



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 10:00 PM GMT

PDB ID : 4WGW
Title : Staphylococcus capitis divalent metal ion transporter (DMT) in complex with manganese
Authors : Ehrnstorfer, I.A.; Geertsma, E.R.; Pardon, E.; Steyaert, J.; Dutzler, R.
Deposited on : 2014-09-19
Resolution : 3.40 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
<http://wwpdb.org/validation/2016/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
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

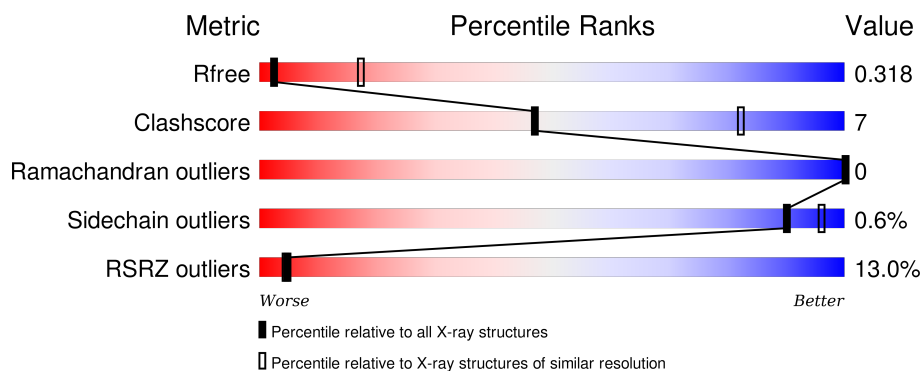
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.40 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}	91344	1476 (3.50-3.30)
Clashscore	102246	1611 (3.50-3.30)
Ramachandran outliers	100387	1571 (3.50-3.30)
Sidechain outliers	100360	1571 (3.50-3.30)
RSRZ outliers	91569	1485 (3.50-3.30)

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. 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>6%</div> <div>76%</div> <div>19%</div> <div>5%</div> </div>
1	C	415	<div> <div>16%</div> <div>75%</div> <div>20%</div> <div>5%</div> </div>
2	B	124	<div> <div>23%</div> <div>88%</div> <div>9%</div> <div>•</div> </div>
2	D	124	<div> <div>14%</div> <div>85%</div> <div>11%</div> <div>•</div> </div>

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	MN	C	501	-	-	-	X

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7948 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	395	Total	C	N	O	S	0	0	0
			3050	2024	485	529	12			
1	C	395	Total	C	N	O	S	0	0	0
			3050	2024	485	529	12			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	41	MET	-	initiating methionine	UNP F9L8R0
A	42	SER	-	expression tag	UNP F9L8R0
A	449	ALA	-	expression tag	UNP F9L8R0
A	450	LEU	-	expression tag	UNP F9L8R0
A	451	GLU	-	expression tag	UNP F9L8R0
A	452	VAL	-	expression tag	UNP F9L8R0
A	453	LEU	-	expression tag	UNP F9L8R0
A	454	PHE	-	expression tag	UNP F9L8R0
A	455	GLN	-	expression tag	UNP F9L8R0
C	41	MET	-	initiating methionine	UNP F9L8R0
C	42	SER	-	expression tag	UNP F9L8R0
C	449	ALA	-	expression tag	UNP F9L8R0
C	450	LEU	-	expression tag	UNP F9L8R0
C	451	GLU	-	expression tag	UNP F9L8R0
C	452	VAL	-	expression tag	UNP F9L8R0
C	453	LEU	-	expression tag	UNP F9L8R0
C	454	PHE	-	expression tag	UNP F9L8R0
C	455	GLN	-	expression tag	UNP F9L8R0

