



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 03:25 AM UTC

PDB ID : 6IJ2 / pdb_00006ij2
Title : Crystal structure of a standalone versatile EAL protein from *Vibrio cholerae* O395 - 5'-pGpG bound form
Authors : Yadav, M.; Pal, K.; Sen, U.
Deposited on : 2018-10-08
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 : 4-5-2 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

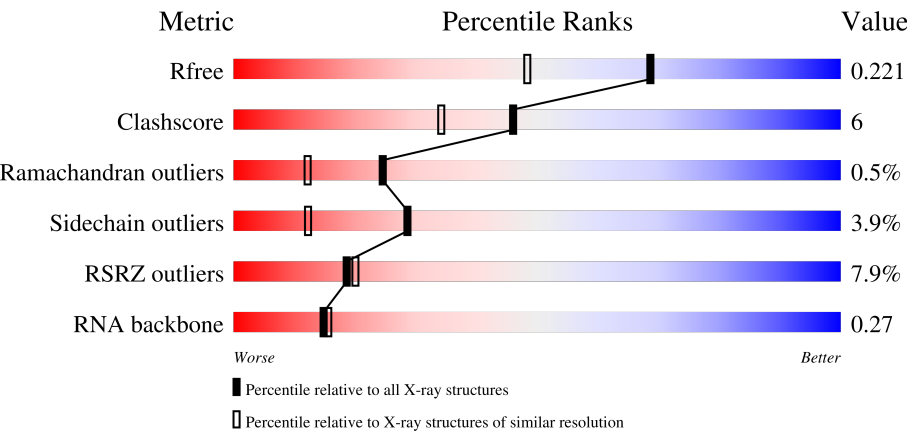
1 Overall quality at a glance i

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}	180053	5551 (1.70-1.70)
Clashscore	190562	5924 (1.70-1.70)
Ramachandran outliers	187476	5846 (1.70-1.70)
Sidechain outliers	187428	5846 (1.70-1.70)
RSRZ outliers	180081	5554 (1.70-1.70)
RNA backbone	3983	1094 (2.20-1.20)

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	257	7% 77%14%• 8%
1	B	257	6% 80%11%• 8%
1	C	257	7% 77%13%• 8%
1	D	257	9% 80%11%• 8%

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Mol	Chain	Length	Quality of chain
2	E	2	 50%50%
2	F	2	 50%50%
2	G	2	 100%
2	H	2	 50%50%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 8373 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 EAL domain protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	236	Total	C	N	O	S	0	0	0
			1889	1212	315	352	10			
1	B	236	Total	C	N	O	S	0	0	0
			1889	1212	315	352	10			
1	C	236	Total	C	N	O	S	0	0	0
			1889	1212	315	352	10			
1	D	236	Total	C	N	O	S	0	0	0
			1889	1212	315	352	10			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	15	SER	CYS	engineered mutation	UNP A0A0H3AJ04
B	15	SER	CYS	engineered mutation	UNP A0A0H3AJ04
C	15	SER	CYS	engineered mutation	UNP A0A0H3AJ04
D	15	SER	CYS	engineered mutation	UNP A0A0H3AJ04

- Molecule 2 is a RNA chain called RNA (5'-R(P*GP*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	2	Total	C	N	O	P	0	0	0
			47	20	10	15	2			
2	F	2	Total	C	N	O	P	0	0	0
			47	20	10	15	2			
2	G	2	Total	C	N	O	P	0	0	0
			47	20	10	15	2			
2	H	2	Total	C	N	O	P	0	0	0
			47	20	10	15	2			

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

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	4	Total Ca 4 4	0	0
3	B	4	Total Ca 4 4	0	0
3	C	4	Total Ca 4 4	0	0
3	D	4	Total Ca 4 4	0	0

