



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 29, 2020 – 09:49 PM BST

PDB ID : 6IJ2
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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.13
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.13

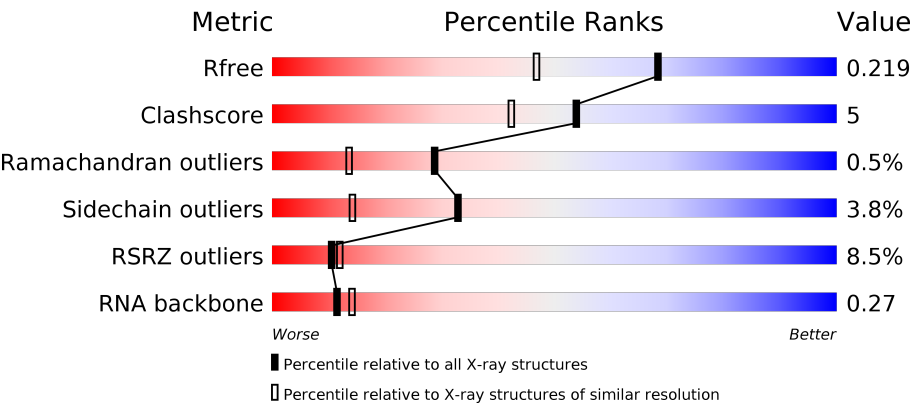
1 Overall quality at a glance i

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.




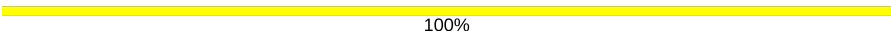

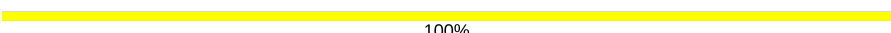
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R _{free}	130704	4298 (1.70-1.70)
Clashscore	141614	4695 (1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (1.70-1.70)
RSRZ outliers	127900	4222 (1.70-1.70)
RNA backbone	3102	1007 (2.38-1.02)

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 on 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	<div><div>8%</div><div><div></div><div>76%</div><div>15%</div><div>• 8%</div></div></div>
1	B	257	<div><div>4%</div><div><div></div><div>81%</div><div>10%</div><div>• 8%</div></div></div>
1	C	257	<div><div>10%</div><div><div></div><div>79%</div><div>11%</div><div>• 8%</div></div></div>
1	D	257	<div><div>10%</div><div><div></div><div>80%</div><div>11%</div><div>• 8%</div></div></div>

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

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
3	CA	D	604	-	-	-	X

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 (three-letter code: CA) (formula: Ca).

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

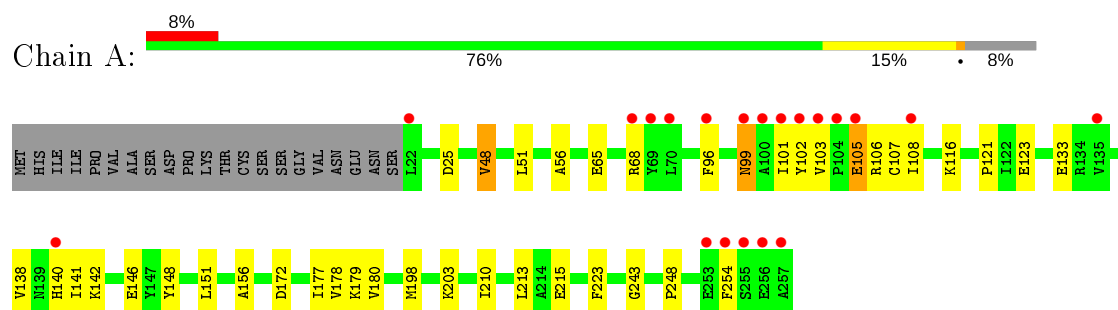
- Molecule 4 is water.

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

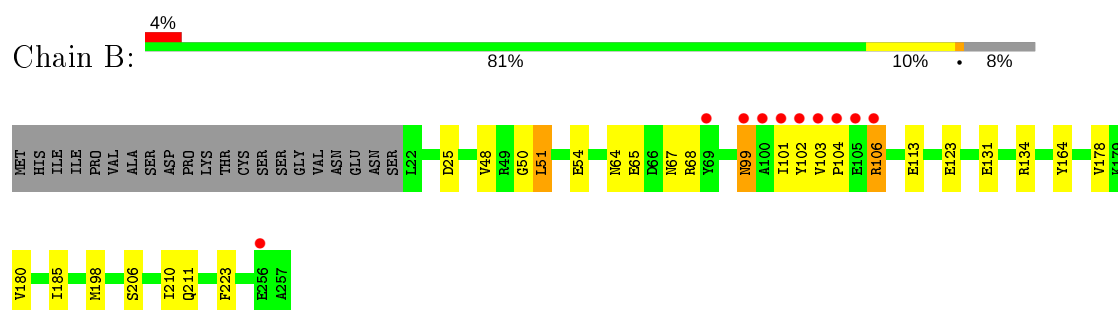
3 Residue-property plots [i](#)

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.