- 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			

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

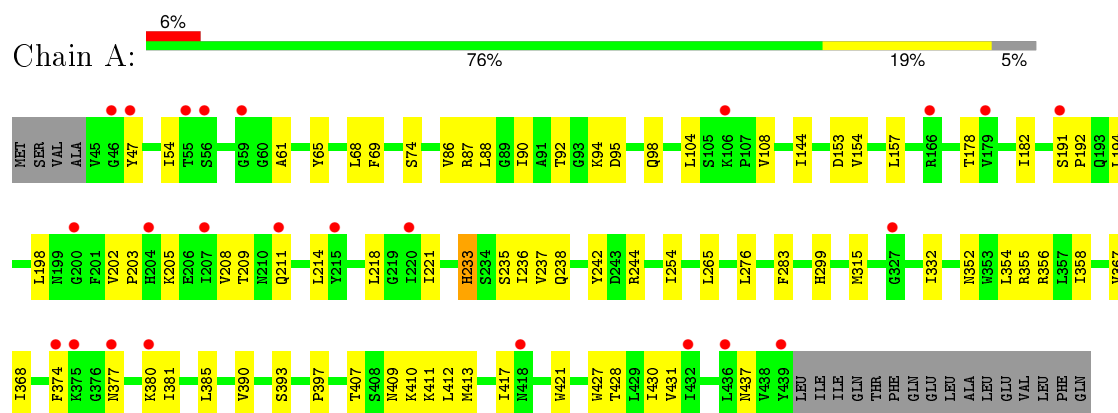
- Molecule 3 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Mn	0	0
			1	1		
3	C	1	Total	Mn	0	0
			1	1		

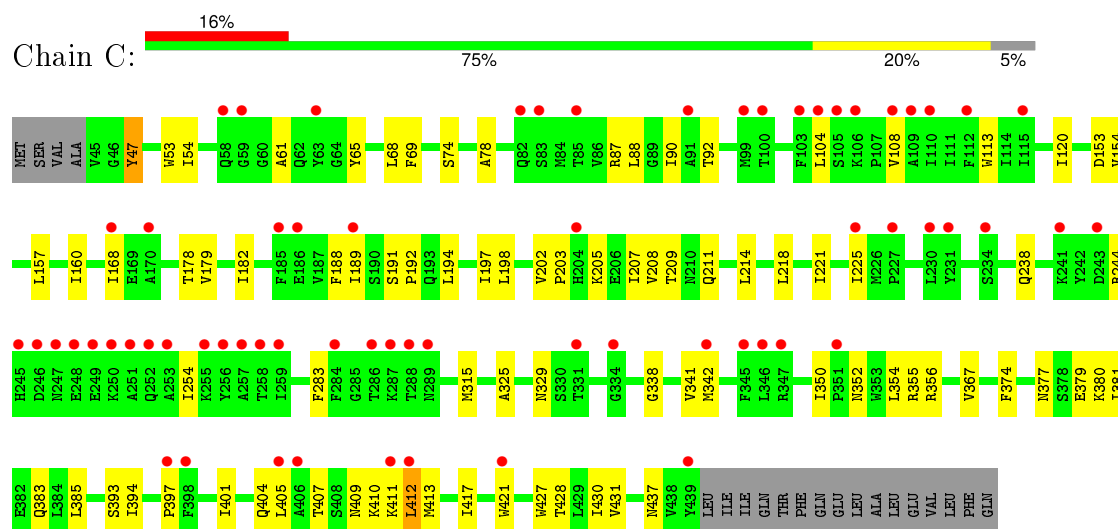
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

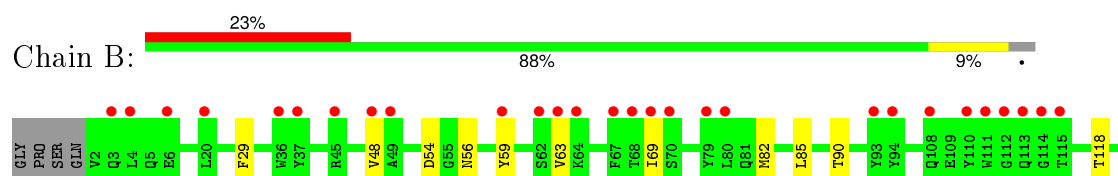
• Molecule 1: Divalent metal cation transporter MntH



