



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 04:02 PM UTC

PDB ID : 6C5W / pdb_00006c5w
Title : Crystal structure of the mitochondrial calcium uniporter
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Deposited on : 2018-01-17
Resolution : 3.10 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

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

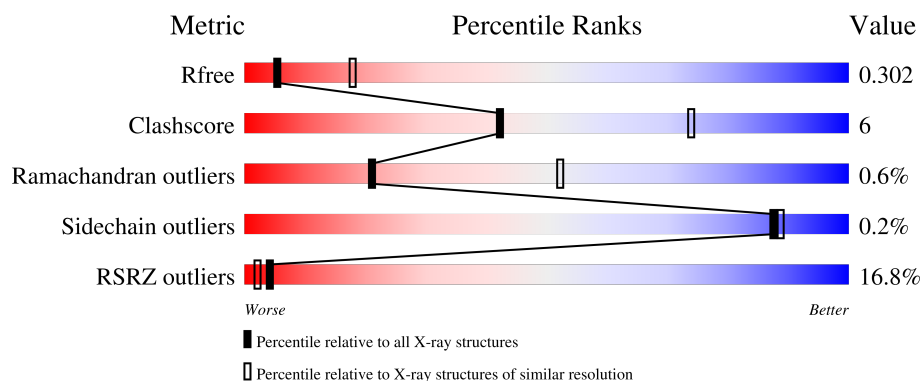
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 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	1456 (3.10-3.10)
Clashscore	190562	1539 (3.10-3.10)
Ramachandran outliers	187476	1467 (3.10-3.10)
Sidechain outliers	187428	1467 (3.10-3.10)
RSRZ outliers	180081	1456 (3.10-3.10)

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	312	15% 78% 13% 9%
1	B	312	9% 57% 12% 30%
2	C	117	7% 89% 11%
2	E	117	34% 79% 21%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5745 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 calcium uniporter.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	285	Total	C	N	O	S	0	1	0
			2193	1407	384	394	8			
1	B	217	Total	C	N	O	S	0	0	0
			1765	1144	308	306	7			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	GLY	deletion	UNP E9DVV4
A	?	-	GLY	deletion	UNP E9DVV4
A	?	-	ASN	deletion	UNP E9DVV4
A	?	-	LYS	deletion	UNP E9DVV4
A	?	-	SER	deletion	UNP E9DVV4
A	?	-	ASN	deletion	UNP E9DVV4
A	?	-	ASP	deletion	UNP E9DVV4
A	?	-	GLY	deletion	UNP E9DVV4
A	?	-	ARG	deletion	UNP E9DVV4
A	?	-	ARG	deletion	UNP E9DVV4
A	?	-	GLU	deletion	UNP E9DVV4
A	?	-	GLU	deletion	UNP E9DVV4
A	?	-	SER	deletion	UNP E9DVV4
A	?	-	ASN	deletion	UNP E9DVV4
A	?	-	GLY	deletion	UNP E9DVV4
A	?	-	ASN	deletion	UNP E9DVV4
B	?	-	GLY	deletion	UNP E9DVV4
B	?	-	GLY	deletion	UNP E9DVV4
B	?	-	ASN	deletion	UNP E9DVV4
B	?	-	LYS	deletion	UNP E9DVV4
B	?	-	SER	deletion	UNP E9DVV4
B	?	-	ASN	deletion	UNP E9DVV4
B	?	-	ASP	deletion	UNP E9DVV4
B	?	-	GLY	deletion	UNP E9DVV4
B	?	-	ARG	deletion	UNP E9DVV4

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Chain	Residue	Modelled	Actual	Comment	Reference
B	?	-	ARG	deletion	UNP E9DVV4
B	?	-	GLU	deletion	UNP E9DVV4
B	?	-	GLU	deletion	UNP E9DVV4
B	?	-	SER	deletion	UNP E9DVV4
B	?	-	ASN	deletion	UNP E9DVV4
B	?	-	GLY	deletion	UNP E9DVV4
B	?	-	ASN	deletion	UNP E9DVV4

