



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 12:20 AM UTC

PDB ID : 3A8K / pdb_00003a8k
Title : Crystal Structure of ETD97N-EHred complex
Authors : Okamura-Ikeda, K.; Hosaka, H.
Deposited on : 2009-10-06
Resolution : 1.95 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:

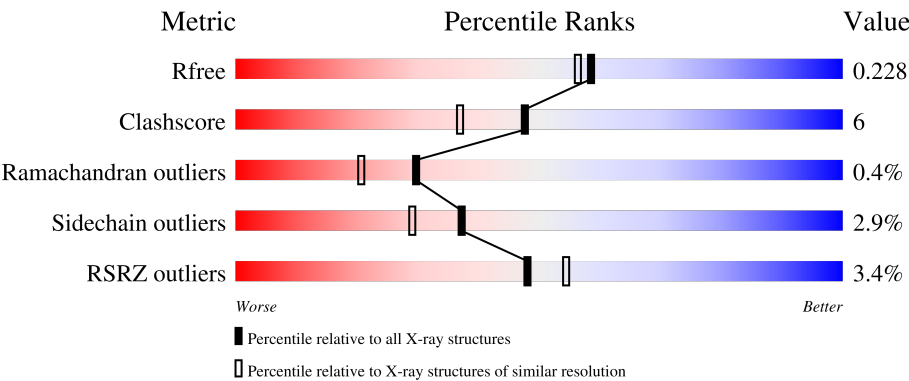
MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.95 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	3494 (1.96-1.96)
Clashscore	190562	3612 (1.96-1.96)
Ramachandran outliers	187476	3587 (1.96-1.96)
Sidechain outliers	187428	3587 (1.96-1.96)
RSRZ outliers	180081	3495 (1.96-1.96)

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	364	2% 86% 14%
1	B	364	2% 84% 14% .
1	C	364	2% 85% 13% ..
1	D	364	3% 83% 15% ..
2	E	129	9% 84% 12% ..

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Mol	Chain	Length	Quality of chain
2	F	129	9% 84% 13%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 14698 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 Aminomethyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	363	Total	C	N	O	S	0	2	0
			2829	1786	496	532	15			
1	B	363	Total	C	N	O	S	0	2	0
			2827	1786	494	532	15			
1	C	362	Total	C	N	O	S	0	0	0
			2809	1774	492	528	15			
1	D	362	Total	C	N	O	S	0	2	0
			2822	1782	495	530	15			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	97	ASN	ASP	engineered mutation	UNP P27248
B	97	ASN	ASP	engineered mutation	UNP P27248
C	97	ASN	ASP	engineered mutation	UNP P27248
D	97	ASN	ASP	engineered mutation	UNP P27248

- Molecule 2 is a protein called Glycine cleavage system H protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	126	Total	C	N	O	S	0	0	0
			958	603	145	206	4			
2	F	126	Total	C	N	O	S	0	0	0
			958	603	145	206	4			

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	370	Total	O	0	0
			370	370		
3	B	352	Total	O	0	0
			352	352		

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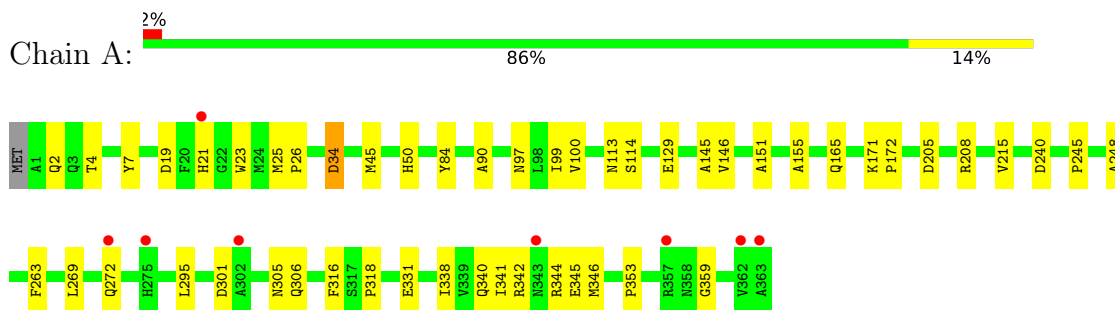
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	C	313	Total 313	O 313	0	0
3	D	298	Total 298	O 298	0	0
3	E	113	Total 113	O 113	0	0
3	F	49	Total 49	O 49	0	0

