



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 9, 2017 – 02:03 PM EST

PDB ID : 5UE8
Title : The crystal structure of Munc13-1 C1C2BMUN domain
Authors : Tomchick, D.R.; Rizo, J.; Xu, J.
Deposited on : 2016-12-29
Resolution : 3.35 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 : unknown
Xtriage (Phenix) : 1.9-1692
EDS : rb-20028442
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) : rb-20028442

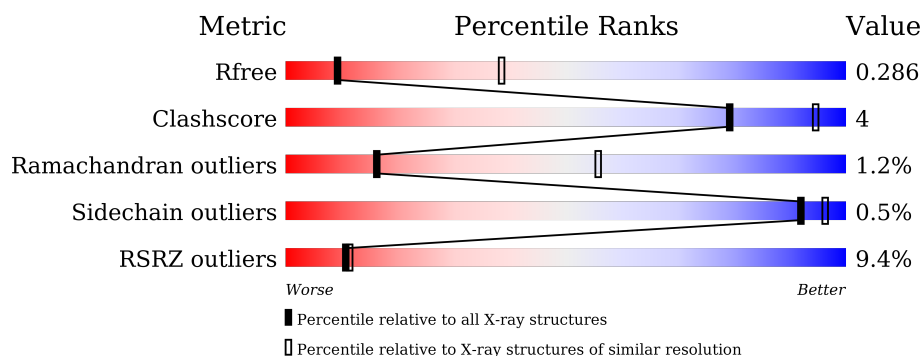
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.35 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	1005 (3.42-3.30)
Clashscore	102246	1076 (3.42-3.30)
Ramachandran outliers	100387	1059 (3.42-3.30)
Sidechain outliers	100360	1058 (3.42-3.30)
RSRZ outliers	91569	1010 (3.42-3.30)

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	961	<div> <div>14%</div> <div> <div></div> <div>80%</div> <div>8%</div> <div>12%</div> </div> </div>
1	B	961	<div> <div>2%</div> <div> <div></div> <div>77%</div> <div>10%</div> <div>13%</div> </div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 27058 atoms, of which 13455 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 Protein unc-13 homolog A.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	847	Total	C	H	N	O	S	0	0	0
			13589	4342	6760	1153	1286	48			
1	B	838	Total	C	H	N	O	S	0	0	0
			13463	4308	6695	1141	1272	47			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	756	TRP	LEU	engineered mutation	UNP Q62768
A	1450	GLU	-	linker	UNP Q62768
A	1451	PHE	-	linker	UNP Q62768
B	756	TRP	LEU	engineered mutation	UNP Q62768
B	1450	GLU	-	linker	UNP Q62768
B	1451	PHE	-	linker	UNP Q62768

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	2	Total	Zn	0	0
			2	2		
2	A	2	Total	Zn	0	0
			2	2		