- Molecule 2 is a protein called nanobody.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	117	Total	C	N	O	S	0	0	0
			893	563	157	169	4			
2	E	117	Total	C	N	O	S	0	0	0
			893	563	157	169	4			

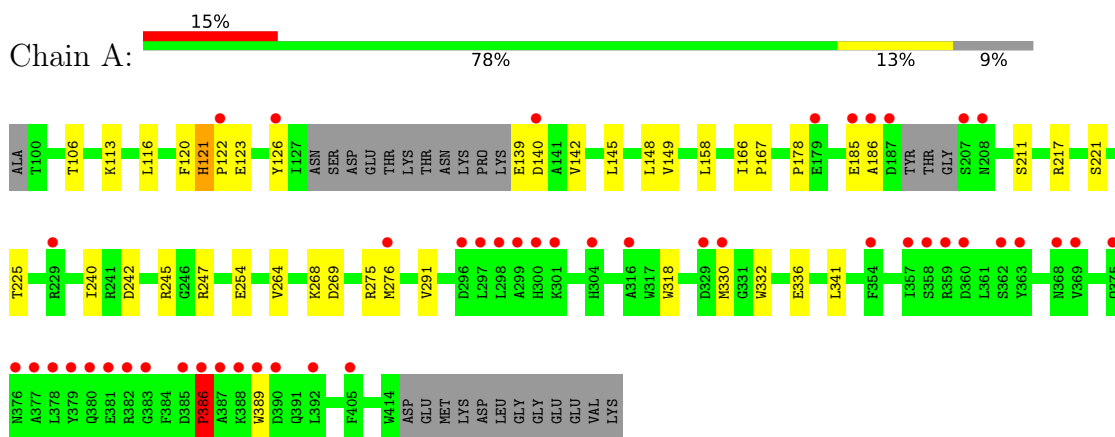
- Molecule 3 is CALCIUM ION (CCD ID: CA) (formula: Ca).

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

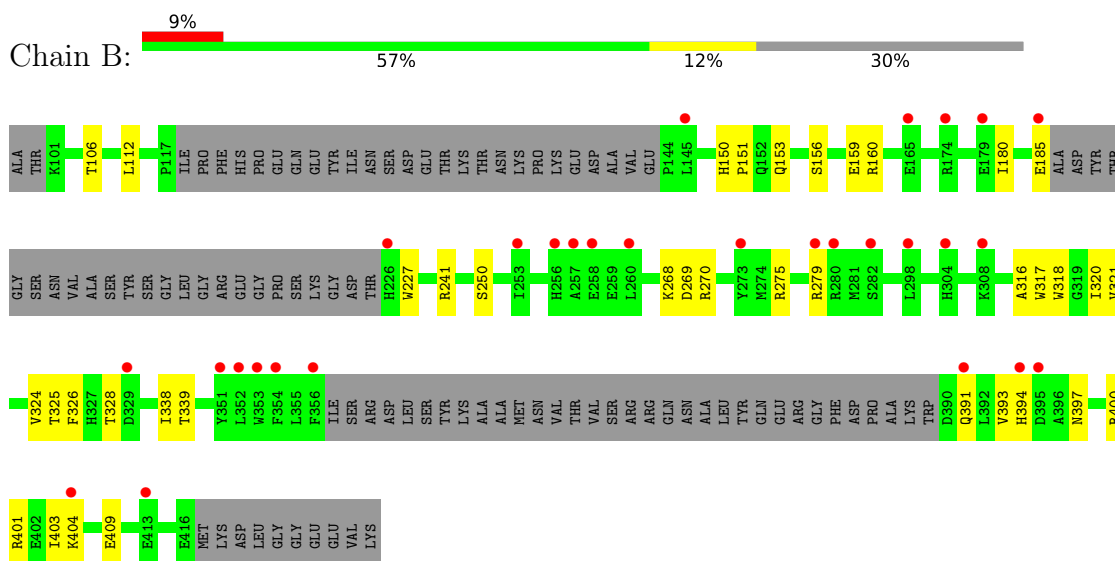
3 Residue-property plots [i](#)