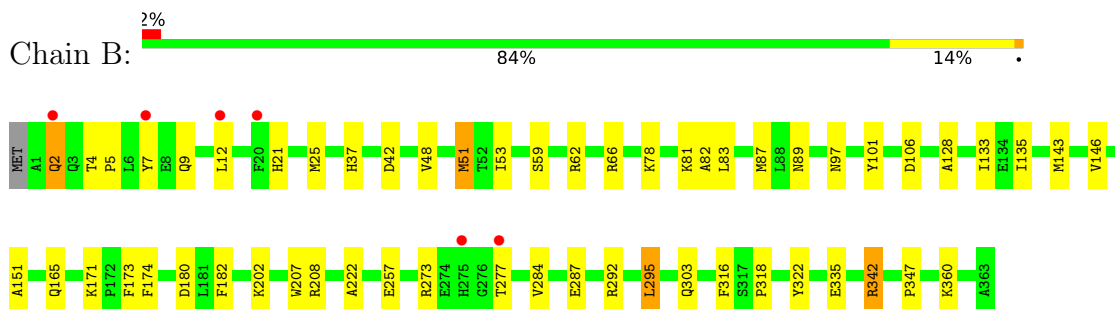
3 Residue-property plots [i](#)

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.

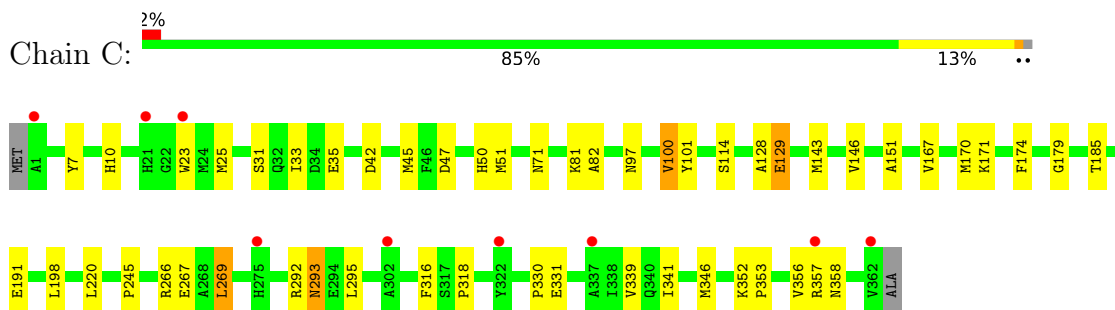
- Molecule 1: Aminomethyltransferase



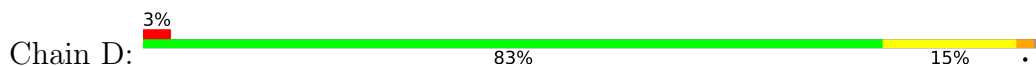
- Molecule 1: Aminomethyltransferase

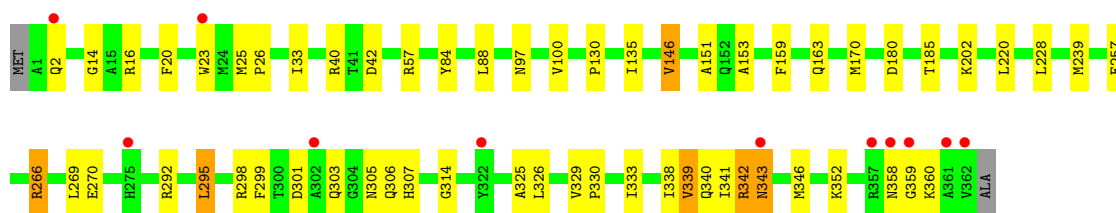


- Molecule 1: Aminomethyltransferase

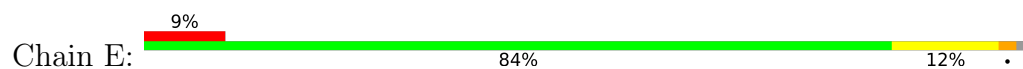


- Molecule 1: Aminomethyltransferase

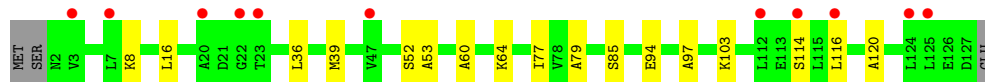
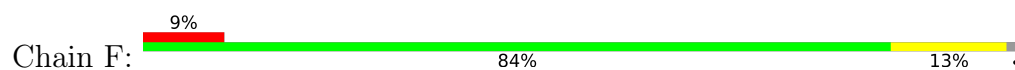