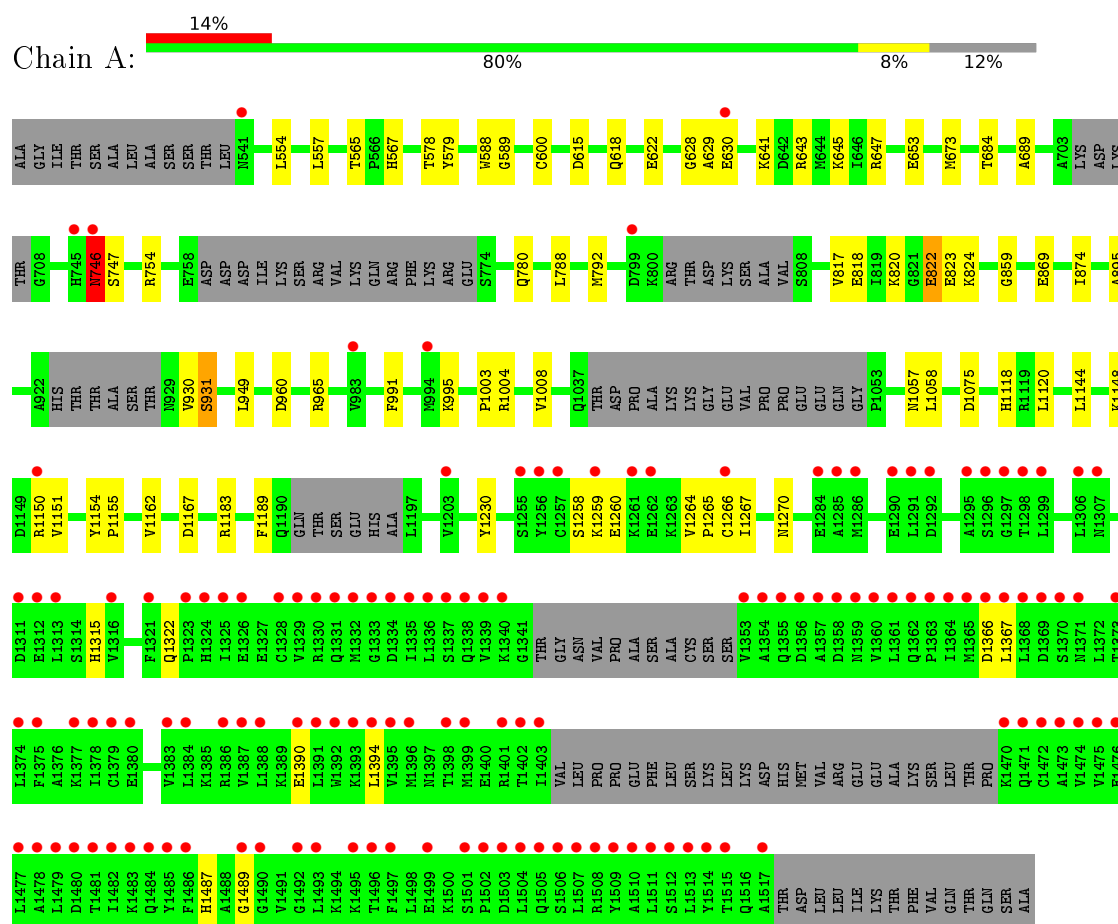
- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Cl	0	0
			1	1		
3	A	1	Total	Cl	0	0
			1	1		

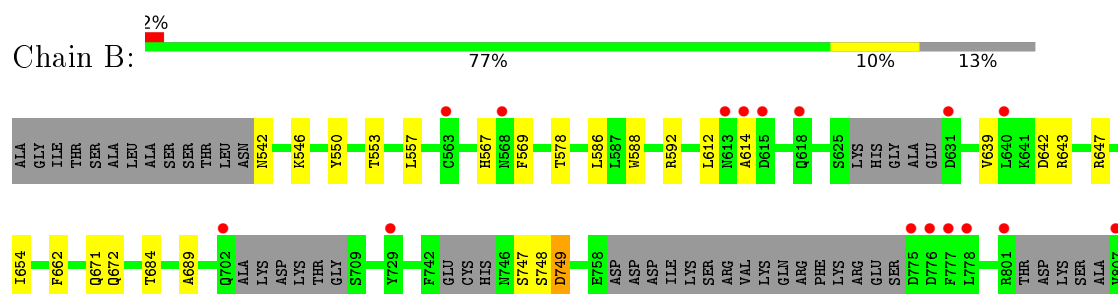
3 Residue-property plots

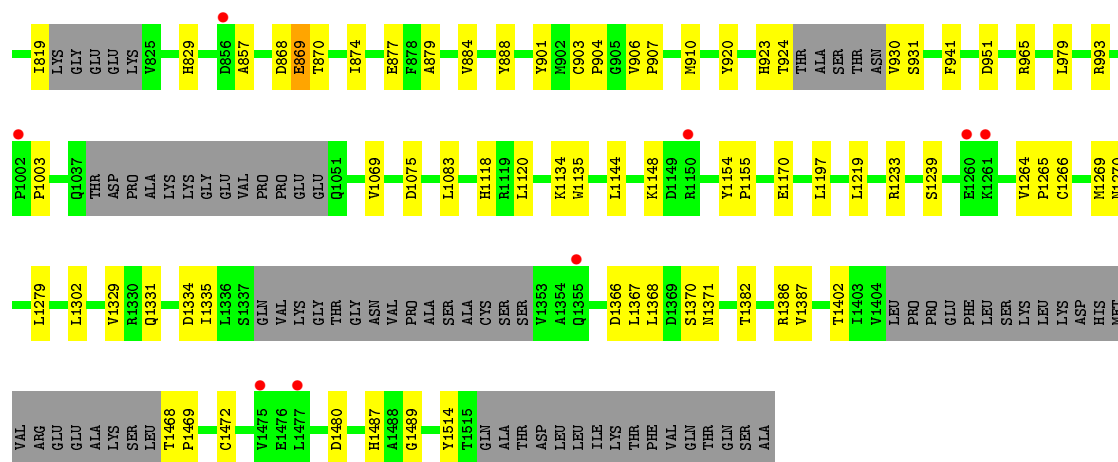
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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: Protein unc-13 homolog A



