	1AX	OAI-CAG-CAJ-OAC
2	B	601	1AX	OAB-CAF-CAK-CAH
2	D	601	1AX	OAI-CAG-CAJ-CAE
2	C	601	1AX	OAI-CAG-CAJ-CAE
2	D	601	1AX	OAA-CAE-CAJ-OAC

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	577/582 (99%)	0.18	7 (1%) 76 76	33, 64, 91, 134	3 (0%)
1	B	569/582 (97%)	0.41	20 (3%) 47 49	30, 68, 121, 143	4 (0%)
1	C	565/582 (97%)	0.38	25 (4%) 39 40	36, 66, 118, 152	1 (0%)
1	D	571/582 (98%)	0.30	24 (4%) 41 42	28, 65, 108, 133	3 (0%)
All	All	2282/2328 (98%)	0.32	76 (3%) 49 51	28, 66, 112, 152	11 (0%)

All (76) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	53	GLY	5.8
1	C	153	PHE	4.5
1	B	493	THR	4.3
1	C	140	ASP	3.9
1	D	557	ALA	3.7
1	B	53	GLY	3.7
1	D	341	PHE	3.4
1	D	41	PHE	3.3
1	B	195	GLY	3.3
1	C	477	MET	3.2
1	D	52	ASP	3.1
1	C	130	THR	3.1
1	C	169	PHE	3.0
1	D	331	ALA	3.0
1	C	523	ASN	3.0
1	C	42	SER	3.0
1	A	485	PHE	2.9
1	D	6	PRO	2.9
1	B	55	GLU	2.9
1	B	554	ALA	2.8
1	C	554	ALA	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	341	PHE	2.8
1	C	134	VAL	2.8
1	B	472	VAL	2.6
1	C	147	LEU	2.6
1	C	5	MET	2.6
1	D	33	GLY	2.6
1	D	330	ILE	2.6
1	B	83	VAL	2.5
1	D	159	ILE	2.5
1	C	32	ASP	2.5
1	C	111	PRO	2.5
1	B	87	ALA	2.4
1	C	108	ALA	2.4
1	B	439	LEU	2.4
1	D	483	ALA	2.4
1	D	55	GLU	2.4
1	B	499	ILE	2.4
1	C	143	GLY	2.4
1	C	492	LEU	2.4
1	C	485	PHE	2.4
1	B	6	PRO	2.4
1	D	132	ASP	2.4
1	C	109	VAL	2.3
1	B	452	LEU	2.3
1	C	144	LEU	2.3
1	D	481	SER	2.3
1	C	488	PHE	2.3
1	D	34	ASP	2.3
1	D	192	SER	2.3
1	B	431	ARG	2.3
1	C	137	TYR	2.2
1	D	493	THR	2.2
1	A	153	PHE	2.2
1	A	523	ASN	2.2
1	B	496	SER	2.2
1	C	478	TYR	2.2
1	D	32	ASP	2.2
1	B	412	ILE	2.1
1	A	5	MET	2.1
1	B	557	ALA	2.1
1	D	51	TYR	2.1
1	A	140	ASP	2.1

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Mol	Chain	Res	Type	RSRZ
1	C	150	LEU	2.1
1	B	485	PHE	2.1
1	B	52	ASP	2.1
1	D	554	ALA	2.1
1	A	339	GLU	2.0
1	D	216	ARG	2.0
1	B	325	ASP	2.0
1	D	332	GLY	2.0
1	A	556	HIS	2.0
1	C	521	PRO	2.0
1	D	61	ARG	2.0
1	D	72[A]	TYR	2.0
1	C	558	ILE	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [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	1AX	B	601	7/11	0.75	0.17	78,86,91,95	0
2	1AX	C	601	9/11	0.78	0.15	67,76,81,82	0
2	1AX	D	601	7/11	0.86	0.11	76,80,82,85	0

6.5 Other polymers [i](#)

There are no such residues in this entry.