



Full wwPDB X-ray Structure Validation Report

Feb 26, 2014 – 07:47 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 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/ValidationPDFNotes.html>

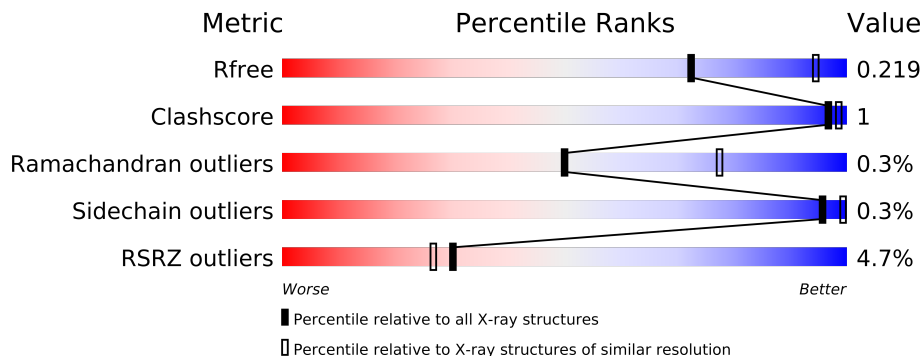
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

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}	66092	1718 (2.60-2.60)
Clashscore	79885	2154 (2.60-2.60)
Ramachandran outliers	78287	2113 (2.60-2.60)
Sidechain outliers	78261	2113 (2.60-2.60)
RSRZ outliers	66119	1718 (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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	431	
1	B	431	
1	C	431	
2	D	21	
2	E	21	
2	F	21	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
3	SO4	A	1302	-	X
3	SO4	A	1303	-	X

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Mol	Type	Chain	Res	Geometry	Electron density
3	SO4	B	1302	-	X
3	SO4	B	1304	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 11056 atoms, of which 0 are hydrogen and 0 are deuterium.

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

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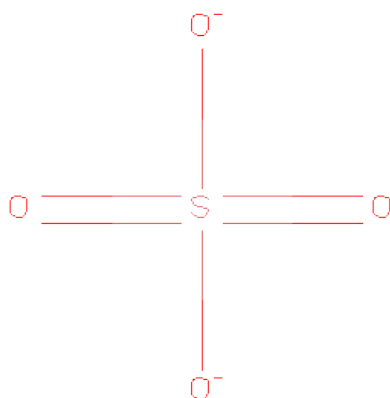
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Chain	Residue	Modelled	Actual	Comment	Reference
C	859	HIS	-	EXPRESSION TAG	UNP Q9LBR1
C	860	HIS	-	EXPRESSION TAG	UNP Q9LBR1
C	861	TYR	-	EXPRESSION TAG	UNP Q9LBR1
C	862	PHE	-	EXPRESSION TAG	UNP Q9LBR1

- Molecule 2 is a protein called Synaptotagmin-2.

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

- Molecule 3 is SULFATE ION (three-letter code: SO₄) (formula: O₄S).



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		

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

- Molecule 4 is water.

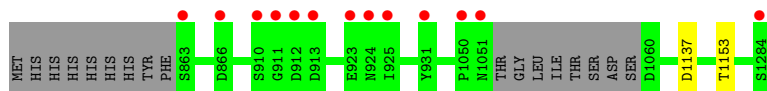
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	176	Total	O	0	0
			176	176		
4	B	156	Total	O	0	0
			156	156		
4	C	90	Total	O	0	0
			90	90		
4	D	3	Total	O	0	0
			3	3		
4	E	2	Total	O	0	0
			2	2		
4	F	3	Total	O	0	0
			3	3		

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: 



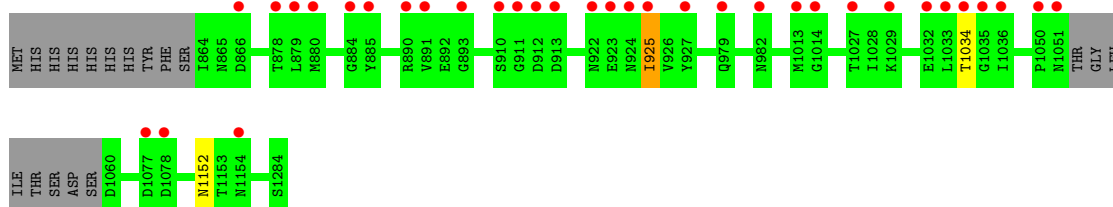
- Molecule 1: Neurotoxin

Chain B: 