• Molecule 1: Protein unc-13 homolog A





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	176.15Å 86.35Å 202.14Å 90.00° 115.54° 90.00°	Depositor
Resolution (Å)	45.60 – 3.35 45.60 – 3.35	Depositor EDS
% Data completeness (in resolution range)	75.3 (45.60-3.35) 75.3 (45.60-3.35)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.33 (at 3.32Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.252 , 0.290 0.248 , 0.286	Depositor DCC
R_{free} test set	1490 reflections (4.98%)	DCC
Wilson B-factor (Å ²)	37.7	Xtriage
Anisotropy	0.799	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 20.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.017 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.84	EDS
Total number of atoms	27058	wwPDB-VP
Average B, all atoms (Å ²)	66.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.48% 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: ZN, CL

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	0.25	0/6965	0.43	0/9403
1	B	0.27	0/6903	0.44	0/9325
All	All	0.26	0/13868	0.43	0/18728

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	6829	6760	6757	40	0
1	B	6768	6695	6698	55	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
All	All	13603	13455	13455	95	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 4.

All (95) 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:642:ASP:OD1	1:B:643:ARG:N	2.20	0.75
1:B:868:ASP:O	1:B:870:THR:N	2.21	0.73
1:A:822:GLU:N	1:A:822:GLU:OE1	2.32	0.61
1:B:879:ALA:HA	1:B:884:VAL:HG22	1.84	0.59
1:A:1366:ASP:OD1	1:A:1367:LEU:N	2.36	0.59
1:A:628:GLY:O	1:A:630:GLU:N	2.36	0.58
1:B:923:HIS:O	1:B:923:HIS:ND1	2.36	0.57
1:A:557:LEU:HD21	1:A:874:ILE:HA	1.88	0.56
1:A:1144:LEU:O	1:A:1148:LYS:N	2.37	0.56
1:A:554:LEU:HD22	1:A:673:MET:HE1	1.88	0.56
1:B:1170:GLU:OE1	1:B:1233:ARG:NH2	2.37	0.55
1:B:557:LEU:O	1:B:647:ARG:NE	2.40	0.55
1:A:1189:PHE:HB3	1:A:1267:ILE:HD11	1.89	0.53
1:B:906:VAL:HG12	1:B:910:MET:HE2	1.92	0.52
1:B:1331:GLN:O	1:B:1335:ILE:HG13	2.10	0.52
1:A:565:THR:OG1	1:A:643:ARG:NH1	2.44	0.49
1:B:979:LEU:HG	1:B:1083:LEU:HD11	1.94	0.49
1:A:689:ALA:HA	1:A:818:GLU:O	2.13	0.49
1:B:1331:GLN:O	1:B:1334:ASP:OD1	2.30	0.48
1:A:557:LEU:O	1:A:647:ARG:NE	2.45	0.48
1:B:1144:LEU:O	1:B:1148:LYS:N	2.45	0.48
1:B:1118:HIS:HB3	1:B:1120:LEU:HD13	1.95	0.48
1:A:1258:SER:O	1:A:1260:GLU:N	2.39	0.47
1:B:557:LEU:HD21	1:B:877:GLU:HB2	1.95	0.47
1:A:822:GLU:O	1:A:824:LYS:N	2.45	0.47
1:A:1264:VAL:O	1:A:1267:ILE:HG13	2.14	0.47
1:A:1057:ASN:OD1	1:A:1058:LEU:N	2.47	0.47
1:A:1315:HIS:ND1	1:A:1390:GLU:OE2	2.47	0.47
1:B:1154:TYR:N	1:B:1155:PRO:CD	2.78	0.47
1:A:788:LEU:HB3	1:A:817:VAL:HG21	1.96	0.47
1:A:578:THR:HG22	1:A:579:TYR:N	2.30	0.46
1:A:1150:ARG:HB3	1:A:1151:VAL:HG12	1.98	0.46
1:A:567:HIS:CE1	1:A:600:CYS:SG	3.08	0.46
1:B:1197:LEU:O	1:B:1270:ASN:HB3	2.15	0.46
1:B:1329:VAL:HG12	1:B:1402:THR:OG1	2.15	0.46
1:B:903:CYS:SG	1:B:904:PRO:HD2	2.55	0.46