• Molecule 1: Divalent metal cation transporter MntH



• Molecule 2: Camelid antibody fragment, nanobody



	Gly	Phe	Ser	Gln	V2	Q5 E6	L11	S17	L20	N35 V36	R38	Q39	P40 P41	L47 V48	A49	V63	L80 D81	M82	L85	T90	G91 Y92	Y93	Y94	C95	I96	S106 A107	Q108	H111 G112	Q113	G114	T115	T118	S121
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4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	114.17Å 114.17Å 257.53Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	19.90 – 3.40 49.44 – 3.40	Depositor EDS
% Data completeness (in resolution range)	100.0 (19.90-3.40) 100.0 (49.44-3.40)	Depositor EDS
R_{merge}	8.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.06 (at 3.40Å)	Xtriage
Refinement program	PHENIX (phenix.refine: dev_1760)	Depositor
R, R_{free}	0.252 , 0.292 0.270 , 0.318	Depositor DCC
R_{free} test set	1342 reflections (4.88%)	DCC
Wilson B-factor (Å ²)	138.0	Xtriage
Anisotropy	0.080	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 99.4	EDS
Estimated twinning fraction	0.029 for -h,-k,l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 27510 reflections	Xtriage
F_o, F_c correlation	0.85	EDS
Total number of atoms	7948	wwPDB-VP
Average B, all atoms (Å ²)	152.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.47% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: MN

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	0.22	0/3112	0.41	0/4235
1	C	0.24	0/3112	0.44	0/4235
2	B	0.21	0/937	0.37	0/1268
2	D	0.20	0/937	0.37	0/1268
All	All	0.23	0/8098	0.42	0/11006

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

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	3050	0	3222	52	0
1	C	3050	0	3222	58	0
2	B	923	0	897	6	0
2	D	923	0	897	8	0
3	A	1	0	0	0	0
3	C	1	0	0	0	0
All	All	7948	0	8238	121	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 7.