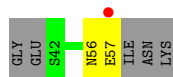
- Molecule 1: Neurotoxin

Chain C: 



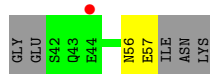
- Molecule 2: Synaptotagmin-2

Chain D: 



- Molecule 2: Synaptotagmin-2

Chain E: 



- Molecule 2: Synaptotagmin-2

Chain F: 

GLY	GLU	S42	D43	E44	D45	N56	E57	ILE	ASN	LYS

4 Data and refinement statistics

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
$\langle I/\sigma(I) \rangle$ ¹	1.97 (at 2.58Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.220 , 0.235 0.202 , 0.219	Depositor DCC
R_{free} test set	4426 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 , 16.2	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	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	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.*

¹Intensities estimated from amplitudes.

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 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3398	0	0	1	0
1	B	3378	0	5	6	0
1	C	3376	0	5	3	0
2	D	138	0	0	1	0
2	E	138	0	0	2	0
2	F	138	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	20	0	0	0	0
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	0	0
4	B	156	0	0	0	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	10	11	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 1.

All (11) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1153:THR:OG1	1:C:925:ILE:HD13	2.01	0.60
1:B:885:TYR:CD1	1:B:925:ILE:CD1	2.89	0.56
1:B:885:TYR:CD1	1:B:925:ILE:HD11	2.41	0.54
1:C:925:ILE:O	1:C:925:ILE:HG13	2.08	0.53
1:B:885:TYR:CB	1:B:925:ILE:HD13	2.38	0.53
1:B:885:TYR:CG	1:B:925:ILE:HD13	2.47	0.50
1:B:885:TYR:CB	1:B:925:ILE:CD1	2.90	0.49
2:E:56:ASN:CA	2:E:57:GLU:CB	2.94	0.46
1:B:1185:ASN:ND2	2:E:56:ASN:O	2.52	0.43
2:D:56:ASN:CA	2:D:57:GLU:CB	2.98	0.42
1:C:925:ILE:O	1:C:925:ILE:CG1	2.69	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	411/431 (95%)	392 (95%)	19 (5%)	0	100	100
1	B	409/431 (95%)	389 (95%)	18 (4%)	2 (0%)	38	67
1	C	409/431 (95%)	386 (94%)	22 (5%)	1 (0%)	56	82
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%)	2	1
All	All	1271/1356 (94%)	1208 (95%)	59 (5%)	4 (0%)	50	77

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 ⓘ

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%)	96	99
1	B	378/395 (96%)	378 (100%)	0	100	100
1	C	377/395 (95%)	375 (100%)	2 (0%)	94	99
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%)	23	44
All	All	1180/1242 (95%)	1176 (100%)	4 (0%)	96	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

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Mol	Chain	Res	Type
2	F	56	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

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	0.34	0	6,6,6	0.14	0
3	SO4	A	1302	-	4,4,4	0.45	0	6,6,6	0.12	0
3	SO4	A	1303	-	4,4,4	0.42	0	6,6,6	0.07	0
3	SO4	A	1304	-	4,4,4	0.41	0	6,6,6	0.11	0
3	SO4	B	1301	-	4,4,4	0.35	0	6,6,6	0.13	0
3	SO4	B	1302	-	4,4,4	0.47	0	6,6,6	0.08	0
3	SO4	B	1303	-	4,4,4	0.42	0	6,6,6	0.08	0
3	SO4	B	1304	-	4,4,4	0.45	0	6,6,6	0.07	0
3	SO4	C	1301	-	4,4,4	0.40	0	6,6,6	0.17	0
3	SO4	C	1302	-	4,4,4	0.38	0	6,6,6	0.17	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	SO4	C	1303	-	4,4,4	0.43	0	6,6,6	0.15	0
3	SO4	E	101	-	4,4,4	0.42	0	6,6,6	0.06	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
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.

