



Full wwPDB X-ray Structure Validation Report ⓘ

May 24, 2020 – 10:26 am BST

PDB ID : 5M94
Title : Crystal structure of Staphylococcus capitis divalent metal ion transporter (DMT) in complex with nanobody
Authors : Dutzler, R.; Ehrnstorfer, I.A.
Deposited on : 2016-10-31
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 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	:	2.11
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)	:	2.11

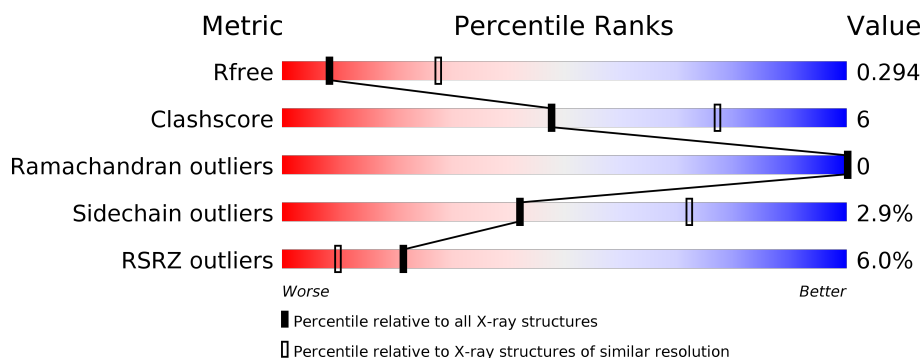
1 Overall quality at a glance

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}	130704	1094 (3.10-3.10)
Clashscore	141614	1184 (3.10-3.10)
Ramachandran outliers	138981	1141 (3.10-3.10)
Sidechain outliers	138945	1141 (3.10-3.10)
RSRZ outliers	127900	1067 (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 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	415	<div> <div>3%</div> <div> <div></div> <div>78%</div> <div>18%</div> <div>••</div> </div> </div>
1	C	415	<div> <div>8%</div> <div> <div></div> <div>80%</div> <div>15%</div> <div>••</div> </div> </div>
2	B	123	<div> <div>8%</div> <div> <div></div> <div>84%</div> <div>14%</div> <div>•</div> </div> </div>
2	D	123	<div> <div>2%</div> <div> <div></div> <div>83%</div> <div>15%</div> <div>•</div> </div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 8048 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 Divalent metal cation transporter MntH.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	401	Total	C	N	O	S	0	0	0
			3101	2060	492	537	12			
1	C	401	Total	C	N	O	S	0	0	0
			3101	2060	492	537	12			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	41	MET	-	initiating methionine	UNP A0A0S4MEX1
A	42	ALA	-	expression tag	UNP A0A0S4MEX1
A	361	SER	ALA	engineered mutation	UNP A0A0S4MEX1
A	449	ALA	-	expression tag	UNP A0A0S4MEX1
A	450	LEU	-	expression tag	UNP A0A0S4MEX1
A	451	GLU	-	expression tag	UNP A0A0S4MEX1
A	452	VAL	-	expression tag	UNP A0A0S4MEX1
A	453	LEU	-	expression tag	UNP A0A0S4MEX1
A	454	PHE	-	expression tag	UNP A0A0S4MEX1
A	455	GLN	-	expression tag	UNP A0A0S4MEX1
C	41	MET	-	initiating methionine	UNP A0A0S4MEX1
C	42	ALA	-	expression tag	UNP A0A0S4MEX1
C	361	SER	ALA	engineered mutation	UNP A0A0S4MEX1
C	449	ALA	-	expression tag	UNP A0A0S4MEX1
C	450	LEU	-	expression tag	UNP A0A0S4MEX1
C	451	GLU	-	expression tag	UNP A0A0S4MEX1
C	452	VAL	-	expression tag	UNP A0A0S4MEX1
C	453	LEU	-	expression tag	UNP A0A0S4MEX1
C	454	PHE	-	expression tag	UNP A0A0S4MEX1
C	455	GLN	-	expression tag	UNP A0A0S4MEX1