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: calcium uniporter

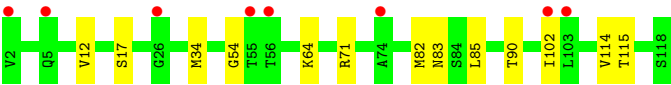


• Molecule 1: calcium uniporter

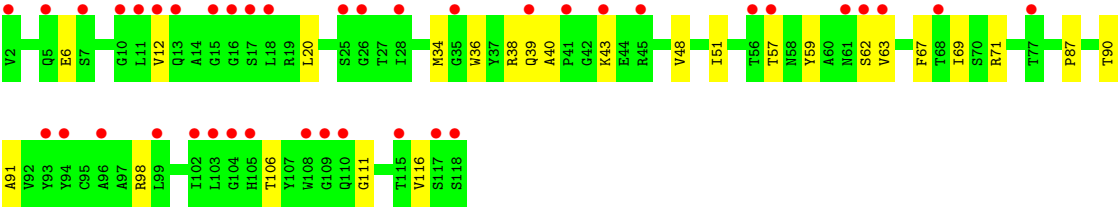
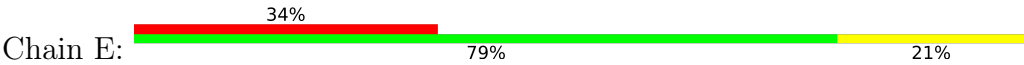


• Molecule 2: nanobody





● Molecule 2: nanobody



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	88.02Å 290.45Å 126.12Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.30 – 3.10 45.30 – 3.10	Depositor EDS
% Data completeness (in resolution range)	78.9 (45.30-3.10) 78.8 (45.30-3.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.64 (at 3.12Å)	Xtriage
Refinement program	phenix.refine 1.11.1_2575, PHENIX 1.11.1_2575	Depositor
R, R_{free}	0.256 , 0.299 0.257 , 0.302	Depositor DCC
R_{free} test set	1218 reflections (4.08%)	wwPDB-VP
Wilson B-factor (Å ²)	56.2	Xtriage
Anisotropy	0.099	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 50.0	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	0.83	EDS
Total number of atoms	5745	wwPDB-VP
Average B, all atoms (Å ²)	75.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.59% 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: 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	0.12	0/2248	0.37	1/3053 (0.0%)
1	B	0.10	0/1809	0.32	0/2447
2	C	0.09	0/914	0.26	0/1239
2	E	0.10	0/914	0.31	0/1239
All	All	0.11	0/5885	0.33	1/7978 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	386	PRO	N-CA-CB	7.20	110.81	103.25

