Full wwPDB X-ray Structure Validation Report ⓘ

Jan 25, 2023 – 10:33 AM EST

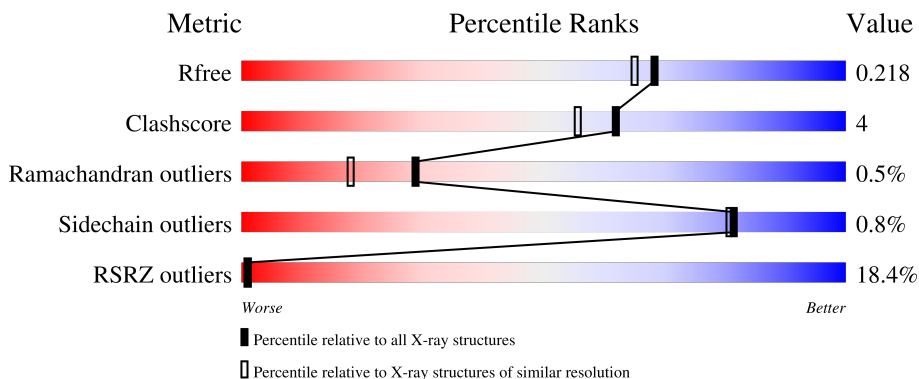|		
PDB ID	:	3PNX
Title	:	Crystal structure of a putative sulfurtransferase dsrE (Swol_2425) from Syntrophomonas wolfei str. Goettingen at 1.92 A resolution
Authors	:	Joint Center for Structural Genomics (JCSG)
Deposited on	:	2010-11-19
Resolution	:	1.92 Å(reported)

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 1.92 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	Percentile Ranks	Value
Rfree		0.218
Clashscore		4
Ramachandran outliers		0.5%
Sidechain outliers		0.8%
RSRZ outliers		18.4%

Worse   *Better*

▮ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	7937 (1.94-1.90)
Clashscore	141614	8644 (1.94-1.90)
Ramachandran outliers	138981	8530 (1.94-1.90)
Sidechain outliers	138945	8530 (1.94-1.90)
RSRZ outliers	127900	7793 (1.94-1.90)

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 of 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 <=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	160	22% / 94% / 6%
1	B	160	15% / 90% / 8%
1	C	160	11% / 91% / 8%
1	D	160	14% / 88% / 12%
1	E	160	23% / 88% / 9%

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Mol	Chain	Length	Quality of chain
1	F	160	

2 Entry composition ⓘ

There are 5 unique types of molecules in this entry. The entry contains 7805 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 Putative sulfurtransferase dsrE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	160	Total	C	N	O	S	Se	0	7	0
			1289	834	196	247	2	10			
1	B	157	Total	C	N	O	S	Se	0	7	0
			1254	813	194	236	2	9			
1	C	157	Total	C	N	O	S	Se	0	10	0
			1273	826	194	241	2	10			
1	D	160	Total	C	N	O	S	Se	0	6	0
			1266	819	192	243	2	10			
1	E	157	Total	C	N	O	S	Se	0	7	0
			1241	804	188	238	2	9			
1	F	157	Total	C	N	O	S	Se	0	4	0
			1245	804	192	238	2	9			

There are 6 discrepancies between the modelled and reference sequences:

| Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	expression tag	UNP Q0AU90
B	0	GLY	-	expression tag	UNP Q0AU90
C	0	GLY	-	expression tag	UNP Q0AU90
D	0	GLY	-	expression tag	UNP Q0AU90
E	0	GLY	-	expression tag	UNP Q0AU90
F	0	GLY	-	expression tag	UNP Q0AU90

- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Cl	0	0
			1	1		
2	D	1	Total	Cl	0	0
			1	1		

- Molecule 3 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	3	Total 3	Na 3	0	0
3	B	1	Total 1	Na 1	0	0
3	C	1	Total 1	Na 1	0	0
3	D	3	Total 3	Na 3	0	0
3	E	1	Total 1	Na 1	0	0
3	F	1	Total 1	Na 1	0	0

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).
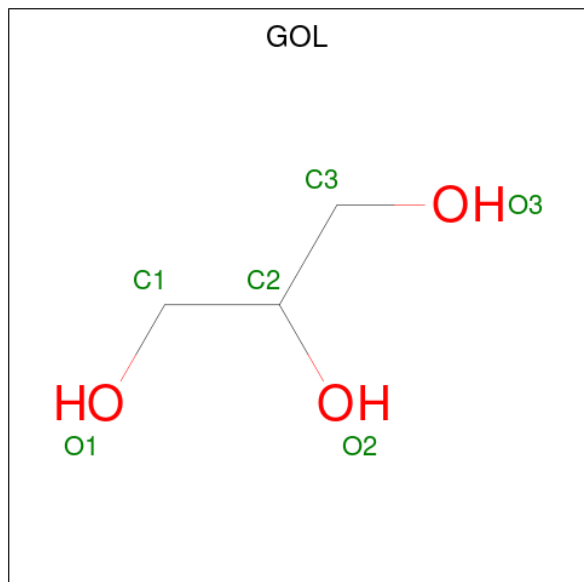
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total 6	C 3	O 3	0	0
4	B	1	Total 12	C 6	O 6	0	1
4	D	1	Total 12	C 6	O 6	0	1
4	D	1	Total 6	C 3	O 3	0	0