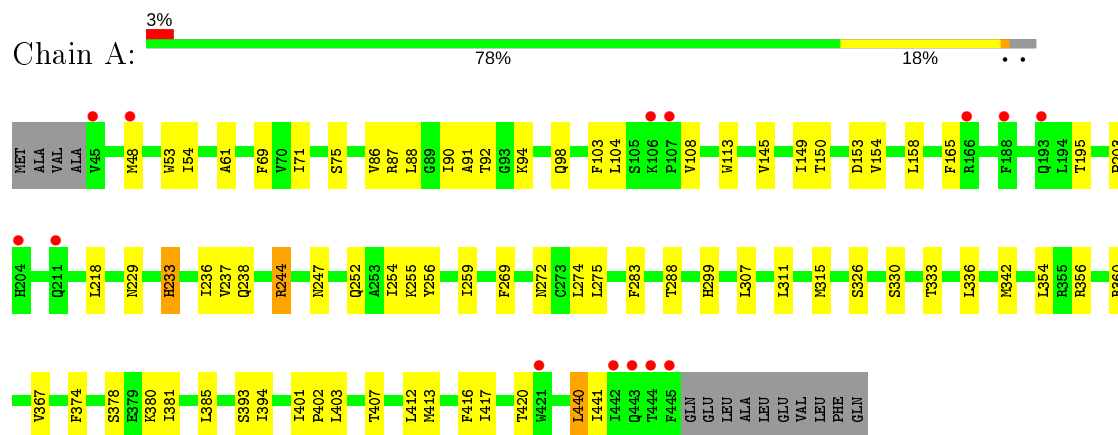
- Molecule 2 is a protein called CAMELID ANTIBODY FRAGMENT, NANOBODY.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	120	Total	C	N	O	S	0	0	0
			923	564	172	183	4			
2	D	120	Total	C	N	O	S	0	0	0
			923	564	172	183	4			

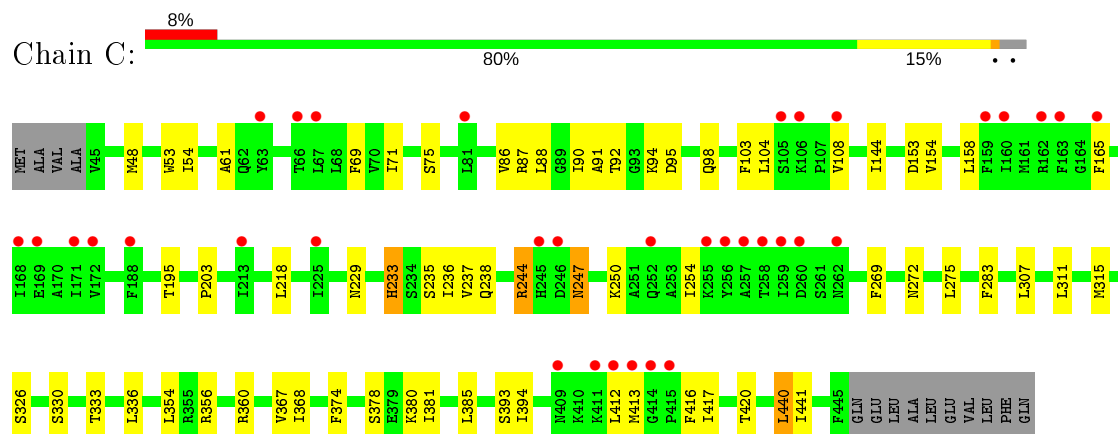
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