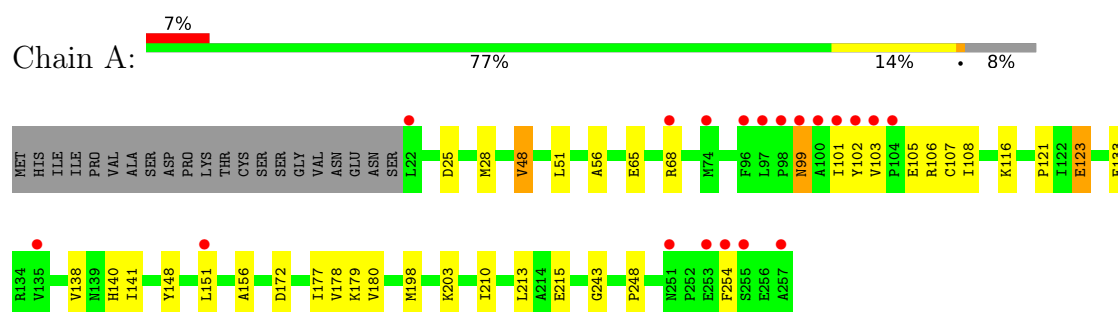
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	124	Total O 124 124	0	0
4	E	4	Total O 4 4	0	0
4	B	169	Total O 169 169	0	0
4	F	10	Total O 10 10	0	0
4	C	157	Total O 157 157	0	0
4	G	6	Total O 6 6	0	0
4	D	134	Total O 134 134	0	0
4	H	9	Total O 9 9	0	0

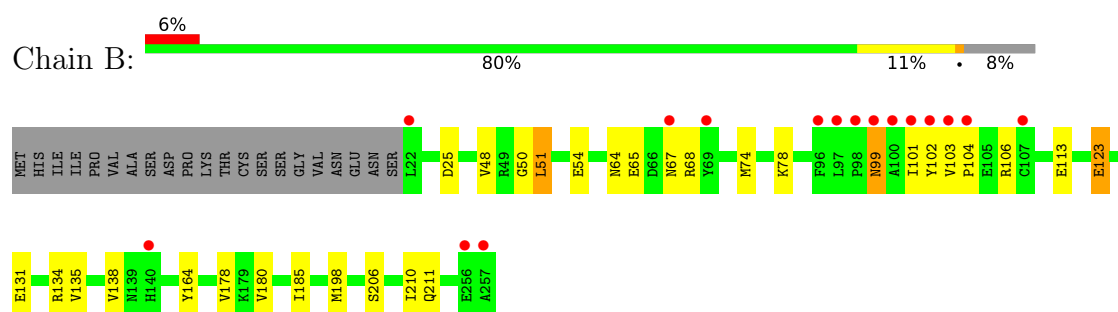
3 Residue-property plots [i](#)

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.

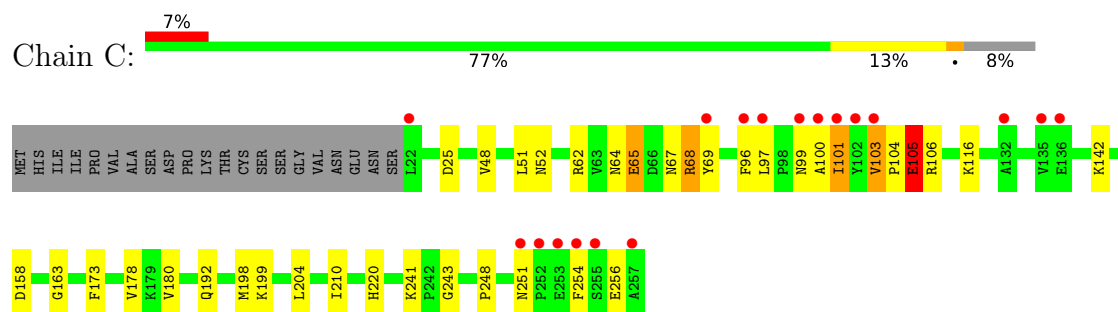
- Molecule 1: EAL domain protein



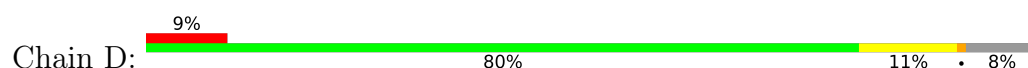
- Molecule 1: EAL domain protein

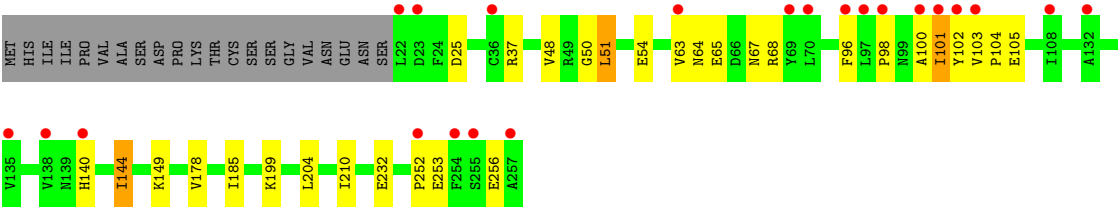


- Molecule 1: EAL domain protein



- Molecule 1: EAL domain protein





● Molecule 2: RNA (5'-R(P*GP*G)-3')



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There are no outlier residues recorded for this chain.

