Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 05:35 PM GMT

PDB ID	:	4ISR
Title	:	Binding domain of Botulinum neurotoxin DC in complex with rat synaptotagmin II
Authors	:	Berntsson, R.P.-A.; Peng, L.; Svensson, L.M.; Dong, M.; Stenmark, P.
Deposited on	:	2013-01-17
Resolution	:	2.59 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

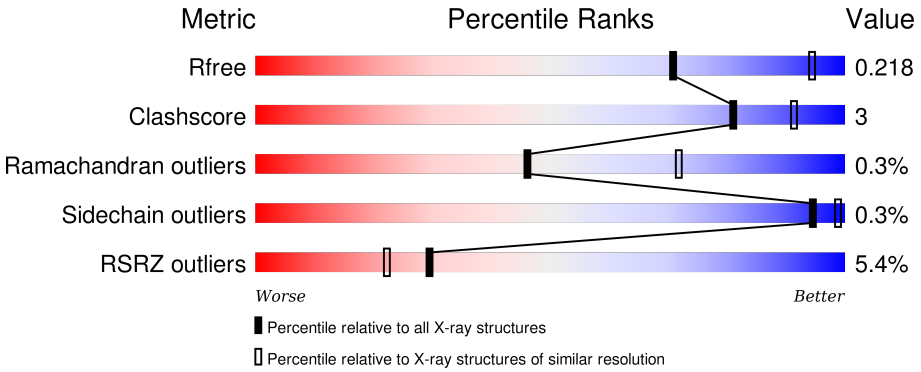
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.59 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	2328 (2.60-2.60)
Clashscore	102246	2679 (2.60-2.60)
Ramachandran outliers	100387	2635 (2.60-2.60)
Sidechain outliers	100360	2635 (2.60-2.60)
RSRZ outliers	91569	2334 (2.60-2.60)

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 <=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	431	3%, 89%, 7%, ·
1	B	431	3%, 91%, 5%, ·
1	C	431	9%, 90%, 6%, ·
2	D	21	5%, 67%, 10%, 24%
2	E	21	5%, 52%, 24%, 24%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	F	21	

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	SO4	A	1302	-	-	-	X
3	SO4	B	1302	-	-	-	X
3	SO4	B	1304	-	-	-	X

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 11056 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 Neurotoxin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	414	Total	C	N	O	S	0	1	0
			3398	2181	561	642	14			
1	B	413	Total	C	N	O	S	0	0	0
			3378	2168	558	638	14			
1	C	413	Total	C	N	O	S	0	0	0
			3376	2167	558	637	14			

There are 27 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	854	MET	-	EXPRESSION TAG	UNP Q9LBR1
A	855	HIS	-	EXPRESSION TAG	UNP Q9LBR1
A	856	HIS	-	EXPRESSION TAG	UNP Q9LBR1
A	857	HIS	-	EXPRESSION TAG	UNP Q9LBR1
A	858	HIS	-	EXPRESSION TAG	UNP Q9LBR1
A	859	HIS	-	EXPRESSION TAG	UNP Q9LBR1
A	860	HIS	-	EXPRESSION TAG	UNP Q9LBR1
A	861	TYR	-	EXPRESSION TAG	UNP Q9LBR1
A	862	PHE	-	EXPRESSION TAG	UNP Q9LBR1
B	854	MET	-	EXPRESSION TAG	UNP Q9LBR1
B	855	HIS	-	EXPRESSION TAG	UNP Q9LBR1
B	856	HIS	-	EXPRESSION TAG	UNP Q9LBR1
B	857	HIS	-	EXPRESSION TAG	UNP Q9LBR1
B	858	HIS	-	EXPRESSION TAG	UNP Q9LBR1
B	859	HIS	-	EXPRESSION TAG	UNP Q9LBR1
B	860	HIS	-	EXPRESSION TAG	UNP Q9LBR1
B	861	TYR	-	EXPRESSION TAG	UNP Q9LBR1
B	862	PHE	-	EXPRESSION TAG	UNP Q9LBR1
C	854	MET	-	EXPRESSION TAG	UNP Q9LBR1
C	855	HIS	-	EXPRESSION TAG	UNP Q9LBR1
C	856	HIS	-	EXPRESSION TAG	UNP Q9LBR1
C	857	HIS	-	EXPRESSION TAG	UNP Q9LBR1
C	858	HIS	-	EXPRESSION TAG	UNP Q9LBR1

Continued on next page...