1:B:747:SER:C	1:B:749:ASP:H	2.18	0.46
1:A:653:GLU:OE1	1:A:653:GLU:N	2.39	0.46
1:B:869:GLU:HG3	1:B:870:THR:N	2.30	0.46
1:B:1279:LEU:HD11	1:B:1302:LEU:HD23	1.97	0.46
1:A:1162:VAL:HG21	1:A:1230:TYR:CZ	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1266:CYS:O	1:B:1270:ASN:ND2	2.49	0.46
1:B:951:ASP:OD1	1:B:993:ARG:NH2	2.49	0.46
1:A:1118:HIS:HB3	1:A:1120:LEU:HD13	1.97	0.45
1:A:1154:TYR:N	1:A:1155:PRO:CD	2.79	0.45
1:B:1334:ASP:OD1	1:B:1335:ILE:N	2.49	0.45
1:A:822:GLU:HG2	1:A:822:GLU:O	2.17	0.45
1:B:550:TYR:O	1:B:553:THR:HG22	2.17	0.45
1:B:588:TRP:H	1:B:592:ARG:HG3	1.82	0.44
1:B:1069:VAL:HG21	1:B:1135:TRP:HZ3	1.83	0.44
1:A:965:ARG:NH1	1:A:1075:ASP:OD1	2.43	0.44
1:B:689:ALA:HB2	1:B:819:ILE:HG22	2.00	0.44
1:B:1239:SER:HA	1:B:1302:LEU:HD22	1.99	0.44
1:B:1468:THR:N	1:B:1469:PRO:CD	2.81	0.44
1:B:901:TYR:O	1:B:907:PRO:HD3	2.18	0.44
1:B:639:VAL:O	1:B:642:ASP:OD1	2.36	0.44
1:A:991:PHE:CE1	1:A:995:LYS:HG3	2.53	0.43
1:A:1487:HIS:NE2	1:A:1489:GLY:O	2.50	0.43
1:A:895:ALA:HA	1:A:949:LEU:HD21	2.01	0.43
1:B:747:SER:O	1:B:749:ASP:N	2.51	0.43
1:A:1264:VAL:HB	1:A:1265:PRO:HD3	2.01	0.43
1:A:930:VAL:HG22	1:A:931:SER:N	2.34	0.43
1:A:746:ASN:ND2	1:A:747:SER:H	2.16	0.42
1:B:569:PHE:CZ	1:B:612:LEU:CD1	3.02	0.42
1:B:642:ASP:OD1	1:B:642:ASP:C	2.57	0.42
1:B:906:VAL:HG12	1:B:910:MET:CE	2.48	0.42
1:B:1134:LYS:HD2	1:B:1219:LEU:O	2.19	0.42
1:B:1487:HIS:NE2	1:B:1489:GLY:O	2.52	0.42
1:B:671:GLN:HG3	1:B:672:GLN:N	2.34	0.42
1:A:1266:CYS:O	1:A:1270:ASN:ND2	2.52	0.42
1:A:615:ASP:HB3	1:A:618:GLN:HB2	2.02	0.42
1:B:888:TYR:CE1	1:B:941:PHE:HA	2.54	0.42
1:B:829:HIS:ND1	1:B:884:VAL:HG12	2.35	0.42
1:B:557:LEU:HD11	1:B:874:ILE:HG23	2.02	0.42
1:B:567:HIS:HB2	1:B:569:PHE:CE2	2.55	0.42
1:A:641:LYS:O	1:A:645:LYS:HG2	2.20	0.42
1:B:578:THR:O	1:B:586:LEU:HD12	2.20	0.42
1:B:557:LEU:HD22	1:B:654:ILE:HD11	2.02	0.42
1:A:754:ARG:NE	1:A:780:GLN:OE1	2.53	0.41
1:B:1329:VAL:CG1	1:B:1402:THR:OG1	2.68	0.41
1:B:1269:MET:HE1	1:B:1387:VAL:CG2	2.50	0.41
1:B:1472:CYS:SG	1:B:1514:TYR:HD2	2.43	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:546:LYS:HG2	1:B:662:PHE:HD2	1.85	0.41
1:A:1322:GLN:OE1	1:A:1394:LEU:HD11	2.21	0.41
1:A:1150:ARG:HB3	1:A:1151:VAL:CG1	2.50	0.41
1:A:588:TRP:CG	1:A:589:GLY:N	2.88	0.41
1:B:1382:THR:O	1:B:1386:ARG:HG2	2.21	0.41
1:B:1264:VAL:HB	1:B:1265:PRO:HD3	2.03	0.41
1:B:923:HIS:O	1:B:924:THR:OG1	2.36	0.41
1:A:1004:ARG:O	1:A:1008:VAL:HG23	2.21	0.40
1:B:1367:LEU:O	1:B:1371:ASN:HB2	2.21	0.40
1:A:618:GLN:O	1:A:622:GLU:HG3	2.21	0.40
1:B:1366:ASP:O	1:B:1370:SER:HB3	2.22	0.40
1:B:930:VAL:O	1:B:930:VAL:HG22	2.20	0.40
1:B:965:ARG:NH1	1:B:1075:ASP:OD1	2.52	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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	829/961 (86%)	761 (92%)	57 (7%)	11 (1%)	15	54
1	B	816/961 (85%)	754 (92%)	53 (6%)	9 (1%)	17	58
All	All	1645/1922 (86%)	1515 (92%)	110 (7%)	20 (1%)	16	56