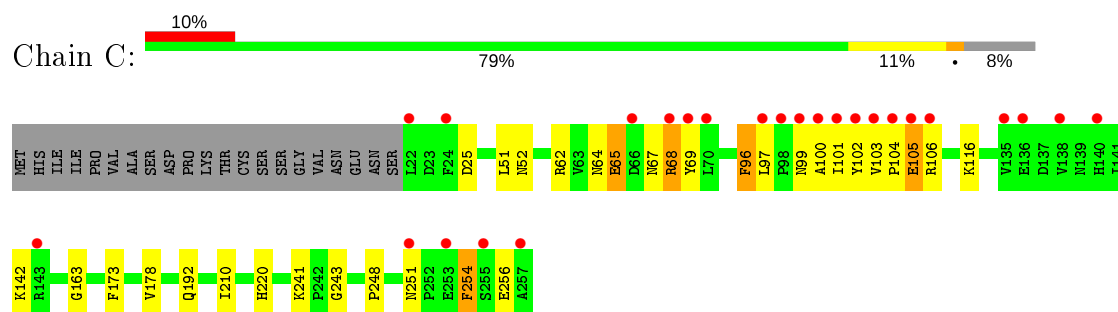
- Molecule 1: EAL domain protein



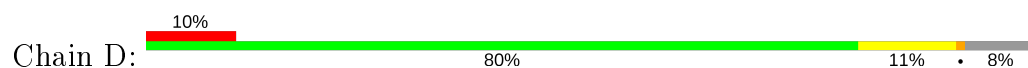
- Molecule 1: EAL domain protein

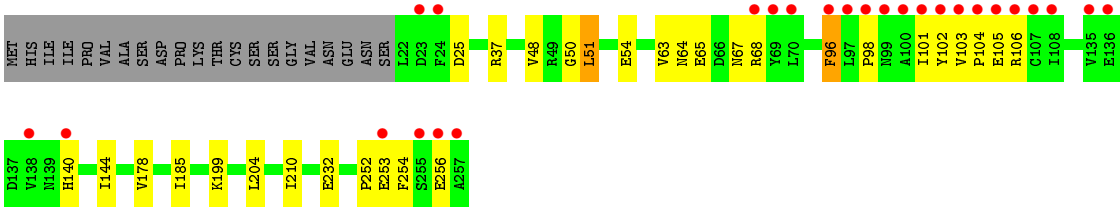


- Molecule 1: EAL domain protein



- Molecule 1: EAL domain protein





● Molecule 2: RNA (5'-R(P*GP*G)-3')



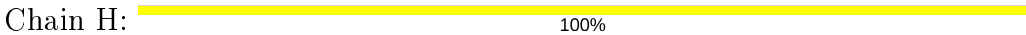
● Molecule 2: RNA (5'-R(P*GP*G)-3')



● Molecule 2: RNA (5'-R(P*GP*G)-3')



● 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	73.48 Å 42.71 Å 158.47 Å 90.00° 94.94° 90.00°	Depositor
Resolution (Å)	51.51 – 1.70 52.63 – 1.70	Depositor EDS
% Data completeness (in resolution range)	98.1 (51.51-1.70) 93.9 (52.63-1.70)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.88 (at 1.70 Å)	Xtriage
Refinement program	PHENIX 1.12 _2829	Depositor
R, R_{free}	0.182 , 0.220 0.182 , 0.219	Depositor DCC
R_{free} test set	5294 reflections (4.95%)	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 , 53.7	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.*

¹ Intensities estimated from amplitudes.

² Theoretical 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: 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	0.35	0/1928	0.52	0/2605
1	B	0.37	0/1928	0.53	0/2605
1	C	0.36	0/1928	0.53	0/2605
1	D	0.33	0/1928	0.51	0/2605
2	E	2.53	2/52 (3.8%)	0.61	0/78
2	F	2.84	2/52 (3.8%)	0.71	0/78
2	G	2.51	2/52 (3.8%)	0.72	0/78
2	H	2.44	1/52 (1.9%)	0.67	0/78
All	All	0.54	7/7920 (0.1%)	0.53	0/10732

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	503	G	OP3-P	-16.52	1.41	1.61
2	H	503	G	OP3-P	-14.71	1.43	1.61
2	G	503	G	OP3-P	-14.37	1.44	1.61
2	E	503	G	OP3-P	-14.02	1.44	1.61
2	E	503	G	O3'-P	-7.38	1.52	1.61
2	F	503	G	O3'-P	-5.63	1.54	1.61
2	G	503	G	O3'-P	-5.17	1.54	1.61

There are no bond angle outliers.