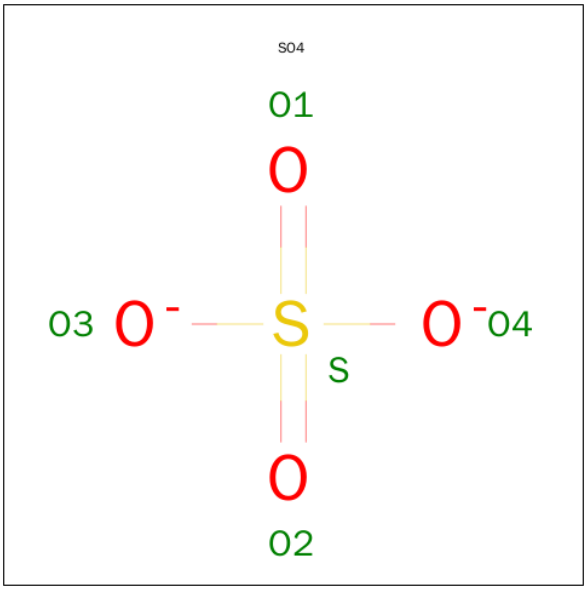
Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
C	859	HIS	-	EXPRESSION TAG	UNP Q9LBR1
C	860	HIS	-	EXPRESSION TAG	UNP Q9LBR1
C	861	TYR	-	EXPRESSION TAG	UNP Q9LBR1
C	862	PHE	-	EXPRESSION TAG	UNP Q9LBR1

- Molecule 2 is a protein called Synaptotagmin-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	16	Total	C	N	O	S	0	0	0
			138	89	21	27	1			
2	E	16	Total	C	N	O	S	0	0	0
			138	89	21	27	1			
2	F	16	Total	C	N	O	S	0	0	0
			138	89	21	27	1			

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	O	S		0	0
			5	4	1			
3	A	1	Total	O	S		0	0
			5	4	1			
3	A	1	Total	O	S		0	0
			5	4	1			
3	A	1	Total	O	S		0	0
			5	4	1			

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total O S 5 4 1	0	0
3	B	1	Total O S 5 4 1	0	0
3	B	1	Total O S 5 4 1	0	0
3	B	1	Total O S 5 4 1	0	0
3	C	1	Total O S 5 4 1	0	0
3	C	1	Total O S 5 4 1	0	0
3	C	1	Total O S 5 4 1	0	0
3	E	1	Total O S 5 4 1	0	0

- Molecule 4 is water.

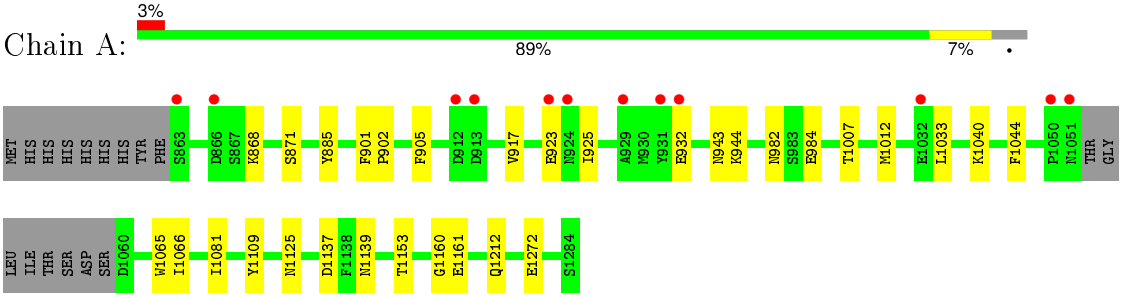
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	176	Total O 176 176	0	0
4	B	156	Total O 156 156	0	0
4	C	90	Total O 90 90	0	0
4	D	3	Total O 3 3	0	0
4	E	2	Total O 2 2	0	0
4	F	3	Total O 3 3	0	0

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.