All (20) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	629	ALA
1	B	749	ASP
1	B	869	GLU
1	A	746	ASN
1	A	820	LYS

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Mol	Chain	Res	Type
1	A	822	GLU
1	A	931	SER
1	A	1259	LYS
1	B	614	ALA
1	B	748	SER
1	B	857	ALA
1	A	823	GLU
1	A	859	GLY
1	B	684	THR
1	A	684	THR
1	A	869	GLU
1	B	931	SER
1	B	1368	LEU
1	A	1003	PRO
1	B	1003	PRO

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	762/861 (88%)	757 (99%)	5 (1%)	88	95
1	B	758/861 (88%)	755 (100%)	3 (0%)	93	97
All	All	1520/1722 (88%)	1512 (100%)	8 (0%)	92	96

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	746	ASN
1	A	792	MET
1	A	960	ASP
1	A	1167	ASP
1	A	1183	ARG
1	B	542	ASN
1	B	920	TYR
1	B	1480	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	746	ASN
1	A	1085	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 6 ligands modelled in this entry, 6 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	847/961 (88%)	0.90	135 (15%) 3 3	18, 51, 175, 205	0
1	B	838/961 (87%)	0.39	24 (2%) 55 56	13, 49, 95, 134	0
All	All	1685/1922 (87%)	0.65	159 (9%) 11 11	13, 51, 161, 205	0

All (159) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1479	LEU	12.1
1	A	1353	VAL	7.5
1	A	1337	SER	7.1
1	A	1364	ILE	7.1
1	A	1332	MET	7.0
1	A	1365	MET	6.9
1	A	1403	ILE	6.6
1	A	1392	TRP	6.4
1	A	1292	ASP	6.3
1	A	1475	VAL	5.7
1	A	1335	ILE	5.5
1	A	1391	LEU	5.5
1	A	1486	PHE	5.4
1	A	1470	LYS	5.3
1	A	1511	LEU	5.3
1	A	1482	ILE	5.3
1	A	1493	LEU	5.3
1	A	1299	LEU	5.2
1	A	1502	PRO	5.2
1	A	1473	ALA	5.1
1	A	1339	VAL	5.0
1	A	1490	GLY	5.0
1	A	1478	ALA	4.9
1	A	1477	LEU	4.9

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Mol	Chain	Res	Type	RSRZ
1	A	1514	TYR	4.9
1	A	1387	VAL	4.8
1	A	1371	ASN	4.7
1	A	1499	GLU	4.7
1	A	1375	PHE	4.6
1	A	1515	THR	4.6
1	A	1325	ILE	4.5
1	A	1378	ILE	4.5
1	A	1359	ASN	4.5
1	A	1380	GLU	4.4
1	A	1354	ALA	4.4
1	A	1476	GLU	4.4
1	A	1395	VAL	4.4
1	A	1510	ALA	4.3
1	A	1333	GLY	4.2
1	A	1336	LEU	4.2
1	A	1503	ASP	4.1
1	A	1355	GLN	4.0
1	A	1362	GLN	4.0
1	A	1504	LEU	4.0
1	A	1340	LYS	4.0
1	A	1298	THR	4.0
1	A	1361	LEU	3.9
1	A	1328	CYS	3.9
1	A	1366	ASP	3.9
1	A	1402	THR	3.9
1	A	1295	ALA	3.8
1	A	1398	THR	3.8
1	A	1290	GLU	3.7
1	A	1259	LYS	3.7
1	A	1360	VAL	3.7
1	A	1331	GLN	3.6
1	A	1474	VAL	3.6
1	A	1399	MET	3.6
1	A	1517	ALA	3.6
1	A	1507	LEU	3.6
1	A	1324	HIS	3.6
1	A	1481	THR	3.5
1	A	1261	LYS	3.5
1	A	1483	LYS	3.5
1	A	1296	SER	3.5
1	A	1369	ASP	3.5