All (121) 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	1.49	0.78
1:C:238:GLN:O	1:C:244:ARG:NH2	2.18	0.77
1:C:417:ILE:HG22	1:C:421:TRP:CD1	2.24	0.72
1:C:205:LYS:O	1:C:209:THR:OG1	2.07	0.72
1:C:188:PHE:O	1:C:189:ILE:HG13	1.94	0.66
1:C:104:LEU:HB3	1:C:108:VAL:HG13	1.78	0.65
1:C:160:ILE:HD11	1:C:168:ILE:HG12	1.77	0.65
1:A:354:LEU:HD11	1:C:354:LEU:HD11	1.79	0.65
1:C:208:VAL:HA	1:C:214:LEU:HD13	1.79	0.64
2:B:48:VAL:HG13	2:B:63:VAL:HG21	1.78	0.64
2:D:48:VAL:HG13	2:D:63:VAL:HG21	1.80	0.64
1:A:238:GLN:O	1:A:244:ARG:NH2	2.31	0.63
1:A:54:ILE:HG21	1:A:385:LEU:HG	1.80	0.62
1:A:157:LEU:HD11	1:A:332:ILE:HD11	1.81	0.61
2:B:90:THR:HG23	2:B:118:THR:HA	1.82	0.61
1:C:211:GLN:NE2	1:C:437:ASN:OD1	2.34	0.60
1:A:211:GLN:NE2	1:A:437:ASN:OD1	2.34	0.60
1:C:74:SER:HB3	1:C:221:ILE:HG12	1.84	0.59
1:C:54:ILE:HG21	1:C:385:LEU:HG	1.84	0.59
2:D:90:THR:HG23	2:D:118:THR:HA	1.85	0.57
2:D:20:LEU:HD12	2:D:80:LEU:HD23	1.85	0.57
1:C:154:VAL:HG13	1:C:356:ARG:HE	1.69	0.57
1:C:342:MET:HE1	1:C:355:ARG:HE	1.69	0.57
1:A:74:SER:HB3	1:A:221:ILE:HG12	1.87	0.57
1:C:417:ILE:HG22	1:C:421:TRP:HD1	1.69	0.56
1:A:104:LEU:HB3	1:A:108:VAL:HG23	1.88	0.56
1:A:90:ILE:HD12	1:A:254:ILE:HG12	1.88	0.56
2:B:82:MET:HB3	2:B:85:LEU:HD21	1.88	0.56
1:A:208:VAL:HA	1:A:214:LEU:HD13	1.87	0.55
1:C:411:LYS:O	1:C:413:MET:HG2	2.07	0.55
1:A:407:THR:O	1:A:413:MET:HB3	2.06	0.55
1:A:409:ASN:O	1:A:410:LYS:NZ	2.39	0.55
1:A:411:LYS:O	1:A:413:MET:HG2	2.07	0.55
1:C:407:THR:O	1:C:413:MET:HB3	2.06	0.55
1:C:409:ASN:O	1:C:410:LYS:NZ	2.39	0.54
1:C:214:LEU:HD11	1:C:430:ILE:HG23	1.88	0.54
1:C:207:ILE:HG13	1:C:208:VAL:HG23	1.90	0.53
1:A:154:VAL:HG13	1:A:356:ARG:HE	1.72	0.52
1:A:205:LYS:O	1:A:209:THR:OG1	2.19	0.52
2:B:59:TYR:HE1	2:B:69:ILE:H	1.57	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:87:ARG:HG2	1:C:254:ILE:HD13	1.91	0.52
1:A:198:LEU:HD22	1:A:203:PRO:HG3	1.92	0.51
1:C:352:ASN:OD1	1:C:355:ARG:NH1	2.44	0.51
1:A:88:LEU:O	1:A:92:THR:OG1	2.25	0.51
1:C:88:LEU:O	1:C:92:THR:OG1	2.24	0.51
2:D:82:MET:HB3	2:D:85:LEU:HD21	1.93	0.51
1:A:218:LEU:O	1:A:393:SER:OG	2.29	0.50
1:C:153:ASP:OD1	1:C:154:VAL:N	2.45	0.50
1:C:61:ALA:HB1	1:C:283:PHE:HB2	1.94	0.49
1:A:428:THR:HA	1:A:431:VAL:HG22	1.95	0.49
2:D:35:ASN:HB2	2:D:96:ASN:HB3	1.94	0.49
2:D:35:ASN:N	2:D:96:ASN:O	2.35	0.49
1:A:354:LEU:HD21	1:C:354:LEU:HD21	1.95	0.48
1:C:218:LEU:O	1:C:393:SER:OG	2.31	0.48
1:A:367:VAL:HG13	1:A:381:ILE:HD11	1.95	0.47
2:B:54:ASP:OD1	2:B:56:ASN:ND2	2.25	0.47
1:A:87:ARG:HH12	1:A:407:THR:HG23	1.80	0.46
1:A:417:ILE:HG22	1:A:421:TRP:CD1	2.49	0.46
1:A:182:ILE:HD13	1:A:315:MET:HB3	1.97	0.46
1:C:350:ILE:O	1:C:355:ARG:NH2	2.48	0.46
1:A:374:PHE:CG	1:A:380:LYS:HG2	2.51	0.46
1:A:61:ALA:HB1	1:A:283:PHE:HB2	1.96	0.46
1:A:214:LEU:HD11	1:A:430:ILE:HG23	1.96	0.46
1:A:95:ASP:HB3	1:A:235:SER:HB2	1.98	0.46
1:A:377:ASN:HB3	1:A:380:LYS:HB2	1.97	0.46
1:A:153:ASP:OD1	1:A:154:VAL:N	2.48	0.46