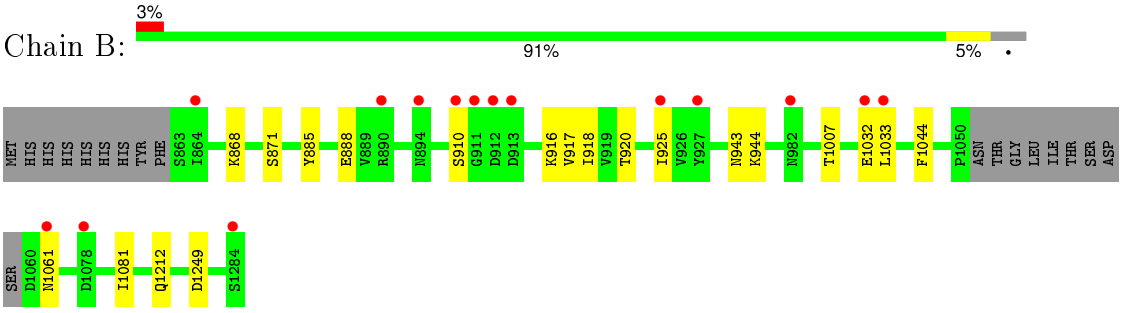
- Molecule 1: Neurotoxin

Chain A:



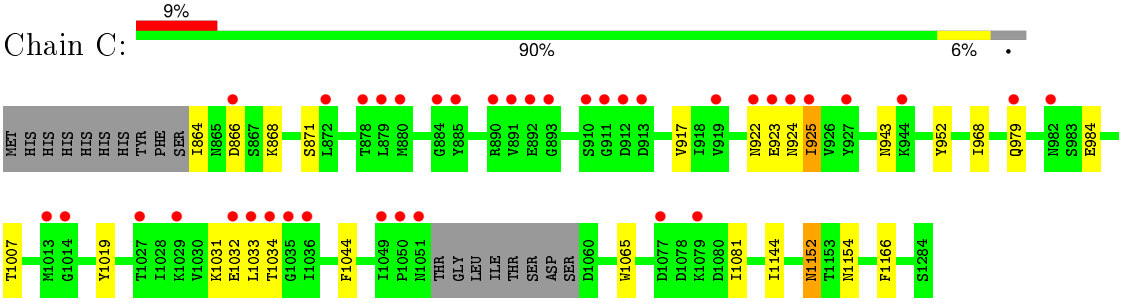
- Molecule 1: Neurotoxin

Chain B:



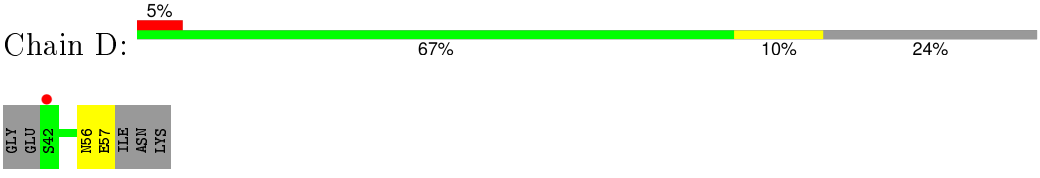
- Molecule 1: Neurotoxin

Chain C:



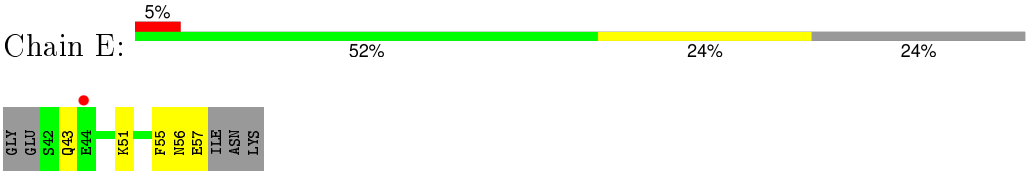
- Molecule 2: Synaptotagmin-2

Chain D:



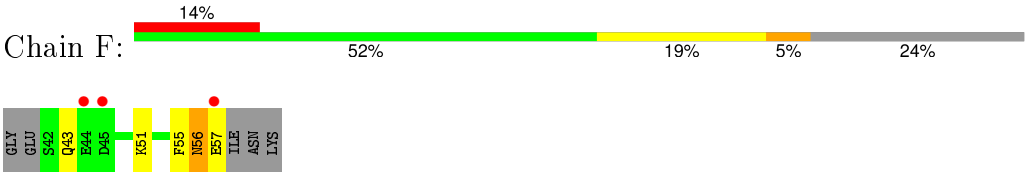
• Molecule 2: Synaptotagmin-2

Chain E:



• Molecule 2: Synaptotagmin-2

Chain F:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	165.24Å 57.78Å 169.56Å 90.00° 118.49° 90.00°	Depositor
Resolution (Å)	47.73 – 2.59 47.73 – 2.59	Depositor EDS
% Data completeness (in resolution range)	99.6 (47.73-2.59) 99.6 (47.73-2.59)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.97 (at 2.58Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.220 , 0.235 0.202 , 0.218	Depositor DCC
R_{free} test set	4425 reflections (5.26%)	DCC
Wilson B-factor (Å^2)	31.6	Xtriage
Anisotropy	0.288	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 42.1	EDS
Estimated twinning fraction	0.017 for -h-l,k,h 0.017 for l,k,-h-l 0.017 for h,-k,-h-l 0.019 for -h-l,-k,l 0.018 for l,-k,h	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Outliers	0 of 88514 reflections	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	11056	wwPDB-VP
Average B, all atoms (Å^2)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.20% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: SO4

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	0.30	0/3476	0.48	0/4704
1	B	0.30	0/3455	0.47	0/4675
1	C	0.30	0/3453	0.47	0/4673
2	D	0.35	0/140	0.50	0/183
2	E	0.35	0/140	0.55	0/183
2	F	0.35	0/140	0.49	0/183
All	All	0.30	0/10804	0.47	0/14601

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	3398	0	3318	19	0
1	B	3378	0	3304	16	0
1	C	3376	0	3299	20	0
2	D	138	0	129	3	0
2	E	138	0	129	9	0
2	F	138	0	129	3	0
3	A	20	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	20	0	0	0	0
3	C	15	0	0	0	0
3	E	5	0	0	0	0
4	A	176	0	0	4	0
4	B	156	0	0	2	0
4	C	90	0	0	0	0
4	D	3	0	0	0	0
4	E	2	0	0	0	0
4	F	3	0	0	0	0
All	All	11056	0	10308	68	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 3.