● Molecule 2: RNA (5'-R(P*GP*G)-3')



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	73.48Å 42.71Å 158.47Å 90.00° 94.94° 90.00°	Depositor
Resolution (Å)	51.51 – 1.70 51.51 – 1.70	Depositor EDS
% Data completeness (in resolution range)	98.1 (51.51-1.70) 93.9 (51.51-1.70)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.88 (at 1.70Å)	Xtriage
Refinement program	PHENIX 1.12_2829	Depositor
R, R_{free}	0.182 , 0.220 0.183 , 0.221	Depositor DCC
R_{free} test set	5294 reflections (4.87%)	wwPDB-VP
Wilson B-factor (Å ²)	25.5	Xtriage
Anisotropy	0.610	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 52.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	8373	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 42.38 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.0578e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.30	0/1928	0.48	0/2605
1	B	0.30	0/1928	0.52	0/2605
1	C	0.32	1/1928 (0.1%)	0.49	0/2605
1	D	0.25	0/1928	0.46	0/2605
2	E	1.32	1/52 (1.9%)	0.74	0/78
2	F	1.46	0/52	0.63	0/78
2	G	1.28	0/52	0.83	0/78
2	H	1.16	0/52	0.72	0/78
All	All	0.36	2/7920 (0.0%)	0.50	0/10732

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	503	G	O3'-P	-5.91	1.52	1.61
1	C	158	ASP	C-O	-5.38	1.17	1.24