• Molecule 2: Glycine cleavage system H protein



• Molecule 2: Glycine cleavage system H protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	54.12Å 88.41Å 97.86Å 91.56° 102.42° 89.59°	Depositor
Resolution (Å)	43.97 – 1.95 43.97 – 1.95	Depositor EDS
% Data completeness (in resolution range)	98.1 (43.97-1.95) 98.1 (43.97-1.95)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.21 (at 1.95Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, R_{free}	0.171 , 0.229 0.171 , 0.228	Depositor DCC
R_{free} test set	6363 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å ²)	21.7	Xtriage
Anisotropy	0.174	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 45.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.059 for -h,k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	14698	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.27% 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: LA2

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	1.33	5/2893 (0.2%)	1.17	4/3917 (0.1%)
1	B	1.32	5/2891 (0.2%)	1.16	4/3914 (0.1%)
1	C	1.30	3/2867 (0.1%)	1.17	10/3884 (0.3%)
1	D	1.28	9/2886 (0.3%)	1.14	3/3909 (0.1%)
2	E	1.13	1/954 (0.1%)	1.07	0/1301
2	F	1.05	2/954 (0.2%)	1.06	0/1301
All	All	1.28	25/13445 (0.2%)	1.15	21/18226 (0.1%)

All (25) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	198	LEU	N-CA	7.62	1.53	1.46
1	D	153	ALA	CA-CB	7.45	1.65	1.53
1	D	339	VAL	CA-CB	6.45	1.63	1.54
1	A	90	ALA	CA-CB	6.43	1.63	1.53
1	A	155	ALA	CA-CB	6.39	1.63	1.53
1	D	33	ILE	CA-CB	5.97	1.61	1.54
1	D	325	ALA	CA-CB	5.90	1.63	1.53
1	D	314	GLY	N-CA	5.90	1.51	1.45
1	A	353	PRO	CA-CB	5.66	1.57	1.53
1	B	222	ALA	C-O	-5.56	1.17	1.24
1	D	88	LEU	N-CA	5.41	1.52	1.45
1	A	248	ALA	CA-CB	5.38	1.60	1.53
1	B	87	MET	CA-C	5.34	1.58	1.52
1	B	133	ILE	CA-CB	5.29	1.60	1.54
1	C	33	ILE	CA-CB	5.24	1.60	1.54
2	E	101	ILE	CA-CB	-5.21	1.50	1.55
2	F	77	ILE	CA-CB	5.21	1.59	1.53
1	D	146	VAL	CA-CB	5.19	1.60	1.54
1	A	19	ASP	CA-C	5.19	1.59	1.52
1	C	35	GLU	C-O	5.16	1.30	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	135	ILE	CA-CB	5.16	1.60	1.54
1	B	182	PHE	C-O	-5.15	1.17	1.24
2	F	114	SER	CA-C	5.09	1.59	1.52
1	B	89	ASN	C-O	5.07	1.30	1.23
1	D	266	ARG	N-CA	5.07	1.52	1.46