All (68) 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:885:TYR:HB3	1:B:925:ILE:CD1	2.08	0.83
2:E:56:ASN:HA	2:E:57:GLU:HG3	1.61	0.83
2:D:56:ASN:HA	2:D:57:GLU:HB2	1.62	0.81
1:A:1125:ASN:HB2	4:A:1566:HOH:O	1.81	0.79
1:C:923:GLU:HB3	1:C:924:ASN:HB2	1.72	0.70
1:B:885:TYR:HB3	1:B:925:ILE:HD13	1.73	0.69
2:D:56:ASN:CA	2:D:57:GLU:HB2	2.23	0.67
1:A:932:GLU:HG3	1:A:1012:MET:HB2	1.77	0.66
2:E:56:ASN:HA	2:E:57:GLU:CG	2.27	0.65
1:C:917:VAL:HB	1:C:1044:PHE:HB2	1.80	0.63
2:E:56:ASN:HA	2:E:57:GLU:CB	2.30	0.62
1:A:1153:THR:OG1	1:C:925:ILE:HD13	2.01	0.60
2:D:56:ASN:HA	2:D:57:GLU:CB	2.33	0.59
1:B:868:LYS:HD3	1:B:871:SER:HB2	1.87	0.57
1:B:885:TYR:CD1	1:B:925:ILE:CD1	2.89	0.56
1:A:1007:THR:HG21	1:A:1081:ILE:HG12	1.88	0.55
1:B:917:VAL:HB	1:B:1044:PHE:HB2	1.88	0.55
1:B:885:TYR:CD1	1:B:925:ILE:HD11	2.41	0.54
1:B:1007:THR:HG21	1:B:1081:ILE:HG12	1.89	0.54
1:C:925:ILE:HG13	1:C:925:ILE:O	2.08	0.53
1:B:885:TYR:CB	1:B:925:ILE:HD13	2.38	0.52
1:A:923:GLU:HG2	1:A:1040:LYS:HG2	1.92	0.52
2:E:56:ASN:HB3	2:E:57:GLU:HB2	1.92	0.52
1:A:905:PHE:CZ	1:A:1066:ILE:HB	2.45	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:56:ASN:HA	2:F:57:GLU:HB2	1.92	0.51
1:A:1212:GLN:HG3	4:A:1484:HOH:O	2.10	0.51
1:A:982:ASN:HD21	2:E:43:GLN:HE22	1.59	0.51
1:C:979:GLN:HG3	1:C:1033:LEU:HD23	1.93	0.51
1:B:885:TYR:CG	1:B:925:ILE:HD13	2.47	0.50
2:E:56:ASN:CA	2:E:57:GLU:HB2	2.43	0.49
1:C:1007:THR:HB	1:C:1019:TYR:HB2	1.93	0.49
1:C:943:ASN:HB2	1:C:1065:TRP:CZ3	2.48	0.49
1:B:910:SER:OG	1:B:1061:ASN:HB3	2.14	0.48
1:A:868:LYS:HD3	1:A:871:SER:HB2	1.95	0.48
1:B:885:TYR:HD1	1:B:925:ILE:HD11	1.77	0.47
1:C:979:GLN:OE1	1:C:984:GLU:HA	2.14	0.47
1:C:864:ILE:HG22	1:C:866:ASP:H	1.79	0.47
1:C:868:LYS:HD3	1:C:871:SER:HB2	1.95	0.47
1:B:916:LYS:HE2	1:B:918:ILE:HD11	1.97	0.47
1:C:1152:ASN:HD21	1:C:1154:ASN:HB2	1.79	0.46
2:E:56:ASN:CA	2:E:57:GLU:CB	2.94	0.46
1:C:952:TYR:HB2	1:C:968:ILE:HG13	1.97	0.46
1:C:943:ASN:HB2	1:C:1065:TRP:HZ3	1.81	0.45
2:E:56:ASN:HA	2:E:57:GLU:HB2	1.99	0.45
2:E:51:LYS:HA	2:E:55:PHE:CD1	2.52	0.45
1:C:1007:THR:HG21	1:C:1081:ILE:HG12	1.98	0.45
1:A:984:GLU:HA	1:A:1033:LEU:HD21	2.00	0.43
2:F:51:LYS:HA	2:F:55:PHE:CD1	2.53	0.43
1:B:943:ASN:HA	1:B:944:LYS:HA	1.71	0.43
2:F:56:ASN:CA	2:F:57:GLU:HB2	2.48	0.43
1:C:1152:ASN:HD22	1:C:1154:ASN:H	1.65	0.43
1:B:1212:GLN:HG3	4:B:1481:HOH:O	2.18	0.42
1:A:901:PHE:CG	1:A:902:PRO:HA	2.53	0.42
1:B:888:GLU:HB3	1:B:920:THR:HB	2.02	0.42
1:A:1109:TYR:CZ	1:A:1139:ASN:HA	2.55	0.41
1:A:885:TYR:HD1	1:A:925:ILE:HG23	1.85	0.41
1:B:1249:ASP:HB3	4:B:1498:HOH:O	2.20	0.41
1:C:924:ASN:O	1:C:925:ILE:HG22	2.20	0.41
1:A:943:ASN:HB2	1:A:1065:TRP:HZ3	1.86	0.41
1:C:1031:LYS:O	1:C:1032:GLU:HB3	2.21	0.41
1:A:1160:GLY:O	1:A:1161:GLU:HB2	2.20	0.41
1:C:1144:ILE:HD13	1:C:1166:PHE:HD1	1.86	0.41
1:A:1272:GLU:HG3	4:A:1568:HOH:O	2.21	0.41
1:A:943:ASN:HB2	1:A:1065:TRP:CZ3	2.56	0.41
1:C:922:ASN:HA	1:C:923:GLU:HA	1.84	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:944:LYS:HD3	4:A:1476:HOH:O	2.21	0.40
1:A:917:VAL:HB	1:A:1044:PHE:HB2	2.03	0.40
1:C:925:ILE:CG1	1:C:925:ILE:O	2.69	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	411/431 (95%)	392 (95%)	19 (5%)	0	100 100
1	B	409/431 (95%)	389 (95%)	18 (4%)	2 (0%)	34 60
1	C	409/431 (95%)	386 (94%)	22 (5%)	1 (0%)	52 77
2	D	14/21 (67%)	14 (100%)	0	0	100 100
2	E	14/21 (67%)	14 (100%)	0	0	100 100
2	F	14/21 (67%)	13 (93%)	0	1 (7%)	1 1
All	All	1271/1356 (94%)	1208 (95%)	59 (5%)	4 (0%)	46 72