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	2193	0	2094	27	0
1	B	1765	0	1770	25	0
2	C	893	0	862	7	0
2	E	893	0	862	14	0
3	A	1	0	0	0	0
All	All	5745	0	5588	71	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 (71) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:90:THR:HG23	2:C:115:THR:HA	1.70	0.72
1:B:150:HIS:HB3	1:B:153:GLN:HG3	1.70	0.72
1:A:221:SER:HB3	1:A:247:ARG:HD3	1.72	0.72
1:A:123:GLU:HG2	1:A:126:TYR:HA	1.70	0.71
1:A:186:ALA:HA	1:A:245:ARG:HE	1.55	0.71
1:A:139:GLU:N	1:A:139:GLU:OE1	2.30	0.65
1:A:185:GLU:HG3	1:A:225:THR:HB	1.78	0.64
1:A:242:ASP:OD1	1:A:245:ARG:NH1	2.31	0.64
2:E:98:ARG:HG2	2:E:106:THR:HG22	1.78	0.63
1:B:268:LYS:O	1:B:275:ARG:NH1	2.33	0.61
1:A:211:SER:O	1:A:245:ARG:NH2	2.36	0.59
1:B:317:TRP:HH2	1:B:338:ILE:HG22	1.67	0.58
2:C:17:SER:OG	2:C:83:ASN:OD1	2.21	0.58
1:B:241:ARG:HD2	1:B:409:GLU:HB3	1.84	0.58
1:B:275:ARG:HG2	1:B:279:ARG:HH21	1.69	0.58
1:A:341:LEU:HD12	1:B:318:TRP:CE2	2.39	0.58
1:B:275:ARG:HG3	1:B:403:ILE:HD11	1.86	0.58
2:E:63:VAL:HG13	2:E:67:PHE:CD2	2.39	0.58
1:A:122:PRO:HG3	1:A:139:GLU:HB2	1.86	0.57
1:B:156:SER:HA	1:B:159:GLU:HG2	1.85	0.57
1:A:126:TYR:OH	1:A:254:GLU:O	2.16	0.55
2:E:38:ARG:HB2	2:E:91:ALA:HB3	1.89	0.55
2:C:34:MET:HB2	2:C:71:ARG:HD2	1.88	0.55
2:C:12:VAL:HG11	2:C:85:LEU:HD13	1.89	0.54
2:E:34:MET:HB2	2:E:71:ARG:HD2	1.89	0.54
1:A:166:ILE:HG12	1:A:167:PRO:HD2	1.89	0.54
2:E:12:VAL:O	2:E:116:VAL:HA	2.08	0.54
1:A:126:TYR:OH	1:A:178:PRO:HB3	2.07	0.54
2:E:51:ILE:HG12	2:E:57:THR:HB	1.90	0.54
1:B:227:TRP:HZ3	1:B:250:SER:HB2	1.74	0.53
1:A:268:LYS:O	1:A:275:ARG:NH1	2.42	0.52
2:C:82:MET:HE1	2:C:114:VAL:HG21	1.93	0.51
2:E:39:GLN:H	2:E:91:ALA:HB1	1.74	0.51
1:A:186:ALA:HA	1:A:245:ARG:NE	2.24	0.51
1:A:332:TRP:CE2	1:A:336:GLU:HB2	2.45	0.50
1:B:150:HIS:ND1	1:B:151:PRO:HD2	2.27	0.50
1:B:394:HIS:HA	1:B:397:ASN:HB2	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:185:GLU:HG2	1:B:227:TRP:CD1	2.47	0.50
2:E:48:VAL:HA	2:E:63:VAL:HG21	1.94	0.49
1:A:149:VAL:HG11	1:A:158:LEU:HD13	1.94	0.49
2:E:40:ALA:HB3	2:E:43:LYS:HB2	1.94	0.49
2:E:87:PRO:O	2:E:90:THR:OG1	2.25	0.49
1:B:159:GLU:HB2	1:B:180:ILE:HG12	1.95	0.48
2:E:38:ARG:NH2	2:E:62:SER:OG	2.47	0.47
1:A:291:VAL:HG11	1:A:386:PRO:HA	1.97	0.47
1:B:324:VAL:O	1:B:328:THR:OG1	2.33	0.47
1:A:140:ASP:OD1	1:A:140:ASP:N	2.47	0.46
1:A:116:LEU:HD11	1:A:145:LEU:HD23	1.98	0.46
2:E:59:TYR:CZ	2:E:69:ILE:HG22	2.50	0.46
1:B:159:GLU:HG3	1:B:160:ARG:N	2.32	0.45
2:C:64:LYS:HE3	2:C:64:LYS:HB2	1.82	0.45
1:B:400:ARG:HA	1:B:403:ILE:HG22	1.98	0.45
1:A:106:THR:HG21	1:A:269:ASP:O	2.17	0.44
1:A:113:LYS:HE3	1:A:148:LEU:HD13	2.00	0.44
1:B:391:GLN:C	1:B:393:VAL:H	2.26	0.43
2:E:6:GLU:OE2	2:E:111:GLY:N	2.45	0.43
1:B:326:PHE:CD2	2:C:54:GLY:HA3	2.53	0.43
1:B:106:THR:HG21	1:B:269:ASP:O	2.18	0.43
1:A:330:MET:HE2	1:A:330:MET:HB3	1.94	0.43
1:B:317:TRP:HZ2	1:B:339:THR:HA	1.84	0.43
1:B:159:GLU:HA	1:B:180:ILE:HD11	2.00	0.42
1:A:318:TRP:CD1	1:A:318:TRP:C	2.96	0.42
1:B:401:ARG:O	1:B:404:LYS:HG2	2.19	0.42
1:B:316:ALA:O	1:B:320:ILE:HG12	2.19	0.42
1:A:120:PHE:O	1:A:121:HIS:HB2	2.20	0.42
2:E:20:LEU:HB3	2:E:36:TRP:CH2	2.54	0.42
1:A:120:PHE:O	1:A:142:VAL:HG12	2.20	0.41
1:A:217:ARG:HG2	1:A:264:VAL:O	2.20	0.41
1:A:240:ILE:HD13	1:A:240:ILE:HA	1.86	0.41
1:B:112:LEU:HD21	1:B:270:ARG:NH1	2.37	0.40
1:B:321:VAL:O	1:B:325:THR:OG1	2.34	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	280/312 (90%)	266 (95%)	11 (4%)	3 (1%)	11	39
1	B	209/312 (67%)	202 (97%)	7 (3%)	0	100	100
2	C	115/117 (98%)	109 (95%)	5 (4%)	1 (1%)	14	44
2	E	115/117 (98%)	108 (94%)	7 (6%)	0	100	100
All	All	719/858 (84%)	685 (95%)	30 (4%)	4 (1%)	21	52