1:A:191:SER:HB2	1:A:194:LEU:HB2	1.97	0.46
1:C:404:GLN:NE2	1:C:417:ILE:HG23	2.31	0.45
2:D:36:TRP:HB2	2:D:49:ALA:HB3	1.97	0.45
1:A:191:SER:HA	1:A:192:PRO:HD3	1.82	0.44
1:C:428:THR:HA	1:C:431:VAL:HG22	1.99	0.44
1:A:68:LEU:HG	1:A:276:LEU:HD22	1.98	0.44
1:C:154:VAL:HG22	1:C:356:ARG:HE	1.82	0.44
1:C:120:ILE:HD13	1:C:338:GLY:HA2	1.98	0.44
1:C:47:TYR:O	1:C:53:TRP:NE1	2.45	0.44
1:A:397:PRO:HG3	1:A:427:TRP:HD1	1.83	0.44
1:C:367:VAL:HG13	1:C:381:ILE:HD11	1.99	0.44
1:C:182:ILE:HD13	1:C:315:MET:HB3	1.99	0.43
1:A:299:HIS:HB3	2:B:29:PHE:HA	2.00	0.43
1:C:377:ASN:HB3	1:C:380:LYS:HB2	2.00	0.43
1:C:397:PRO:HG3	1:C:427:TRP:HD1	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:401:ILE:O	1:C:405:LEU:HD13	2.19	0.43
1:C:78:ALA:HB2	1:C:225:ILE:HG12	2.00	0.43
1:A:244:ARG:HD3	1:A:244:ARG:HA	1.75	0.43
1:C:90:ILE:HD12	1:C:254:ILE:HG12	2.01	0.43
1:A:233:HIS:HA	1:A:236:ILE:HG22	2.00	0.43
1:A:242:TYR:O	1:A:244:ARG:NH1	2.52	0.43
1:C:178:THR:O	1:C:182:ILE:HG13	2.19	0.42
1:A:69:PHE:CD1	1:A:202:VAL:HB	2.54	0.42
2:D:37:TYR:CZ	2:D:47:LEU:HD23	2.54	0.42
1:C:69:PHE:CD1	1:C:202:VAL:HB	2.55	0.42
1:C:157:LEU:O	1:C:160:ILE:HG22	2.18	0.42
1:A:352:ASN:HA	1:A:355:ARG:HG2	2.02	0.42
1:C:194:LEU:HA	1:C:194:LEU:HD23	1.94	0.42
1:A:86:VAL:HG13	1:A:237:VAL:HG21	2.02	0.42
1:C:203:PRO:O	1:C:205:LYS:N	2.53	0.42
1:C:197:ILE:HG23	1:C:198:LEU:HG	2.00	0.42
1:C:325:ALA:O	1:C:329:ASN:ND2	2.53	0.42
1:C:188:PHE:C	1:C:189:ILE:HG13	2.40	0.42
1:A:410:LYS:HA	1:A:410:LYS:NZ	2.35	0.42
1:C:120:ILE:HD11	1:C:341:VAL:HG21	2.01	0.41
1:C:394:ILE:HD13	1:C:431:VAL:HB	2.02	0.41
1:C:410:LYS:HA	1:C:410:LYS:NZ	2.35	0.41
1:C:374:PHE:CG	1:C:380:LYS:HG2	2.55	0.41
1:A:178:THR:O	1:A:182:ILE:HG13	2.21	0.41
1:C:113:TRP:CD1	1:C:341:VAL:HG12	2.56	0.41
1:C:379:GLU:O	1:C:383:GLN:HG3	2.21	0.41
1:A:144:ILE:HD11	1:A:368:ILE:HG23	2.02	0.41
1:A:393:SER:HA	1:A:427:TRP:HZ2	1.85	0.41
1:A:98:GLN:H	1:A:98:GLN:HG2	1.62	0.41
1:C:179:VAL:HA	1:C:182:ILE:HD12	2.03	0.41
1:C:65:TYR:HB3	1:C:68:LEU:HD12	2.03	0.41
1:C:191:SER:HA	1:C:192:PRO:HD3	1.81	0.41
1:C:254:ILE:CD1	1:C:412:LEU:HD21	2.51	0.41
1:A:390:VAL:O	1:A:393:SER:HB2	2.21	0.41
1:C:244:ARG:HA	1:C:244:ARG:HD3	1.71	0.41
1:A:65:TYR:HB3	1:A:68:LEU:HD12	2.03	0.40
1:A:94:LYS:HB3	1:A:95:ASP:H	1.78	0.40
1:A:87:ARG:HG2	1:A:254:ILE:HD13	2.02	0.40
1:A:355:ARG:HA	1:A:358:ILE:HD12	2.02	0.40
1:A:265:LEU:HA	1:A:265:LEU:HD23	1.95	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	393/415 (95%)	372 (95%)	21 (5%)	0	100	100
1	C	393/415 (95%)	368 (94%)	25 (6%)	0	100	100
2	B	118/124 (95%)	118 (100%)	0	0	100	100
2	D	118/124 (95%)	118 (100%)	0	0	100	100
All	All	1022/1078 (95%)	976 (96%)	46 (4%)	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	333/351 (95%)	330 (99%)	3 (1%)	84	94
1	C	333/351 (95%)	331 (99%)	2 (1%)	90	96
2	B	98/101 (97%)	98 (100%)	0	100	100
2	D	98/101 (97%)	98 (100%)	0	100	100
All	All	862/904 (95%)	857 (99%)	5 (1%)	90	96