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	1033	LEU
2	F	43	GLN
1	B	1032	GLU
1	C	925	ILE

5.3.2 Protein sidechains (i)

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	380/395 (96%)	379 (100%)	1 (0%)	94 99
1	B	378/395 (96%)	378 (100%)	0	100 100
1	C	377/395 (95%)	375 (100%)	2 (0%)	92 98
2	D	15/19 (79%)	15 (100%)	0	100 100
2	E	15/19 (79%)	15 (100%)	0	100 100
2	F	15/19 (79%)	14 (93%)	1 (7%)	20 40
All	All	1180/1242 (95%)	1176 (100%)	4 (0%)	94 99

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1137	ASP
1	C	1034	THR
1	C	1152	ASN
2	F	56	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	1089	GLN
1	B	1162	ASN
1	B	1223	GLN
1	C	1063	ASN
1	C	1152	ASN
1	C	1154	ASN
2	E	43	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)

12 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	SO4	A	1301	-	4,4,4	0.29	0	6,6,6	0.14	0
3	SO4	A	1302	-	4,4,4	0.40	0	6,6,6	0.13	0
3	SO4	A	1303	-	4,4,4	0.37	0	6,6,6	0.08	0
3	SO4	A	1304	-	4,4,4	0.36	0	6,6,6	0.11	0
3	SO4	B	1301	-	4,4,4	0.30	0	6,6,6	0.14	0
3	SO4	B	1302	-	4,4,4	0.42	0	6,6,6	0.09	0
3	SO4	B	1303	-	4,4,4	0.37	0	6,6,6	0.08	0
3	SO4	B	1304	-	4,4,4	0.40	0	6,6,6	0.07	0
3	SO4	C	1301	-	4,4,4	0.35	0	6,6,6	0.18	0
3	SO4	C	1302	-	4,4,4	0.33	0	6,6,6	0.18	0
3	SO4	C	1303	-	4,4,4	0.38	0	6,6,6	0.17	0
3	SO4	E	101	-	4,4,4	0.37	0	6,6,6	0.07	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	SO4	A	1301	-	-	0/0/0/0	0/0/0/0
3	SO4	A	1302	-	-	0/0/0/0	0/0/0/0
3	SO4	A	1303	-	-	0/0/0/0	0/0/0/0
3	SO4	A	1304	-	-	0/0/0/0	0/0/0/0
3	SO4	B	1301	-	-	0/0/0/0	0/0/0/0
3	SO4	B	1302	-	-	0/0/0/0	0/0/0/0
3	SO4	B	1303	-	-	0/0/0/0	0/0/0/0
3	SO4	B	1304	-	-	0/0/0/0	0/0/0/0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	SO4	C	1301	-	-	0/0/0/0	0/0/0/0
3	SO4	C	1302	-	-	0/0/0/0	0/0/0/0
3	SO4	C	1303	-	-	0/0/0/0	0/0/0/0
3	SO4	E	101	-	-	0/0/0/0	0/0/0/0