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	1889	0	1866	27	0
1	B	1889	0	1866	17	0
1	C	1889	0	1866	22	0
1	D	1889	0	1866	17	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	3	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	81	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 5.

All (81) 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:A:180:VAL:HG11	1:A:198:MET:HE1	1.80	0.64
1:C:178:VAL:HG23	1:C:210:ILE:HG21	1.78	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:65:GLU:HG2	1:C:68:ARG:HH12	1.63	0.63
1:C:241:LYS:NZ	4:C:704:HOH:O	2.31	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
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:105:GLU:HG2	1:A:106:ARG:H	1.69	0.56
1:B:134:ARG:HG3	1:C:163:GLY:HA2	1.86	0.55
1:A:123:GLU:CD	1:A:123:GLU:H	2.11	0.53
1:A:179:LYS:HE3	1:A:215:GLU:OE1	2.08	0.53
1:A:142:LYS:NZ	1:A:146:GLU:OE1	2.35	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:A:101:ILE:C	1:A:103:VAL:H	2.17	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:123:GLU:CD	1:B:123:GLU:H	2.17	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:48:VAL:HG13	2:F:504:G:O6	2.15	0.47
1:C:142:LYS:HG3	1:C:173:PHE:HB3	1.98	0.46
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: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:198:MET:HA	1:B:198:MET:HE2	2.01	0.42
1:B:99:ASN:O	1:B:101:ILE:HD12	2.19	0.42
1:C:99:ASN:C	1:C:101:ILE:H	2.23	0.42
1:A:156:ALA:HA	1:A:177:ILE:O	2.20	0.41
1:C:254:PHE:O	4:C:701:HOH:O	2.22	0.41
1:A:203:LYS:HZ1	1:B:206:SER:CB	2.34	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:101:ILE:HG13	1:A:101:ILE:H	1.75	0.41
1:A:101:ILE:HD12	1:A:102:TYR:N	2.36	0.41
1:A:48:VAL:HG12	1:A:56:ALA:HA	2.02	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:104:PRO:C	1:C:106:ARG:H	2.24	0.41
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%)	34	18
1	C	234/257 (91%)	222 (95%)	9 (4%)	3 (1%)	12	2
1	D	234/257 (91%)	221 (94%)	12 (5%)	1 (0%)	34	18
All	All	936/1028 (91%)	890 (95%)	41 (4%)	5 (0%)	29	13

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%)	193 (95%)	10 (5%)	25	9
1	B	203/222 (91%)	197 (97%)	6 (3%)	41	22
1	C	203/222 (91%)	195 (96%)	8 (4%)	32	13
1	D	203/222 (91%)	196 (97%)	7 (3%)	37	18
All	All	812/888 (91%)	781 (96%)	31 (4%)	33	14

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	48	VAL
1	A	96	PHE
1	A	99	ASN
1	A	105	GLU
1	A	107	CYS
1	A	116	LYS

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Mol	Chain	Res	Type
1	A	133	GLU
1	A	141	ILE
1	A	223	PHE
1	A	254	PHE
1	B	51	LEU
1	B	99	ASN
1	B	106	ARG
1	B	113	GLU
1	B	185	ILE
1	B	223	PHE
1	C	52	ASN
1	C	65	GLU
1	C	96	PHE
1	C	102	TYR
1	C	116	LYS
1	C	192	GLN
1	C	251	ASN
1	C	254	PHE
1	D	51	LEU
1	D	96	PHE
1	D	106	ARG
1	D	185	ILE
1	D	204	LEU
1	D	253	GLU
1	D	254	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 monosaccharides 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%)	0.49	20 (8%) 10 12	24, 40, 97, 148	0
1	B	236/257 (91%)	0.21	10 (4%) 36 40	20, 32, 76, 134	0
1	C	236/257 (91%)	0.50	25 (10%) 6 7	21, 36, 97, 131	0
1	D	236/257 (91%)	0.46	26 (11%) 5 6	23, 38, 102, 120	0
2	E	2/2 (100%)	-0.44	0 100 100	46, 46, 46, 50	0
2	F	2/2 (100%)	-0.70	0 100 100	30, 30, 30, 32	0
2	G	2/2 (100%)	-0.70	0 100 100	36, 36, 36, 41	0
2	H	2/2 (100%)	-0.67	0 100 100	42, 42, 42, 46	0
All	All	952/1036 (91%)	0.41	81 (8%) 10 12	20, 36, 95, 148	0