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	121	HIS
1	A	386	PRO
2	C	102	ILE
1	A	389	TRP

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	209/260 (80%)	207 (99%)	2 (1%)	68	79
1	B	181/260 (70%)	181 (100%)	0	100	100
2	C	92/92 (100%)	92 (100%)	0	100	100
2	E	92/92 (100%)	92 (100%)	0	100	100
All	All	574/704 (82%)	572 (100%)	2 (0%)	87	87

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	276[A]	MET
1	A	276[B]	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	287	GLN
2	C	32	HIS
2	E	39	GLN

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](#)

Of 1 ligands modelled in this entry, 1 is 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 ⓘ

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	285/312 (91%)	0.84	47 (16%)	4	2	15, 53, 162, 218	1 (0%)
1	B	217/312 (69%)	0.77	29 (13%)	7	4	22, 60, 123, 164	0
2	C	117/117 (100%)	0.43	8 (6%)	23	12	28, 49, 80, 111	0
2	E	117/117 (100%)	1.77	40 (34%)	1	0	76, 145, 191, 207	0
All	All	736/858 (85%)	0.90	124 (16%)	4	2	15, 62, 169, 218	1 (0%)

All (124) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	385	ASP	8.0
1	A	186	ALA	6.5
1	A	297	LEU	6.3
2	E	103	LEU	6.3
1	A	354	PHE	6.1
1	A	360	ASP	5.6
2	E	102	ILE	5.3
1	A	359	ARG	5.2
1	A	362	SER	5.0
2	E	105	HIS	5.0
1	B	256	HIS	5.0
1	A	296	ASP	4.8
2	E	17	SER	4.8
1	A	357	ILE	4.6
1	B	273	TYR	4.6
1	A	358	SER	4.4
1	A	126	TYR	4.4
2	E	117	SER	4.3
1	A	363	TYR	4.2
1	A	300	HIS	4.2
2	E	104	GLY	4.1