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	47	TYR
1	A	233	HIS

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Mol	Chain	Res	Type
1	A	412	LEU
1	C	47	TYR
1	C	412	LEU

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

Mol	Chain	Res	Type
1	A	238	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](#)

Of 2 ligands modelled in this entry, 2 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

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	395/415 (95%)	0.37	24 (6%) 25 23	86, 133, 206, 279	0
1	C	395/415 (95%)	0.93	65 (16%) 2 2	85, 166, 255, 339	0
2	B	120/124 (96%)	1.16	28 (23%) 1 1	94, 132, 173, 179	0
2	D	120/124 (96%)	0.52	17 (14%) 4 3	98, 131, 177, 213	0
All	All	1030/1078 (95%)	0.70	134 (13%) 5 4	85, 140, 231, 339	0

All (134) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	246	ASP	16.5
1	C	412	LEU	9.3
1	A	204	HIS	9.2
1	C	247	ASN	8.0
1	C	252	GLN	7.5
1	C	411	LYS	7.4
1	C	103	PHE	6.8
1	C	248	GLU	5.6
2	B	111	TRP	5.5
1	C	245	HIS	5.3
1	C	256	TYR	4.8
1	C	259	ILE	4.7
1	C	63	TYR	4.5
1	C	112	PHE	4.5
2	B	36	TRP	4.5
2	B	48	VAL	4.4
2	D	106	SER	4.4
2	B	113	GLN	4.4
1	C	289	ASN	4.3
1	C	231	TYR	4.3
1	C	82	GLN	4.3