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	179	GLY	CA-C-N	-7.93	109.97	122.73
1	C	179	GLY	C-N-CA	-7.93	109.97	122.73
1	C	129	GLU	CA-C-N	-6.84	112.75	119.87
1	C	129	GLU	C-N-CA	-6.84	112.75	119.87
1	C	71	ASN	N-CA-C	-6.64	101.96	110.53
1	A	34	ASP	CB-CA-C	-6.38	100.19	110.79
1	C	266	ARG	NE-CZ-NH2	-6.38	113.46	119.20
1	B	21	HIS	CB-CA-C	-5.95	103.12	111.80
1	B	335	GLU	N-CA-C	5.90	120.09	113.01
1	A	34	ASP	N-CA-CB	-5.45	102.11	110.12
1	B	51	MET	CA-C-N	-5.42	115.52	123.00
1	B	51	MET	C-N-CA	-5.42	115.52	123.00
1	C	167	VAL	N-CA-C	5.31	117.28	112.29
1	A	263	PHE	N-CA-C	-5.27	101.28	109.24
1	A	26	PRO	CB-CA-C	-5.24	105.12	111.46
1	C	31	SER	N-CA-C	5.22	115.94	107.23
1	D	266	ARG	CG-CD-NE	-5.19	100.59	112.00
1	C	45	MET	N-CA-C	5.08	117.10	109.23
1	C	7	TYR	N-CA-C	5.04	116.46	111.07
1	D	329	VAL	CA-C-N	5.01	124.94	119.78
1	D	329	VAL	C-N-CA	5.01	124.94	119.78

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	2829	0	2792	35	0
1	B	2827	0	2792	34	0
1	C	2809	0	2768	27	0
1	D	2822	0	2785	37	0
2	E	958	0	909	10	0
2	F	958	0	909	7	0
3	A	370	0	0	5	0
3	B	352	0	0	7	0
3	C	313	0	0	6	0
3	D	298	0	0	7	0
3	E	113	0	0	2	0
3	F	49	0	0	0	0
All	All	14698	0	12955	147	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 6.