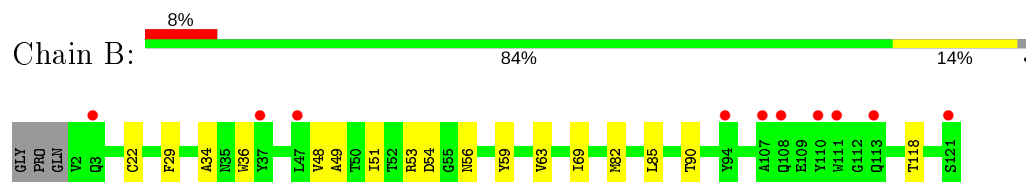
- Molecule 1: Divalent metal cation transporter MntH



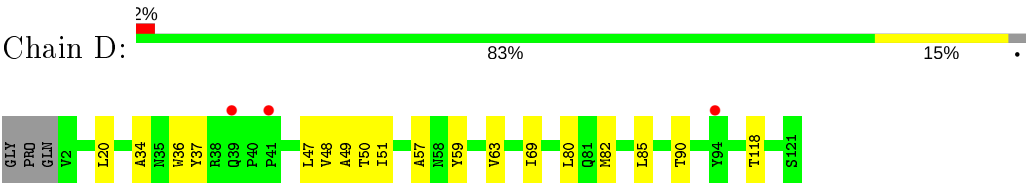
- Molecule 1: Divalent metal cation transporter MntH



- Molecule 2: CAMELID ANTIBODY FRAGMENT, NANOBODY



- Molecule 2: CAMELID ANTIBODY FRAGMENT, NANOBODY



4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	114.35Å 114.35Å 257.87Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	19.93 – 3.10 46.22 – 3.10	Depositor EDS
% Data completeness (in resolution range)	99.4 (19.93-3.10) 99.4 (46.22-3.10)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.73 (at 3.12Å)	Xtriage
Refinement program	PHENIX (1.10_2155: ???)	Depositor
R, R_{free}	0.237 , 0.273 0.250 , 0.294	Depositor DCC
R_{free} test set	1784 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	118.3	Xtriage
Anisotropy	0.081	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 89.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.026 for -h,-k,l	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	8048	wwPDB-VP
Average B, all atoms (Å ²)	131.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.55% 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](#)

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	0.26	0/3164	0.41	0/4306
1	C	0.26	0/3164	0.41	0/4306
2	B	0.25	0/937	0.46	0/1268
2	D	0.25	0/937	0.46	0/1268
All	All	0.26	0/8202	0.42	0/11148