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Mol	Chain	Res	Type	RSRZ
1	A	1313	LEU	3.5
1	A	1394	LEU	3.5
1	A	1505	GLN	3.5
1	A	1374	LEU	3.5
1	A	1396	MET	3.4
1	A	1356	ASP	3.4
1	A	1338	GLN	3.3
1	A	1291	LEU	3.3
1	A	1388	LEU	3.3
1	A	1326	GLU	3.3
1	A	1367	LEU	3.2
1	A	1312	GLU	3.2
1	A	1489	GLY	3.2
1	A	1484	GLN	3.1
1	A	1485	TYR	3.1
1	A	1386	ARG	3.1
1	A	1472	CYS	3.1
1	A	1330	ARG	3.1
1	A	1480	ASP	3.1
1	A	1323	PRO	3.0
1	B	1150	ARG	3.0
1	B	563	CYS	3.0
1	A	1377	LYS	3.0
1	A	746	ASN	3.0
1	A	1256	TYR	2.9
1	A	1286	MET	2.9
1	A	1513	LEU	2.8
1	A	1321	PHE	2.8
1	B	776	ASP	2.8
1	A	1307	ASN	2.8
1	A	1471	GLN	2.8
1	A	1509	TYR	2.8
1	A	1150	ARG	2.8
1	A	1501	SER	2.8
1	A	1379	CYS	2.7
1	A	1363	PRO	2.7
1	B	568	ASN	2.7
1	B	775	ASP	2.6
1	A	1497	PHE	2.6
1	A	1266	CYS	2.6
1	A	1383	VAL	2.5
1	A	1370	SER	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	801	ARG	2.5
1	B	729	TYR	2.5
1	A	1255	SER	2.5
1	A	1384	LEU	2.5
1	A	745	HIS	2.5
1	B	1355	GLN	2.5
1	B	778	LEU	2.5
1	A	1334	ASP	2.5
1	A	1203	VAL	2.5
1	A	1390	GLU	2.5
1	A	983	VAL	2.5
1	A	1492	GLY	2.5
1	B	1477	LEU	2.5
1	B	856	ASP	2.4
1	A	1284	GLU	2.4
1	A	799	ASP	2.4
1	A	1358	ASP	2.4
1	A	1401	ARG	2.4
1	A	1508	ARG	2.4
1	B	1475	VAL	2.4
1	A	1262	GLU	2.4
1	B	618	GLN	2.4
1	B	613	ASN	2.4
1	A	1329	VAL	2.3
1	A	1285	ALA	2.3
1	A	630	GLU	2.3
1	A	1512	SER	2.3
1	B	807	VAL	2.3
1	B	614	ALA	2.3
1	B	702	GLN	2.3
1	B	777	PHE	2.3
1	A	1368	LEU	2.2
1	A	1311	ASP	2.2
1	B	1260	GLU	2.2
1	A	1373	THR	2.2
1	A	1357	ALA	2.2
1	B	640	LEU	2.2
1	B	615	ASP	2.2
1	B	1261	LYS	2.2
1	A	1495	LYS	2.2
1	A	1257	CYS	2.1
1	B	1002	PRO	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	1496	THR	2.1
1	A	1316	VAL	2.1
1	A	1393	LYS	2.1
1	B	631	ASP	2.1
1	A	1306	LEU	2.1
1	A	994	MET	2.1
1	A	541	ASN	2.0
1	A	1506	SER	2.0
1	A	1297	GLY	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 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(\AA^2)	Q<0.9
2	ZN	A	1702	1/1	0.95	0.13	-1.22	23,23,23,23	0
2	ZN	B	1603	1/1	0.96	0.09	-1.75	58,58,58,58	0
2	ZN	A	1701	1/1	0.99	0.13	-1.96	15,15,15,15	0
2	ZN	B	1602	1/1	0.95	0.07	-2.61	80,80,80,80	0
3	CL	B	1601	1/1	0.93	0.16	-	8,8,8,8	0
3	CL	A	1703	1/1	0.96	0.19	-	8,8,8,8	0

6.5 Other polymers [i](#)

There are no such residues in this entry.