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Mol	Chain	Res	Type	RSRZ
2	E	118	SER	4.1
2	E	18	LEU	4.0
2	E	11	LEU	3.9
2	C	103	LEU	3.9
1	A	380	GLN	3.9
1	A	375	GLN	3.8
1	B	394	HIS	3.8
2	E	43	LYS	3.8
1	A	381	GLU	3.8
1	A	377	ALA	3.7
2	E	41	PRO	3.7
1	B	304	HIS	3.7
2	C	102	ILE	3.7
1	A	187	ASP	3.7
2	E	62	SER	3.6
2	E	57	THR	3.6
1	B	413	GLU	3.6
1	A	140	ASP	3.6
1	B	282	SER	3.6
1	B	391	GLN	3.5
1	A	379	TYR	3.5
1	B	404	LYS	3.5
1	A	378	LEU	3.4
1	A	330	MET	3.4
2	E	35	GLY	3.4
1	A	387	ALA	3.4
1	A	298	LEU	3.3
1	B	165	GLU	3.3
2	E	109	GLY	3.3
1	B	145	LEU	3.3
2	E	12	VAL	3.3
1	A	386	PRO	3.2
1	A	229	ARG	3.1
2	E	94	TYR	3.1
2	E	13	GLN	3.1
1	B	351	TYR	3.1
1	A	299	ALA	3.0
1	A	390	ASP	3.0
2	C	74	ALA	3.0
2	E	45	ARG	3.0
1	B	354	PHE	3.0
2	E	15	GLY	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	276[A]	MET	3.0
1	B	257	ALA	3.0
2	E	2	VAL	2.9
1	A	392	LEU	2.9
2	E	93	TYR	2.9
2	E	115	THR	2.9
2	E	96	ALA	2.9
1	A	122	PRO	2.8
1	A	369	VAL	2.8
1	B	226	HIS	2.7
1	A	388	LYS	2.7
2	E	26	GLY	2.7
2	C	55	THR	2.7
1	A	316	ALA	2.7
1	A	382	ARG	2.6
1	B	356	PHE	2.6
1	A	304	HIS	2.6
1	B	353	TRP	2.6
1	A	179	GLU	2.6
2	E	5	GLN	2.6
1	B	329	ASP	2.5
1	B	352	LEU	2.5
1	B	279	ARG	2.5
1	B	185	GLU	2.5
1	B	253	ILE	2.5
1	B	298	LEU	2.5
1	B	179	GLU	2.5
2	E	63	VAL	2.5
1	A	207	SER	2.5
1	A	389	TRP	2.4
2	E	61	ASN	2.4
2	C	5	GLN	2.4
2	E	16	GLY	2.3
2	E	99	LEU	2.3
1	B	280	ARG	2.3
2	E	28	ILE	2.3
2	E	56	THR	2.3
2	C	56	THR	2.3
1	B	260	LEU	2.3
1	A	376	ASN	2.3
2	E	39	GLN	2.3
1	B	308	LYS	2.3

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Mol	Chain	Res	Type	RSRZ
2	C	26	GLY	2.3
2	E	10	GLY	2.3
2	E	7	SER	2.2
2	E	110	GLN	2.2
1	A	208	ASN	2.2
1	A	405	PHE	2.2
1	A	368	ASN	2.2
2	E	68	THR	2.2
1	A	383	GLY	2.2
1	A	301	LYS	2.1
1	B	174	ARG	2.1
2	E	77	THR	2.1
1	A	185	GLU	2.1
2	C	2	VAL	2.1
2	E	108	TRP	2.1
1	B	258	GLU	2.1
2	E	25	SER	2.0
1	B	395	ASP	2.0
1	A	329	ASP	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($\text{\AA}^2$)	Q<0.9
3	CA	A	501	1/1	0.98	0.11	32,32,32,32	1

6.5 Other polymers [i](#)

There are no such residues in this entry.