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Mol	Chain	Res	Type	RSRZ
2	B	79	TYR	4.1
1	A	418	ASN	4.1
2	D	114	GLY	4.0
1	C	189	ILE	3.8
1	C	186	GLU	3.8
1	A	377	ASN	3.8
2	B	62	SER	3.7
1	C	91	ALA	3.7
1	C	406	ALA	3.7
1	C	250	LYS	3.6
1	A	439	TYR	3.6
2	B	67	PHE	3.6
1	A	55	THR	3.6
1	C	255	LYS	3.5
1	C	204	HIS	3.5
1	C	59	GLY	3.5
2	D	92	VAL	3.5
1	C	243	ASP	3.5
1	C	288	THR	3.5
1	C	345	PHE	3.4
2	B	70	SER	3.4
1	C	104	LEU	3.4
2	D	94	TYR	3.4
2	B	20	LEU	3.3
2	B	93	TYR	3.3
1	A	200	GLY	3.3
1	C	227	PRO	3.3
1	A	106	LYS	3.3
2	D	113	GLN	3.3
2	B	94	TYR	3.3
1	A	56	SER	3.2
1	A	374	PHE	3.2
1	C	110	ILE	3.2
2	B	69	ILE	3.2
2	B	115	THR	3.2
1	A	179	VAL	3.1
1	A	207	ILE	3.1
1	A	215	TYR	3.1
1	A	375	LYS	3.1
2	B	59	TYR	3.1
2	B	108	GLN	3.1
1	C	439	TYR	3.1

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Mol	Chain	Res	Type	RSRZ
2	B	63	VAL	3.0
2	D	111	TRP	3.0
1	C	108	VAL	3.0
1	C	251	ALA	3.0
1	C	334	GLY	3.0
2	D	108	GLN	3.0
1	C	253	ALA	2.9
2	D	115	THR	2.9
2	D	11	LEU	2.9
1	C	106	LYS	2.9
2	B	64	LYS	2.8
2	D	41	PRO	2.8
1	C	105	SER	2.8
2	B	112	GLY	2.7
2	B	80	LEU	2.7
2	D	39	GLN	2.7
1	C	258	THR	2.7
2	D	6	GLU	2.7
2	B	68	THR	2.7
1	C	83	SER	2.7
1	C	100	THR	2.7
1	A	191	SER	2.6
1	C	99	MET	2.6
1	C	170	ALA	2.6
1	C	351	PRO	2.6
1	C	230	LEU	2.6
1	A	380	LYS	2.6
1	C	241	LYS	2.6
1	C	286	THR	2.6
1	A	166	ARG	2.6
1	C	287	LYS	2.6
2	D	107	ALA	2.5
2	D	95	CYS	2.5
1	A	211	GLN	2.5
1	A	436	LEU	2.5
2	B	49	ALA	2.5
2	B	37	TYR	2.4
1	C	234	SER	2.4
1	C	58	GLN	2.4
2	D	17	SER	2.4
1	C	405	LEU	2.4
1	A	59	GLY	2.4

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Mol	Chain	Res	Type	RSRZ
2	B	6	GLU	2.4
1	C	115	ILE	2.4
2	D	5	GLN	2.4
1	C	398	PHE	2.3
1	C	284	PHE	2.3
1	C	346	LEU	2.3
1	A	46	GLY	2.3
1	C	109	ALA	2.3
1	A	432	ILE	2.3
2	B	3	GLN	2.3
2	B	114	GLY	2.3
1	C	249	GLU	2.3
2	B	45	ARG	2.3
1	A	327	GLY	2.2
1	C	397	PRO	2.2
2	B	4	LEU	2.2
1	C	257	ALA	2.2
1	C	421	TRP	2.2
1	A	47	TYR	2.2
1	C	185	PHE	2.2
1	A	220	ILE	2.2
2	D	112	GLY	2.1
1	C	347	ARG	2.1
1	C	342	MET	2.1
1	C	225	ILE	2.1
2	B	110	TYR	2.1
1	C	168	ILE	2.0
1	C	331	THR	2.0
1	C	85	THR	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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
3	MN	C	501	1/1	0.94	0.47	2.89	326,326,326,326	0
3	MN	A	501	1/1	0.88	0.14	-2.28	173,173,173,173	0

6.5 Other polymers [i](#)

There are no such residues in this entry.