All (147) 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:298:ARG:HH12	1:D:340:GLN:HE21	1.12	0.97
1:C:97:ASN:HB2	3:C:698:HOH:O	1.71	0.89
1:D:180[A]:ASP:OD2	1:D:202:LYS:HD2	1.74	0.87
1:D:26:PRO:HG2	3:D:845:HOH:O	1.81	0.81
1:C:146:VAL:HG12	1:C:151:ALA:HB1	1.63	0.80
1:C:341:ILE:HD12	1:C:346:MET:HG3	1.63	0.78
1:D:298:ARG:NH1	1:D:340:GLN:HE21	1.81	0.77
1:D:180[A]:ASP:OD1	3:D:690:HOH:O	2.03	0.75
1:D:40:ARG:O	3:D:850:HOH:O	2.04	0.75
1:B:48:VAL:HB	1:B:51:MET:HE2	1.70	0.72
1:B:81[A]:LYS:NZ	3:B:908:HOH:O	2.23	0.72
1:D:257:GLU:OE2	3:D:880:HOH:O	2.09	0.71
1:A:341:ILE:O	1:A:344:ARG:HG2	1.92	0.69
1:D:292:ARG:H	1:D:295:LEU:HD22	1.57	0.69
1:A:340:GLN:HG3	1:A:345:GLU:OE1	1.93	0.68
1:C:293:ASN:ND2	3:C:723:HOH:O	2.26	0.67
1:D:298:ARG:HH12	1:D:340:GLN:NE2	1.89	0.67
1:A:331:GLU:HA	1:A:331:GLU:OE1	1.93	0.67
1:D:180[A]:ASP:OD2	1:D:202:LYS:CD	2.43	0.66
1:C:97:ASN:CB	3:C:698:HOH:O	2.38	0.64
1:D:352:LYS:HE2	3:D:883:HOH:O	1.97	0.63
2:E:18:LYS:NZ	3:E:284:HOH:O	2.16	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:298:ARG:HH22	1:D:340:GLN:NE2	1.97	0.63
1:D:25:MET:HB2	1:D:220:LEU:HD11	1.81	0.63
1:B:81[A]:LYS:HE3	1:B:173:PHE:O	2.00	0.62
1:B:287[B]:GLU:OE2	1:B:347:PRO:HD2	2.00	0.62
1:D:343:ASN:HD22	1:D:343:ASN:N	1.98	0.61
1:D:266:ARG:O	1:D:270:GLU:HG2	2.00	0.61
1:A:338:ILE:HG21	1:A:345:GLU:HB3	1.81	0.61
2:F:116:LEU:HD22	2:F:120:ALA:HB1	1.82	0.61
1:B:78:LYS:HE2	1:B:174:PHE:HZ	1.66	0.60
1:A:341:ILE:O	1:A:342:ARG:HG2	2.02	0.60
1:B:7:TYR:CD1	1:B:7:TYR:C	2.80	0.59
1:B:257:GLU:OE1	3:B:891:HOH:O	2.17	0.59
1:C:50:HIS:CD2	1:C:114:SER:HB2	2.38	0.59
1:C:267:GLU:HG3	3:C:608:HOH:O	2.02	0.59
1:A:113:ASN:HB3	3:A:748:HOH:O	2.03	0.58
1:B:81[A]:LYS:HD2	1:B:174:PHE:CE1	2.39	0.57
1:B:9:GLN:HE21	1:B:207:TRP:HD1	1.52	0.57
1:D:298:ARG:HH22	1:D:340:GLN:HE22	1.51	0.57
1:B:208:ARG:HD3	3:B:770:HOH:O	2.07	0.55
1:D:341:ILE:HD12	1:D:346:MET:HG3	1.88	0.55
2:F:79:ALA:HB3	2:F:103:LYS:HB2	1.88	0.55
1:C:51:MET:HE2	1:C:143:MET:HE2	1.89	0.55
1:D:228:LEU:CD1	1:D:326:LEU:HG	2.36	0.55
2:F:116:LEU:HD22	2:F:120:ALA:CB	2.37	0.54
1:B:97:ASN:ND2	3:B:703:HOH:O	2.40	0.54
1:B:2:GLN:HG3	1:D:130:PRO:HB3	1.90	0.54
1:A:146:VAL:HG12	1:A:151:ALA:HB1	1.90	0.53
1:B:292:ARG:H	1:B:295:LEU:HD22	1.71	0.53
2:E:39:MET:CE	2:E:42:VAL:HB	2.39	0.53
2:F:94:GLU:HB3	2:F:97:ALA:HB3	1.89	0.53
1:B:128:ALA:HB3	1:B:135:ILE:HD11	1.90	0.52
2:E:116:LEU:HD23	2:E:116:LEU:N	2.24	0.52
1:C:170:MET:HE3	1:C:185:THR:HG23	1.91	0.52
1:B:12:LEU:O	1:B:12:LEU:HD23	2.10	0.51
2:E:125:LEU:O	2:E:127:ASP:N	2.44	0.51
1:A:2:GLN:O	1:A:23:TRP:HA	2.11	0.51
1:D:170:MET:HE3	1:D:185:THR:HG23	1.93	0.51
1:A:341:ILE:HD12	1:A:346:MET:HG3	1.93	0.50
1:C:25:MET:HB2	1:C:220:LEU:HD11	1.93	0.50
2:F:39:MET:SD	2:F:60:ALA:HB1	2.51	0.50
1:D:159:PHE:HB3	1:D:163:GLN:HB2	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:316:PHE:O	1:C:318:PRO:HD3	2.12	0.50
1:A:4:THR:HG23	1:A:25:MET:HE1	1.94	0.50
1:C:292:ARG:HD2	3:C:764:HOH:O	2.10	0.50
1:A:240:ASP:OD2	3:A:841:HOH:O	2.19	0.49
1:D:146:VAL:HG12	1:D:151:ALA:HB1	1.94	0.49
1:B:83:LEU:C	1:B:83:LEU:HD12	2.37	0.49
1:B:316:PHE:O	1:B:318:PRO:HD3	2.12	0.49
1:A:338:ILE:CG2	1:A:345:GLU:HB3	2.43	0.49
1:D:84:TYR:CE1	1:D:97:ASN:HB2	2.48	0.49