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	1889	0	1866	27	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	1889	0	1866	18	0
1	C	1889	0	1866	26	0
1	D	1889	0	1866	19	0
2	E	47	0	23	0	0
2	F	47	0	23	1	0
2	G	47	0	23	0	0
2	H	47	0	23	1	0
3	A	4	0	0	0	0
3	B	4	0	0	0	0
3	C	4	0	0	0	0
3	D	4	0	0	0	0
4	A	124	0	0	0	0
4	B	169	0	0	1	0
4	C	157	0	0	4	0
4	D	134	0	0	1	0
4	E	4	0	0	0	0
4	F	10	0	0	0	0
4	G	6	0	0	0	0
4	H	9	0	0	0	0
All	All	8373	0	7556	88	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 (88) 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:B:25:ASP:HB3	1:B:51:LEU:HD21	1.60	0.81
1:A:99:ASN:N	1:A:99:ASN:OD1	2.23	0.71
1:B:211:GLN:NE2	4:B:701:HOH:O	2.25	0.70
1:C:65:GLU:HG2	1:C:68:ARG:NH1	2.06	0.69
1:C:25:ASP:HB3	1:C:51:LEU:HD21	1.74	0.68
1:B:64:ASN:H	1:B:67:ASN:HB2	1.62	0.65
1:D:25:ASP:HB3	1:D:51:LEU:HD21	1.76	0.65
1:D:96:PHE:HZ	1:D:101:ILE:HG13	1.61	0.65
1:B:180:VAL:HG11	1:B:198:MET:HE1	1.77	0.64
1:C:178:VAL:HG23	1:C:210:ILE:HG21	1.78	0.64
1:C:65:GLU:HG2	1:C:68:ARG:HH12	1.63	0.63
1:A:180:VAL:HG11	1:A:198:MET:HE1	1.81	0.63
1:B:178:VAL:HG23	1:B:210:ILE:HG21	1.82	0.62
1:C:62:ARG:O	1:C:67:ASN:ND2	2.32	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:180:VAL:HG11	1:C:198:MET:HE1	1.82	0.61
1:C:64:ASN:H	1:C:67:ASN:HB2	1.64	0.61
1:A:99:ASN:HB3	1:A:102:TYR:HB3	1.83	0.60
1:D:178:VAL:HG23	1:D:210:ILE:HG21	1.83	0.60
1:A:179:LYS:HD2	1:A:213:LEU:HD22	1.84	0.59
1:D:37:ARG:HD3	1:D:232:GLU:OE2	2.03	0.59
1:D:64:ASN:H	1:D:67:ASN:HB2	1.66	0.59
1:A:178:VAL:HG23	1:A:210:ILE:HG21	1.85	0.58
1:A:123:GLU:CD	1:A:123:GLU:H	2.11	0.58
1:A:105:GLU:HG2	1:A:106:ARG:H	1.69	0.56
1:B:74:MET:HE2	1:B:78:LYS:HE2	1.88	0.55
1:B:134:ARG:HG3	1:C:163:GLY:HA2	1.86	0.55
1:A:179:LYS:HE3	1:A:215:GLU:OE1	2.08	0.53
1:A:101:ILE:C	1:A:103:VAL:H	2.17	0.53
1:B:123:GLU:H	1:B:123:GLU:CD	2.17	0.52
1:A:68:ARG:NH1	1:A:101:ILE:HG21	2.25	0.51
1:A:68:ARG:CZ	1:A:101:ILE:HG21	2.41	0.51
1:B:50:GLY:HA3	1:B:54:GLU:HB2	1.93	0.51
1:C:100:ALA:O	1:C:103:VAL:HB	2.11	0.51
1:A:179:LYS:HD3	1:A:213:LEU:HD13	1.92	0.50
1:C:69:TYR:CE1	1:C:103:VAL:HG23	2.47	0.50
1:D:140:HIS:O	1:D:144:ILE:HD12	2.12	0.50
1:D:63:VAL:HG12	1:D:68:ARG:HG3	1.94	0.49
1:D:96:PHE:CZ	1:D:101:ILE:HG13	2.44	0.49
1:C:220:HIS:HD2	4:C:839:HOH:O	1.96	0.49
1:D:199:LYS:HD3	4:D:738:HOH:O	2.12	0.49
1:C:104:PRO:O	1:C:106:ARG:N	2.46	0.48
1:C:199:LYS:NZ	4:C:710:HOH:O	2.46	0.48
1:A:121:PRO:HB2	1:A:123:GLU:HG2	1.94	0.48
1:D:252:PRO:O	1:D:256:GLU:HG2	2.13	0.48
1:D:65:GLU:HA	1:D:68:ARG:HD2	1.95	0.48
1:B:101:ILE:O	1:B:103:VAL:N	2.47	0.47
1:B:131:GLU:HG2	1:B:164:TYR:CD2	2.49	0.47
1:B:65:GLU:HB2	1:B:68:ARG:HH21	1.80	0.47
1:A:108:ILE:HD13	1:A:151:LEU:HD12	1.95	0.47
1:C:243:GLY:HA3	1:C:248:PRO:HG3	1.96	0.47
1:A:65:GLU:HA	1:A:68:ARG:CZ	2.45	0.47
1:D:102:TYR:HA	1:D:140:HIS:NE2	2.29	0.47
1:D:103:VAL:HG12	1:D:105:GLU:HG2	1.96	0.47
1:B:48:VAL:HG13	2:F:504:G:O6	2.15	0.47
1:C:99:ASN:C	1:C:101:ILE:H	2.23	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:142:LYS:HG3	1:C:173:PHE:HB3	1.98	0.46
1:C:104:PRO:C	1:C:106:ARG:H	2.24	0.45
1:C:96:PHE:HD1	1:C:97:LEU:N	2.15	0.45
1:D:101:ILE:O	1:D:103:VAL:N	2.50	0.45
1:C:69:TYR:HE1	1:C:103:VAL:HG23	1.82	0.44
1:D:48:VAL:HG13	2:H:504:G:O6	2.18	0.44
1:D:101:ILE:HD13	1:D:104:PRO:HA	2.00	0.43
1:A:138:VAL:HG11	1:A:172:ASP:OD2	2.18	0.43
1:C:68:ARG:HD3	1:C:99:ASN:O	2.19	0.43
1:B:65:GLU:HA	1:B:68:ARG:NE	2.33	0.43
1:D:100:ALA:C	1:D:102:TYR:H	2.26	0.43
1:B:104:PRO:O	1:B:106:ARG:N	2.45	0.42
1:A:25:ASP:HB3	1:A:51:LEU:HD11	2.02	0.42
1:A:108:ILE:HD12	1:A:148:TYR:CE1	2.55	0.42
1:B:99:ASN:O	1:B:101:ILE:HD12	2.19	0.42
1:B:198:MET:HA	1:B:198:MET:HE2	2.01	0.42
1:A:156:ALA:HA	1:A:177:ILE:O	2.20	0.41
1:C:104:PRO:C	1:C:106:ARG:N	2.78	0.41
1:C:254:PHE:O	4:C:701:HOH:O	2.22	0.41
1:D:50:GLY:HA3	1:D:54:GLU:HB2	2.03	0.41
1:C:65:GLU:OE1	1:C:68:ARG:NH2	2.54	0.41
1:A:48:VAL:HG12	1:A:56:ALA:HA	2.02	0.41
1:A:101:ILE:H	1:A:101:ILE:HG13	1.75	0.41
1:A:101:ILE:HD12	1:A:102:TYR:N	2.36	0.41
1:C:105:GLU:OE1	1:C:106:ARG:NH1	2.53	0.41
1:A:68:ARG:NH2	1:A:101:ILE:HG21	2.36	0.41
1:C:198:MET:HA	1:C:198:MET:HE2	2.03	0.41
1:D:103:VAL:C	1:D:105:GLU:H	2.28	0.41
1:C:241:LYS:NZ	4:C:704:HOH:O	2.31	0.41
1:A:203:LYS:HZ2	1:B:206:SER:CB	2.34	0.40
1:A:28:MET:HE1	1:A:48:VAL:HG23	2.02	0.40
1:A:103:VAL:HA	1:A:140:HIS:NE2	2.36	0.40
1:A:243:GLY:HA3	1:A:248:PRO:HG3	2.03	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	234/257 (91%)	224 (96%)	10 (4%)	0	100	100
1	B	234/257 (91%)	223 (95%)	10 (4%)	1 (0%)	30	16
1	C	234/257 (91%)	222 (95%)	9 (4%)	3 (1%)	9	2
1	D	234/257 (91%)	221 (94%)	12 (5%)	1 (0%)	30	16
All	All	936/1028 (91%)	890 (95%)	41 (4%)	5 (0%)	24	12