5.7 Other polymers ⓘ

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	414/431 (96%)	-0.03	13 (3%) 47 43	20, 31, 60, 89	0
1	B	413/431 (95%)	-0.03	10 (2%) 56 53	17, 31, 74, 99	0
1	C	413/431 (95%)	0.28	34 (8%) 12 9	24, 45, 96, 135	0
2	D	16/21 (76%)	0.65	1 (6%) 19 16	29, 47, 76, 78	0
2	E	16/21 (76%)	0.90	1 (6%) 19 16	27, 39, 64, 64	0
2	F	16/21 (76%)	0.91	2 (12%) 5 3	38, 53, 76, 77	0
All	All	1288/1356 (94%)	0.10	61 (4%) 30 27	17, 35, 82, 135	0

All (61) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	927	TYR	5.8
1	B	925	ILE	5.4
1	C	1050	PRO	5.4
1	B	912	ASP	4.7
1	C	923	GLU	4.3
1	C	1033	LEU	4.1
1	C	979	GLN	3.9
1	A	912	ASP	3.6
1	C	1051	ASN	3.5
1	C	884	GLY	3.5
1	A	923	GLU	3.4
1	C	912	ASP	3.4
1	C	913	ASP	3.4
1	C	1013	MET	3.3
1	C	922	ASN	3.2
1	C	1034	THR	3.2
1	B	927	TYR	3.1
1	C	1029	LYS	3.1
1	C	925	ILE	3.0

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Mol	Chain	Res	Type	RSRZ
1	C	982	ASN	3.0
1	B	911	GLY	3.0
1	C	885	TYR	2.9
1	A	1051	ASN	2.9
1	B	913	ASP	2.9
2	F	57	GLU	2.9
1	B	894	ASN	2.9
1	C	890	ARG	2.8
1	C	911	GLY	2.8
1	C	893	GLY	2.8
1	C	1027	THR	2.7
1	B	1061	ASN	2.6
1	C	1014	GLY	2.5
1	A	913	ASP	2.5
1	B	910	SER	2.5
1	C	878	THR	2.5
1	C	880	MET	2.5
2	D	57	GLU	2.5
1	C	879	LEU	2.4
1	B	890	ARG	2.4
1	A	925	ILE	2.4
1	C	924	ASN	2.3
1	C	910	SER	2.3
1	B	1078	ASP	2.3
1	C	866	ASP	2.3
1	C	1078	ASP	2.2
1	C	1035	GLY	2.2
1	C	1154	ASN	2.2
1	A	931[A]	TYR	2.2
1	A	924	ASN	2.1
1	A	866	ASP	2.1
1	A	1284	SER	2.1
1	A	910	SER	2.1
1	C	1032	GLU	2.1
1	C	1077	ASP	2.1
2	E	44	GLU	2.1
1	A	1050	PRO	2.1
1	C	891	VAL	2.1
1	A	911	GLY	2.1
1	C	1036	ILE	2.0
2	F	45	ASP	2.0
1	A	863	SER	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 ⓘ

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	RSR	LLDF	B-factors(Å ²)	Q<0.9
3	SO4	B	1302	5/5	0.20	5.76	61,62,62,64	0
3	SO4	A	1303	5/5	0.30	3.55	86,87,89,89	0
3	SO4	B	1304	5/5	0.30	3.30	77,78,80,81	0
3	SO4	A	1302	5/5	0.20	2.93	63,65,67,67	0
3	SO4	C	1302	5/5	0.17	1.84	62,63,63,64	0
3	SO4	E	101	5/5	0.21	0.89	62,62,64,64	0
3	SO4	A	1304	5/5	0.16	0.86	68,68,69,69	0
3	SO4	C	1303	5/5	0.21	0.69	70,70,71,71	0
3	SO4	B	1303	5/5	0.28	0.56	73,73,74,75	0
3	SO4	A	1301	5/5	0.14	-0.09	33,33,34,34	0
3	SO4	B	1301	5/5	0.11	-1.41	27,27,27,27	0
3	SO4	C	1301	5/5	0.10	-1.41	44,44,45,45	0

6.5 Other polymers ⓘ

There are no such residues in this entry.