1:D:25:MET:CB	1:D:220:LEU:HD11	2.42	0.49
1:B:284:VAL:HG13	1:B:322:TYR:CE1	2.47	0.49
1:A:345:GLU:C	1:A:346:MET:HE2	2.38	0.48
1:D:298:ARG:NH2	1:D:340:GLN:NE2	2.61	0.48
1:B:146:VAL:HG12	1:B:151:ALA:HB1	1.95	0.48
2:E:3:VAL:O	2:E:3:VAL:HG12	2.14	0.47
1:D:358:ASN:C	1:D:360:LYS:H	2.23	0.47
2:E:123:ALA:HA	2:E:126:GLU:HB2	1.97	0.47
1:D:299:PHE:CE2	1:D:333:ILE:HA	2.50	0.47
1:A:344:ARG:HG3	1:A:346:MET:HE3	1.98	0.46
1:A:359:GLY:HA3	3:A:859:HOH:O	2.15	0.46
1:B:25:MET:HE2	1:B:25:MET:HA	1.96	0.46
1:B:78:LYS:NZ	1:B:81[B]:LYS:HD2	2.30	0.46
1:C:81:LYS:HD3	1:C:174:PHE:CZ	2.51	0.46
1:A:50:HIS:CD2	1:A:114:SER:HB2	2.51	0.46
2:E:17:ARG:NH2	3:E:236:HOH:O	2.49	0.46
1:C:82:ALA:HB2	1:C:101:TYR:CD2	2.50	0.46
1:B:53:ILE:HD11	1:B:143:MET:HE2	1.98	0.45
2:F:52:SER:O	2:F:53:ALA:C	2.59	0.45
1:A:359:GLY:CA	3:A:859:HOH:O	2.65	0.45
1:A:21:HIS:N	3:A:946:HOH:O	2.46	0.45
1:C:352:LYS:HB3	1:C:353:PRO:HD2	1.99	0.45
1:A:301:ASP:CG	1:A:305:ASN:HB2	2.42	0.44
1:B:180:ASP:OD2	1:B:202:LYS:HD2	2.17	0.44
1:B:202:LYS:HE2	3:B:869:HOH:O	2.17	0.44
1:D:301:ASP:OD2	1:D:305:ASN:HB2	2.16	0.44
1:D:358:ASN:O	1:D:360:LYS:N	2.50	0.44
1:C:356:VAL:HG12	1:C:357:ARG:N	2.33	0.44
1:D:358:ASN:C	1:D:360:LYS:N	2.76	0.44
1:A:129:GLU:OE2	1:C:23:TRP:HZ2	2.01	0.44
1:B:82:ALA:HB2	1:B:101:TYR:CD2	2.53	0.44
1:C:191:GLU:OE1	1:C:358:ASN:HA	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:59:SER:HA	1:B:106:ASP:OD1	2.18	0.43
1:B:9:GLN:HE21	1:B:207:TRP:CD1	2.33	0.43
1:C:128:ALA:O	1:C:129:GLU:C	2.61	0.43
1:D:298:ARG:NH1	1:D:340:GLN:NE2	2.55	0.43
1:A:4:THR:CG2	1:A:25:MET:HE1	2.48	0.43
1:A:171:LYS:HD3	1:A:172:PRO:HD3	2.00	0.43
1:B:4:THR:HG23	1:B:25:MET:HE1	2.01	0.43
1:C:50:HIS:HD2	1:C:114:SER:CB	2.32	0.43
1:A:346:MET:HE2	1:A:346:MET:HA	2.01	0.43
1:A:25:MET:HA	1:A:25:MET:HE2	2.00	0.43
1:A:7:TYR:C	1:A:7:TYR:CD2	2.97	0.42
1:B:171:LYS:NZ	2:E:85:SER:O	2.52	0.42
1:C:245:PRO:HD2	1:C:269:LEU:HD11	2.01	0.42
1:A:45:MET:HB3	1:A:215:VAL:HG11	2.01	0.42
1:A:205:ASP:OD1	1:A:208[B]:ARG:NH1	2.52	0.42
1:B:62:ARG:O	1:B:66:ARG:HG3	2.19	0.42
2:E:52:SER:O	2:E:53:ALA:C	2.61	0.42
1:B:4:THR:HB	1:B:5:PRO:CD	2.50	0.42
1:C:10:HIS:CE1	1:C:47:ASP:HB2	2.55	0.42
1:A:342:ARG:O	1:A:342:ARG:CG	2.67	0.42
1:A:344:ARG:CG	1:A:346:MET:HE3	2.50	0.42
1:B:81[A]:LYS:CD	1:B:174:PHE:CE1	3.03	0.41
1:D:2:GLN:NE2	3:D:695:HOH:O	2.47	0.41
2:F:39:MET:HB3	2:F:39:MET:HE3	1.52	0.41
1:A:45:MET:HA	1:A:145:ALA:O	2.20	0.41
1:A:84:TYR:CE1	1:A:97:ASN:HB2	2.56	0.41
1:A:245:PRO:HG2	1:A:269:LEU:HD11	2.03	0.41
1:D:307:HIS:HB3	1:D:330:PRO:HG2	2.02	0.41
1:A:4:THR:HG23	1:A:25:MET:CE	2.49	0.41
1:B:277:THR:C	3:B:615:HOH:O	2.64	0.41
1:C:50:HIS:CD2	1:C:114:SER:CB	3.03	0.41
1:D:14:GLY:O	1:D:16:ARG:NH1	2.48	0.41
2:E:6:GLU:OE2	2:E:6:GLU:N	2.35	0.41
1:A:316:PHE:O	1:A:318:PRO:HD3	2.20	0.41
1:C:293:ASN:CG	3:C:723:HOH:O	2.62	0.41
1:D:57[B]:ARG:HG2	3:D:848:HOH:O	2.21	0.41
1:B:37:HIS:HD2	3:B:785:HOH:O	2.02	0.41
1:D:20:PHE:O	1:D:23:TRP:HB2	2.21	0.41
1:D:342:ARG:HB3	1:D:343:ASN:H	1.44	0.41
1:C:51:MET:CE	1:C:143:MET:CE	3.00	0.40
1:A:341:ILE:HG22	1:A:342:ARG:HD2	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:51:MET:CE	1:C:143:MET:HE1	2.51	0.40
1:C:82:ALA:HA	1:C:100:VAL:O	2.22	0.40