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	102	TYR
1	C	68	ARG
1	D	98	PRO
1	C	256	GLU
1	C	105	GLU

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	203/222 (91%)	195 (96%)	8 (4%)	28	12
1	B	203/222 (91%)	196 (97%)	7 (3%)	32	16
1	C	203/222 (91%)	193 (95%)	10 (5%)	22	8
1	D	203/222 (91%)	196 (97%)	7 (3%)	32	16
All	All	812/888 (91%)	780 (96%)	32 (4%)	28	12

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	48	VAL
1	A	99	ASN
1	A	107	CYS
1	A	116	LYS
1	A	123	GLU
1	A	133	GLU
1	A	141	ILE
1	A	254	PHE
1	B	51	LEU
1	B	99	ASN
1	B	113	GLU
1	B	123	GLU
1	B	135	VAL
1	B	138	VAL
1	B	185	ILE
1	C	48	VAL
1	C	52	ASN
1	C	65	GLU
1	C	101	ILE
1	C	103	VAL
1	C	105	GLU
1	C	116	LYS
1	C	192	GLN
1	C	204	LEU
1	C	251	ASN
1	D	51	LEU
1	D	101	ILE
1	D	144	ILE
1	D	149	LYS
1	D	185	ILE
1	D	204	LEU
1	D	253	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	154	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	E	1/2 (50%)	0	0
2	F	1/2 (50%)	0	0
2	G	1/2 (50%)	0	0
2	H	1/2 (50%)	0	0
All	All	4/8 (50%)	0	0

There are no RNA backbone outliers to report.

There are no RNA pucker outliers to report.