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, 95^{th} 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	414/431 (96%)	0.04	12 (2%) 55 48	20, 31, 60, 89	0
1	B	413/431 (95%)	0.09	15 (3%) 46 38	17, 31, 74, 99	0
1	C	413/431 (95%)	0.43	38 (9%) 11 7	24, 45, 96, 135	0
2	D	16/21 (76%)	0.66	1 (6%) 23 17	29, 47, 76, 78	0
2	E	16/21 (76%)	0.82	1 (6%) 23 17	27, 39, 64, 64	0
2	F	16/21 (76%)	1.51	3 (18%) 2 1	38, 53, 76, 77	0
All	All	1288/1356 (94%)	0.22	70 (5%) 29 22	17, 35, 82, 135	0

All (70) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	927	TYR	6.9
1	C	1050	PRO	6.2
1	B	912	ASP	5.1
1	B	925	ILE	5.1
1	C	922	ASN	4.6
1	C	979	GLN	4.4
1	C	912	ASP	4.3
1	C	923	GLU	4.3
1	C	1033	LEU	4.2
1	A	923	GLU	4.0
1	C	925	ILE	3.9
1	C	913	ASP	3.8
1	C	884	GLY	3.6
1	A	1051	ASN	3.5
1	A	912	ASP	3.5
1	C	890	ARG	3.5
1	B	911	GLY	3.4
1	C	1013	MET	3.4
1	C	1051	ASN	3.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	C	911	GLY	3.3
1	B	894	ASN	3.3
1	B	913	ASP	3.2
1	C	1034	THR	3.2
1	C	879	LEU	3.1
1	B	927	TYR	3.1
2	F	45	ASP	3.1
1	B	1061	ASN	3.0
2	F	57	GLU	3.0
1	C	893	GLY	3.0
1	B	982	ASN	3.0
1	C	880	MET	2.9
1	C	878	THR	2.9
2	F	44	GLU	2.9
1	C	924	ASN	2.8
1	C	885	TYR	2.8
1	C	910	SER	2.7
1	C	1027	THR	2.7
1	A	1050	PRO	2.7
1	C	1035	GLY	2.7
1	C	866	ASP	2.6
1	B	910	SER	2.6
1	C	891	VAL	2.6
1	A	863	SER	2.6
1	A	1032	GLU	2.5
1	B	1284	SER	2.5
1	A	866	ASP	2.5
1	C	892	GLU	2.5
1	C	919	VAL	2.5
1	C	1014	GLY	2.4
1	C	982	ASN	2.4
1	C	1036	ILE	2.4
1	C	1049	ILE	2.4
1	A	924	ASN	2.3
1	C	872	LEU	2.3
1	C	1077	ASP	2.3
1	B	1033	LEU	2.3
1	B	890	ARG	2.3
1	A	913	ASP	2.2
1	C	1029	LYS	2.2
1	C	1079	LYS	2.2
1	B	1078	ASP	2.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	864	ILE	2.2
2	D	42	SER	2.2
1	A	931[A]	TYR	2.1
1	A	932	GLU	2.1
1	C	1032	GLU	2.1
1	C	944	LYS	2.1
1	B	1032	GLU	2.1
1	A	929	ALA	2.1
2	E	44	GLU	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, 95^{th} 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	SO4	B	1302	5/5	0.82	0.20	6.69	61,62,62,64	0
3	SO4	A	1302	5/5	0.83	0.21	3.96	63,65,67,67	0
3	SO4	B	1304	5/5	0.81	0.32	3.61	77,78,80,81	0
3	SO4	A	1301	5/5	0.98	0.16	0.64	33,33,34,34	0
3	SO4	B	1303	5/5	0.87	0.30	0.58	73,73,74,75	0
3	SO4	B	1301	5/5	0.99	0.13	-1.11	27,27,27,27	0
3	SO4	C	1301	5/5	0.98	0.11	-1.46	44,44,45,45	0
3	SO4	C	1303	5/5	0.95	0.24	-	70,70,71,71	0
3	SO4	A	1304	5/5	0.95	0.19	-	68,68,69,69	0
3	SO4	C	1302	5/5	0.92	0.18	-	62,63,63,64	0
3	SO4	E	101	5/5	0.97	0.15	-	62,62,64,64	0
3	SO4	A	1303	5/5	0.91	0.25	-	86,87,89,89	0

6.5 Other polymers (i)

There are no such residues in this entry.