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	3101	0	3279	43	0
1	C	3101	0	3279	38	0
2	B	923	0	897	12	0
2	D	923	0	897	10	0
All	All	8048	0	8352	100	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 (100) 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:A:94:LYS:HD3	1:A:238:GLN:HE22	1.51	0.73
1:C:94:LYS:HD3	1:C:238:GLN:HE22	1.54	0.73
1:C:154:VAL:HG22	1:C:356:ARG:HE	1.57	0.69
2:D:20:LEU:HD12	2:D:80:LEU:HD23	1.78	0.66
1:A:154:VAL:HG22	1:A:356:ARG:HE	1.60	0.64
2:D:82:MET:HB3	2:D:85:LEU:HD21	1.79	0.64
2:D:90:THR:HG23	2:D:118:THR:HA	1.80	0.63
1:A:413:MET:HB3	1:A:416:PHE:O	1.99	0.62
1:A:54:ILE:HG21	1:A:385:LEU:HG	1.82	0.62
1:C:218:LEU:O	1:C:393:SER:OG	2.17	0.61
1:A:354:LEU:HD11	1:C:354:LEU:HD11	1.82	0.61
2:D:48:VAL:HG13	2:D:63:VAL:HG21	1.83	0.61
1:C:54:ILE:HG21	1:C:385:LEU:HG	1.81	0.61
2:D:36:TRP:HB2	2:D:49:ALA:HB3	1.83	0.61
1:A:218:LEU:O	1:A:393:SER:OG	2.16	0.60
1:C:413:MET:HB3	1:C:416:PHE:O	2.02	0.60
1:C:86:VAL:HG13	1:C:237:VAL:HG21	1.84	0.60
2:B:48:VAL:HG13	2:B:63:VAL:HG21	1.83	0.59
2:B:36:TRP:HB2	2:B:49:ALA:HB3	1.84	0.58
1:A:87:ARG:HG2	1:A:254:ILE:HD13	1.86	0.58
1:A:367:VAL:HG13	1:A:381:ILE:HD11	1.85	0.58
2:B:82:MET:HB3	2:B:85:LEU:HD21	1.87	0.57
1:C:104:LEU:HB3	1:C:108:VAL:HG23	1.87	0.57
1:A:90:ILE:HD12	1:A:254:ILE:HG12	1.86	0.57
1:C:87:ARG:HG2	1:C:254:ILE:HD13	1.84	0.57
1:A:86:VAL:HG13	1:A:237:VAL:HG21	1.85	0.57
2:D:20:LEU:HB2	2:D:80:LEU:HB3	1.88	0.55
1:C:88:LEU:O	1:C:92:THR:OG1	2.22	0.55
2:B:59:TYR:HE1	2:B:69:ILE:H	1.54	0.55
1:A:233:HIS:HA	1:A:236:ILE:HG22	1.89	0.55
1:A:104:LEU:HB3	1:A:108:VAL:HG23	1.89	0.55
1:C:233:HIS:HA	1:C:236:ILE:HG22	1.89	0.55
1:A:394:ILE:HD12	1:A:441:ILE:HD11	1.88	0.54
1:A:88:LEU:O	1:A:92:THR:OG1	2.22	0.54
2:B:90:THR:HG23	2:B:118:THR:HA	1.89	0.53
1:A:307:LEU:HD21	1:A:315:MET:HG3	1.91	0.52
1:A:94:LYS:HB3	1:A:98:GLN:OE1	2.09	0.52
1:A:48:MET:O	1:A:326:SER:HB2	2.10	0.51
1:C:48:MET:O	1:C:326:SER:HB2	2.10	0.51
1:C:90:ILE:HD12	1:C:254:ILE:HG12	1.91	0.51
1:C:394:ILE:HD12	1:C:441:ILE:HD11	1.92	0.51
1:A:61:ALA:HB1	1:A:283:PHE:HB2	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:69:PHE:CE1	1:A:203:PRO:HG3	2.47	0.50
1:C:71:ILE:HD13	1:C:272:ASN:HB3	1.93	0.49
1:C:94:LYS:HB3	1:C:98:GLN:OE1	2.12	0.49
1:C:218:LEU:HD12	1:C:440:LEU:HD13	1.95	0.49
1:C:61:ALA:HB1	1:C:283:PHE:HB2	1.95	0.48
1:A:71:ILE:HD13	1:A:272:ASN:HB3	1.96	0.48
1:A:288:THR:HB	2:B:53:ARG:HH12	1.79	0.47
1:A:145:VAL:O	1:A:149:ILE:HG13	2.14	0.47
1:A:311:LEU:O	1:A:315:MET:HG2	2.14	0.47
1:A:153:ASP:N	1:A:153:ASP:OD1	2.47	0.47
1:A:374:PHE:CD1	1:A:380:LYS:HG2	2.50	0.47