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	363/364 (100%)	353 (97%)	10 (3%)	0	100	100
1	B	363/364 (100%)	354 (98%)	7 (2%)	2 (1%)	21	12
1	C	360/364 (99%)	349 (97%)	10 (3%)	1 (0%)	36	28
1	D	362/364 (100%)	352 (97%)	8 (2%)	2 (1%)	21	12
2	E	123/129 (95%)	119 (97%)	3 (2%)	1 (1%)	16	8
2	F	123/129 (95%)	119 (97%)	4 (3%)	0	100	100
All	All	1694/1714 (99%)	1646 (97%)	42 (2%)	6 (0%)	30	21

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	E	126	GLU
1	D	359	GLY
1	C	42	ASP
1	B	42	ASP
1	B	342	ARG
1	D	42	ASP

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	293/292 (100%)	286 (98%)	7 (2%)	43	36
1	B	293/292 (100%)	286 (98%)	7 (2%)	43	36
1	C	291/292 (100%)	283 (97%)	8 (3%)	39	32
1	D	293/292 (100%)	283 (97%)	10 (3%)	32	23
2	E	100/103 (97%)	96 (96%)	4 (4%)	28	17
2	F	100/103 (97%)	96 (96%)	4 (4%)	28	17
All	All	1370/1374 (100%)	1330 (97%)	40 (3%)	37	29

All (40) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	34	ASP
1	A	99	ILE
1	A	100	VAL
1	A	165	GLN
1	A	272	GLN
1	A	295	LEU
1	A	306	GLN
1	B	2	GLN
1	B	165	GLN
1	B	273	ARG
1	B	295	LEU
1	B	303	GLN
1	B	342	ARG
1	B	360	LYS
1	C	100	VAL
1	C	171	LYS
1	C	269	LEU
1	C	293	ASN
1	C	295	LEU
1	C	330	PRO
1	C	331	GLU
1	C	339	VAL

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Mol	Chain	Res	Type
1	D	100	VAL
1	D	239	MET
1	D	269	LEU
1	D	295	LEU
1	D	303	GLN
1	D	306	GLN
1	D	338	ILE
1	D	339	VAL
1	D	342	ARG
1	D	343	ASN
2	E	11	LYS
2	E	12	GLU
2	E	109	GLU
2	E	116	LEU
2	F	8	LYS
2	F	16	LEU
2	F	36	LEU
2	F	85	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (25) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	2	GLN
1	A	37	HIS
1	A	126	GLN
1	A	152	GLN
1	A	237	GLN
1	A	272	GLN
1	A	358	ASN
1	B	3	GLN
1	B	9	GLN
1	B	21	HIS
1	B	37	HIS
1	B	97	ASN
1	B	113	ASN
1	B	358	ASN
1	C	2	GLN
1	C	3	GLN
1	C	37	HIS
1	C	293	ASN
1	C	303	GLN
1	D	3	GLN