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 16 ligands modelled in this entry, 16 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	236/257 (91%)	0.58	19 (8%)	18 19	24, 40, 97, 148	0
1	B	236/257 (91%)	0.29	16 (6%)	23 25	20, 32, 76, 134	0
1	C	236/257 (91%)	0.48	18 (7%)	20 21	21, 36, 97, 131	0
1	D	236/257 (91%)	0.53	22 (9%)	14 15	23, 38, 102, 120	0
2	E	2/2 (100%)	0.18	0	100 100	46, 46, 46, 50	0
2	F	2/2 (100%)	-0.61	0	100 100	30, 30, 30, 32	0
2	G	2/2 (100%)	-0.16	0	100 100	36, 36, 36, 41	0
2	H	2/2 (100%)	-0.04	0	100 100	42, 42, 42, 46	0
All	All	952/1036 (91%)	0.47	75 (7%)	18 20	20, 36, 95, 148	0

All (75) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	103	VAL	6.6
1	A	101	ILE	6.1
1	A	102	TYR	5.2
1	B	99	ASN	5.0
1	B	103	VAL	4.8
1	A	135	VAL	4.4
1	A	254	PHE	4.3
1	A	100	ALA	4.3
1	C	135	VAL	4.2
1	B	102	TYR	4.2
1	D	252	PRO	4.2
1	C	252	PRO	4.1
1	B	101	ILE	4.1
1	D	101	ILE	4.1
1	A	255	SER	4.1
1	D	257	ALA	4.0

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Mol	Chain	Res	Type	RSRZ
1	A	97	LEU	3.9
1	C	22	LEU	3.9
1	D	102	TYR	3.8
1	A	257	ALA	3.7
1	B	100	ALA	3.5
1	C	101	ILE	3.4
1	D	100	ALA	3.4
1	B	69	TYR	3.3
1	C	100	ALA	3.3
1	C	251	ASN	3.3
1	D	97	LEU	3.2
1	D	254	PHE	3.2
1	C	103	VAL	3.2
1	C	257	ALA	3.1
1	B	98	PRO	3.0
1	C	69	TYR	3.0
1	A	22	LEU	3.0
1	B	67	ASN	2.9
1	C	102	TYR	2.9
1	B	107	CYS	2.9
1	B	104	PRO	2.8
1	D	108	ILE	2.8
1	B	140	HIS	2.8
1	A	104	PRO	2.7
1	B	97	LEU	2.7
1	D	22	LEU	2.7
1	D	98	PRO	2.6
1	C	136	GLU	2.6
1	D	132	ALA	2.6
1	A	68	ARG	2.5
1	A	253	GLU	2.5
1	B	257	ALA	2.5
1	A	96	PHE	2.4
1	C	253	GLU	2.4
1	D	70	LEU	2.4
1	D	140	HIS	2.4
1	C	254	PHE	2.3
1	D	255	SER	2.3
1	A	151	LEU	2.3
1	C	99	ASN	2.3
1	C	97	LEU	2.3
1	B	96	PHE	2.3

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Mol	Chain	Res	Type	RSRZ
1	D	103	VAL	2.3
1	B	256	GLU	2.2
1	B	22	LEU	2.2
1	C	255	SER	2.2
1	A	74	MET	2.2
1	A	251	ASN	2.2
1	C	96	PHE	2.2
1	D	36	CYS	2.1
1	C	132	ALA	2.1
1	D	135	VAL	2.1
1	D	69	TYR	2.1
1	A	98	PRO	2.1
1	D	96	PHE	2.1
1	D	23	ASP	2.0
1	D	63	VAL	2.0
1	D	138	VAL	2.0
1	A	99	ASN	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
3	CA	D	604	1/1	0.45	0.23	242,242,242,242	0
3	CA	C	604	1/1	0.50	0.24	154,154,154,154	0
3	CA	A	604	1/1	0.87	0.23	84,84,84,84	0
3	CA	B	604	1/1	0.91	0.18	74,74,74,74	0
3	CA	D	603	1/1	0.93	0.19	67,67,67,67	0
3	CA	A	603	1/1	0.96	0.22	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	CA	C	603	1/1	0.97	0.25	43,43,43,43	0
3	CA	A	601	1/1	0.98	0.08	29,29,29,29	0
3	CA	C	602	1/1	0.98	0.06	26,26,26,26	0
3	CA	B	603	1/1	0.98	0.20	41,41,41,41	0
3	CA	D	601	1/1	0.99	0.07	30,30,30,30	0
3	CA	C	601	1/1	0.99	0.04	23,23,23,23	0
3	CA	A	602	1/1	0.99	0.05	26,26,26,26	0
3	CA	D	602	1/1	1.00	0.05	25,25,25,25	0
3	CA	B	602	1/1	1.00	0.01	23,23,23,23	0
3	CA	B	601	1/1	1.00	0.05	23,23,23,23	0

6.5 Other polymers [i](#)

There are no such residues in this entry.