1:A:374:PHE:CG	1:A:380:LYS:HG2	2.50	0.47
1:C:53:TRP:HA	1:C:275:LEU:HD13	1.97	0.46
1:C:69:PHE:CE1	1:C:203:PRO:HG3	2.51	0.46
1:C:229:ASN:O	1:C:233:HIS:HB2	2.15	0.46
2:D:34:ALA:HB3	2:D:51:ILE:HG22	1.98	0.46
1:C:311:LEU:O	1:C:315:MET:HG2	2.16	0.46
1:A:113:TRP:HE1	1:A:342:MET:HA	1.82	0.45
1:A:229:ASN:O	1:A:233:HIS:HB2	2.16	0.45
1:C:307:LEU:HD21	1:C:315:MET:HG3	1.98	0.45
1:A:299:HIS:HB3	2:B:29:PHE:HA	1.99	0.44
1:C:374:PHE:CG	1:C:380:LYS:HG2	2.53	0.44
2:B:54:ASP:OD2	2:B:56:ASN:ND2	2.30	0.44
1:A:75:SER:OG	1:A:269:PHE:HB2	2.17	0.44
1:A:53:TRP:HA	1:A:275:LEU:HD13	2.00	0.44
1:A:378:SER:O	1:A:381:ILE:HG22	2.18	0.43
1:C:367:VAL:HG13	1:C:381:ILE:HD11	1.99	0.43
1:C:95:ASP:HB3	1:C:235:SER:HB2	2.00	0.43
1:C:94:LYS:HA	1:C:94:LYS:HD3	1.80	0.43
1:C:153:ASP:N	1:C:153:ASP:OD1	2.51	0.42
1:C:144:ILE:HD11	1:C:368:ILE:HG23	2.01	0.42
2:B:59:TYR:HB3	2:B:63:VAL:HG23	2.02	0.42
1:C:103:PHE:CZ	1:C:412:LEU:HD11	2.54	0.42
1:C:378:SER:O	1:C:381:ILE:HG22	2.19	0.42
2:B:59:TYR:CE1	2:B:69:ILE:HG22	2.54	0.42
2:D:37:TYR:CZ	2:D:47:LEU:HD23	2.54	0.42
1:A:255:LYS:O	1:A:259:ILE:HG12	2.19	0.42
1:C:381:ILE:HD12	1:C:381:ILE:HA	1.95	0.42
1:A:91:ALA:O	1:A:244:ARG:NH1	2.53	0.42
1:A:403:LEU:O	1:A:407:THR:OG1	2.19	0.41
1:C:90:ILE:HD11	1:C:237:VAL:HG22	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:218:LEU:HD12	1:A:440:LEU:HD13	2.01	0.41
1:A:150:THR:O	1:A:360:ARG:NH1	2.49	0.41
1:C:75:SER:OG	1:C:269:PHE:HB2	2.21	0.41
1:C:247:ASN:O	1:C:250:LYS:HB2	2.20	0.41
1:A:252:GLN:HG2	1:A:256:TYR:CE2	2.56	0.41
1:A:103:PHE:CZ	1:A:412:LEU:HD11	2.56	0.41
1:A:90:ILE:HD11	1:A:237:VAL:HG22	2.02	0.41
1:A:244:ARG:O	1:A:244:ARG:HD2	2.21	0.41
2:B:34:ALA:HB3	2:B:51:ILE:HG22	2.01	0.41
1:C:103:PHE:HZ	1:C:412:LEU:HD11	1.85	0.41
1:C:153:ASP:OD2	1:C:360:ARG:NH1	2.46	0.41
2:D:59:TYR:HE1	2:D:69:ILE:H	1.69	0.41
1:A:103:PHE:HZ	1:A:412:LEU:HD11	1.87	0.40
1:C:91:ALA:O	1:C:244:ARG:NH1	2.54	0.40
1:A:401:ILE:HB	1:A:402:PRO:HD3	2.03	0.40
2:B:22:CYS:HB2	2:B:36:TRP:CZ2	2.57	0.40
2:D:50:THR:O	2:D:57:ALA:HA	2.20	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	399/415 (96%)	389 (98%)	10 (2%)	0	100	100
1	C	399/415 (96%)	388 (97%)	11 (3%)	0	100	100
2	B	118/123 (96%)	117 (99%)	1 (1%)	0	100	100
2	D	118/123 (96%)	118 (100%)	0	0	100	100
All	All	1034/1076 (96%)	1012 (98%)	22 (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	339/350 (97%)	326 (96%)	13 (4%)	33	66
1	C	339/350 (97%)	327 (96%)	12 (4%)	36	68
2	B	98/100 (98%)	98 (100%)	0	100	100
2	D	98/100 (98%)	98 (100%)	0	100	100
All	All	874/900 (97%)	849 (97%)	25 (3%)	42	72