All (81) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	102	TYR	13.6
1	B	102	TYR	13.5
1	A	101	ILE	10.8
1	C	101	ILE	8.7
1	A	257	ALA	8.1
1	D	101	ILE	7.9
1	C	69	TYR	7.8
1	A	100	ALA	7.3
1	A	104	PRO	7.3
1	A	102	TYR	7.1
1	D	102	TYR	6.3
1	D	97	LEU	6.3
1	C	99	ASN	6.2
1	C	257	ALA	6.0
1	D	69	TYR	5.9
1	A	135	VAL	5.9

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Mol	Chain	Res	Type	RSRZ
1	D	107	CYS	5.9
1	A	103	VAL	5.7
1	C	22	LEU	5.5
1	A	255	SER	5.5
1	D	103	VAL	5.5
1	B	100	ALA	5.4
1	B	103	VAL	5.2
1	D	70	LEU	5.0
1	A	69	TYR	4.8
1	D	104	PRO	4.6
1	C	106	ARG	4.5
1	B	101	ILE	4.5
1	C	100	ALA	4.5
1	A	256	GLU	4.5
1	B	99	ASN	4.5
1	B	104	PRO	4.4
1	D	257	ALA	4.4
1	C	253	GLU	4.3
1	D	99	ASN	4.2
1	C	104	PRO	4.2
1	C	105	GLU	4.2
1	A	105	GLU	4.2
1	C	24	PHE	4.1
1	A	99	ASN	3.9
1	D	100	ALA	3.8
1	C	70	LEU	3.8
1	D	106	ARG	3.5
1	D	140	HIS	3.5
1	D	138	VAL	3.5
1	C	136	GLU	3.4
1	D	108	ILE	3.4
1	C	135	VAL	3.4
1	D	255	SER	3.3
1	D	253	GLU	3.3
1	A	68	ARG	3.3
1	C	251	ASN	3.3
1	D	68	ARG	3.3
1	A	140	HIS	3.2
1	A	70	LEU	3.1
1	D	256	GLU	3.1
1	D	23	ASP	3.1
1	D	98	PRO	3.0

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Mol	Chain	Res	Type	RSRZ
1	D	105	GLU	3.0
1	A	254	PHE	2.8
1	C	103	VAL	2.8
1	A	22	LEU	2.8
1	C	255	SER	2.7
1	C	68	ARG	2.6
1	B	69	TYR	2.6
1	C	138	VAL	2.6
1	A	253	GLU	2.6
1	A	96	PHE	2.6
1	C	140	HIS	2.5
1	D	136	GLU	2.5
1	B	105	GLU	2.4
1	C	98	PRO	2.3
1	A	108	ILE	2.3
1	B	106	ARG	2.3
1	C	143	ARG	2.3
1	D	24	PHE	2.2
1	C	97	LEU	2.2
1	D	135	VAL	2.2
1	C	66	ASP	2.2
1	B	256	GLU	2.1
1	D	96	PHE	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 monosaccharides 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.

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	CA	D	604	1/1	-0.11	0.66	242,242,242,242	0
3	CA	C	604	1/1	0.48	0.31	154,154,154,154	0
3	CA	A	604	1/1	0.86	0.14	84,84,84,84	0
3	CA	B	604	1/1	0.91	0.12	74,74,74,74	0
3	CA	D	603	1/1	0.97	0.14	67,67,67,67	0
3	CA	A	603	1/1	0.98	0.18	57,57,57,57	0
3	CA	B	603	1/1	0.98	0.12	41,41,41,41	0
3	CA	A	601	1/1	0.98	0.04	29,29,29,29	0
3	CA	C	603	1/1	0.99	0.17	43,43,43,43	0
3	CA	B	602	1/1	0.99	0.09	23,23,23,23	0
3	CA	C	602	1/1	0.99	0.06	26,26,26,26	0
3	CA	A	602	1/1	1.00	0.05	26,26,26,26	0
3	CA	C	601	1/1	1.00	0.06	23,23,23,23	0
3	CA	D	602	1/1	1.00	0.05	25,25,25,25	0
3	CA	B	601	1/1	1.00	0.05	23,23,23,23	0
3	CA	D	601	1/1	1.00	0.04	30,30,30,30	0

6.5 Other polymers [i](#)

There are no such residues in this entry.