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Mol	Chain	Res	Type
1	D	9	GLN
1	D	237	GLN
1	D	340	GLN
1	D	343	ASN
2	F	31	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 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	LA2	E	64	2	17,19,20	0.59	0	12,21,23	0.98	0
2	LA2	F	64	2	17,19,20	0.67	0	12,21,23	1.34	1 (8%)

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	LA2	E	64	2	-	4/18/20/22	-
2	LA2	F	64	2	-	3/18/20/22	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	64	LA2	C7-C8-S8	-3.53	110.06	113.74

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	E	64	LA2	C6-C7-C8-S8
2	F	64	LA2	C5-C6-C7-C8
2	F	64	LA2	C2-C3-C4-C5
2	F	64	LA2	CA-CB-CG-CD
2	E	64	LA2	CA-CB-CG-CD
2	E	64	LA2	CE-CD-CG-CB
2	E	64	LA2	C4-C5-C6-S6

There are no ring outliers.

No monomer is involved in short contacts.

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	363/364 (99%)	-0.32	8 (2%) 62 69	9, 17, 38, 55	2 (0%)
1	B	363/364 (99%)	-0.27	6 (1%) 69 76	7, 18, 39, 57	3 (0%)
1	C	362/364 (99%)	-0.08	9 (2%) 58 65	13, 22, 43, 56	1 (0%)
1	D	362/364 (99%)	0.01	11 (3%) 52 59	11, 22, 42, 63	2 (0%)
2	E	125/129 (96%)	0.31	12 (9%) 13 15	17, 26, 48, 68	0
2	F	125/129 (96%)	0.82	11 (8%) 15 18	22, 36, 49, 57	0
All	All	1700/1714 (99%)	-0.06	57 (3%) 48 54	7, 21, 44, 68	8 (0%)

All (57) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	363	ALA	4.0
1	D	362	VAL	3.9
2	E	125	LEU	3.9
1	C	322	TYR	3.8
1	D	359	GLY	3.4
1	B	2	GLN	3.3
1	C	302	ALA	3.3
1	B	7	TYR	3.2
1	D	302	ALA	3.2
1	C	275	HIS	3.1
1	D	23	TRP	3.1
1	D	361	ALA	3.1
2	E	124	LEU	3.1
2	E	3	VAL	3.1
1	B	275	HIS	2.9
1	A	302	ALA	2.9
2	F	114	SER	2.9
2	E	126	GLU	2.8
2	F	22	GLY	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	357	ARG	2.8
2	F	23	THR	2.7
2	E	123	ALA	2.7
1	A	343	ASN	2.7
1	C	362	VAL	2.6
2	F	125	LEU	2.6
1	B	12	LEU	2.5
1	C	1	ALA	2.5
1	A	362	VAL	2.5
1	D	275	HIS	2.4
1	C	357	ARG	2.4
2	E	115	LEU	2.4
2	F	124	LEU	2.4
2	E	118	ALA	2.4
1	A	21	HIS	2.4
1	C	23	TRP	2.4
2	F	116	LEU	2.3
2	F	20	ALA	2.3
1	A	275	HIS	2.3
2	E	20	ALA	2.3
2	E	127	ASP	2.3
1	D	357	ARG	2.3
1	D	322	TYR	2.2
1	C	21	HIS	2.2
1	A	272	GLN	2.2
1	D	2	GLN	2.2
2	F	7	LEU	2.2
2	F	112	LEU	2.2
1	B	20	PHE	2.1
2	E	7	LEU	2.1
1	D	343	ASN	2.1
2	F	3	VAL	2.1
2	E	4	PRO	2.1
1	C	337	ALA	2.1
1	B	277	THR	2.0
1	D	358	ASN	2.0
2	F	47	VAL	2.0
2	E	114	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($\text{\AA}^2$)	Q<0.9
2	LA2	F	64	20/21	0.95	0.09	23,31,39,44	0
2	LA2	E	64	20/21	0.96	0.07	19,24,32,43	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.