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	158	LEU
1	A	165	PHE
1	A	195	THR
1	A	233	HIS
1	A	244	ARG
1	A	247	ASN
1	A	274	LEU
1	A	330	SER
1	A	333	THR
1	A	336	LEU
1	A	417	ILE
1	A	420	THR
1	A	440	LEU
1	C	158	LEU
1	C	165	PHE
1	C	195	THR
1	C	233	HIS
1	C	244	ARG
1	C	247	ASN
1	C	330	SER
1	C	333	THR
1	C	336	LEU
1	C	417	ILE
1	C	420	THR
1	C	440	LEU

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

Mol	Chain	Res	Type
1	A	238	GLN
1	C	238	GLN
2	D	13	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 carbohydrates 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	401/415 (96%)	-0.03	14 (3%) 44 23	63, 113, 166, 226	0
1	C	401/415 (96%)	0.17	35 (8%) 10 4	75, 147, 219, 277	0
2	B	120/123 (97%)	0.21	10 (8%) 11 4	83, 114, 157, 195	0
2	D	120/123 (97%)	-0.19	3 (2%) 57 34	88, 115, 156, 200	0
All	All	1042/1076 (96%)	0.06	62 (5%) 21 10	63, 121, 198, 277	0

All (62) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	415	PRO	7.3
1	C	414	GLY	6.2
1	C	259	ILE	6.0
1	C	168	ILE	5.1
1	A	421	TRP	4.7
1	C	245	HIS	4.7
1	A	442	ILE	4.7
1	C	262	ASN	4.5
1	A	443	GLN	4.5
1	C	188	PHE	4.3
1	A	188	PHE	4.1
1	C	169	GLU	3.9
1	A	211	GLN	3.8
1	C	213	ILE	3.8
1	C	108	VAL	3.7
2	B	108	GLN	3.7
1	C	106	LYS	3.6
1	A	106	LYS	3.4
1	A	45	VAL	3.4
1	C	255	LYS	3.3
1	C	256	TYR	3.3

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Mol	Chain	Res	Type	RSRZ
2	B	121	SER	3.3
2	B	37	TYR	3.3
1	C	411	LYS	3.3
1	C	159	PHE	3.3
1	A	444	THR	3.2
1	A	204	HIS	3.2
2	D	94	TYR	3.0
1	C	172	VAL	3.0
2	B	111	TRP	2.9
1	C	258	THR	2.9
1	C	246	ASP	2.8
1	C	81	LEU	2.8
1	A	48	MET	2.7
2	B	107	ALA	2.7
1	A	193	GLN	2.7
2	B	3	GLN	2.7
1	C	67	LEU	2.6
1	C	66	THR	2.6
1	C	105	SER	2.6
1	C	413	MET	2.5
2	B	47	LEU	2.4
2	D	39	GLN	2.4
1	C	171	ILE	2.3
1	A	166	ARG	2.3
1	A	445	PHE	2.3
1	C	252	GLN	2.3
2	B	113	GLN	2.3
2	B	94	TYR	2.3
1	C	165	PHE	2.3
1	C	63	TYR	2.2
1	C	163	PHE	2.2
1	C	160	ILE	2.2
1	C	412	LEU	2.2
1	C	225	ILE	2.2
1	A	107	PRO	2.2
1	C	260	ASP	2.2
2	D	41	PRO	2.2
1	C	162	ARG	2.2
2	B	110	TYR	2.1
1	C	257	ALA	2.1
1	C	409	ASN	2.1

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 carbohydrates 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.