- Molecule 5 is water.

| Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	38	Total 40	O 40	0	2
5	B	29	Total 30	O 30	0	1
5	C	39	Total 39	O 39	0	0
5	D	28	Total 29	O 29	0	1
5	E	27	Total 27	O 27	0	0
5	F	24	Total 24	O 24	0	0

3 Residue-property plots ⓘ

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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: Putative sulfurtransferase dsrE
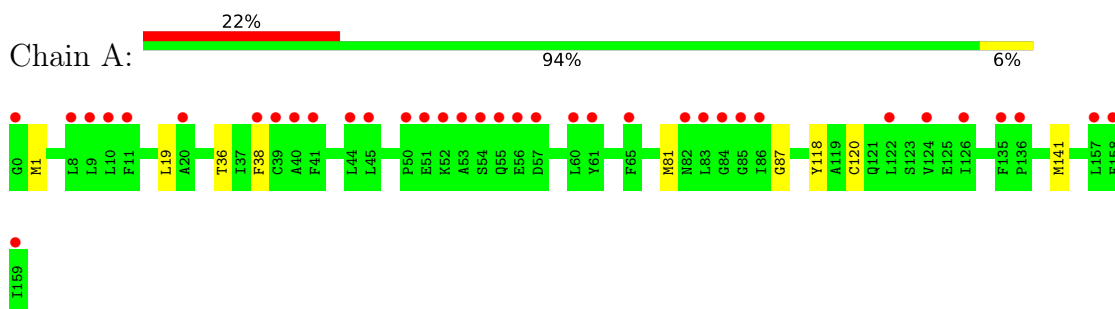
Chain A:

- Molecule 1: Putative sulfurtransferase dsrE

Chain B:
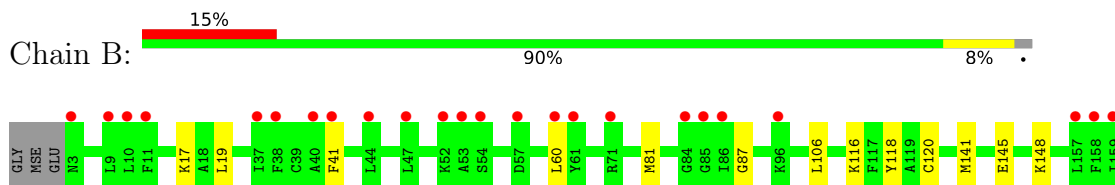
- Molecule 1: Putative sulfurtransferase dsrE
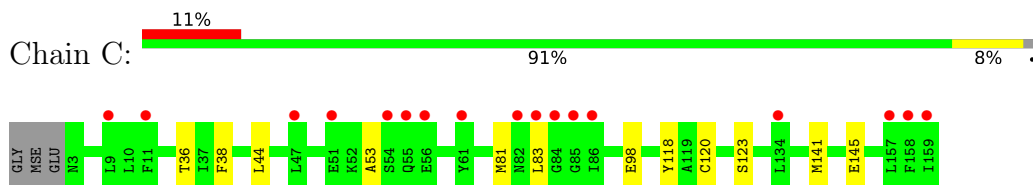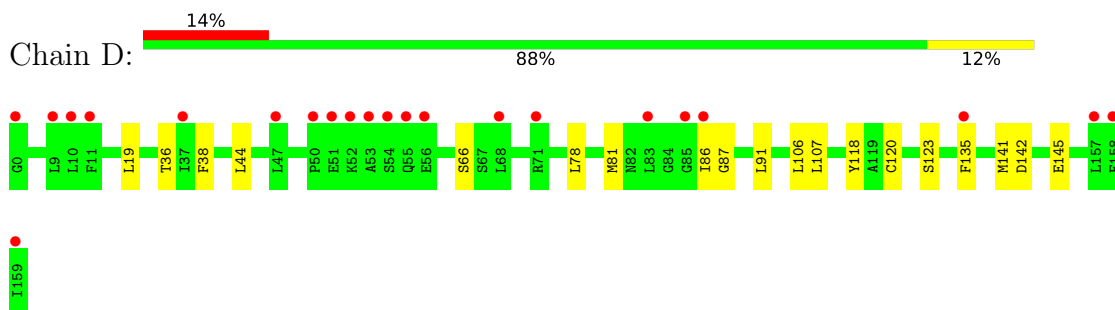
Chain C:
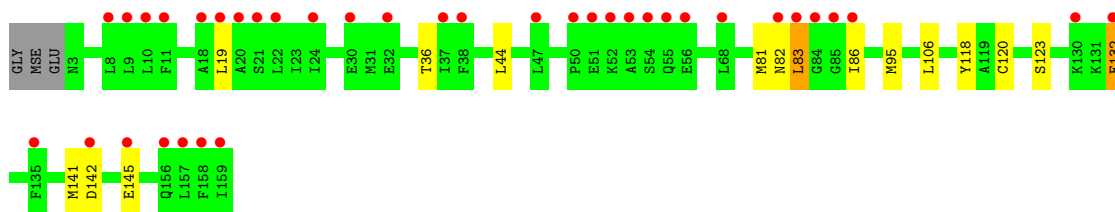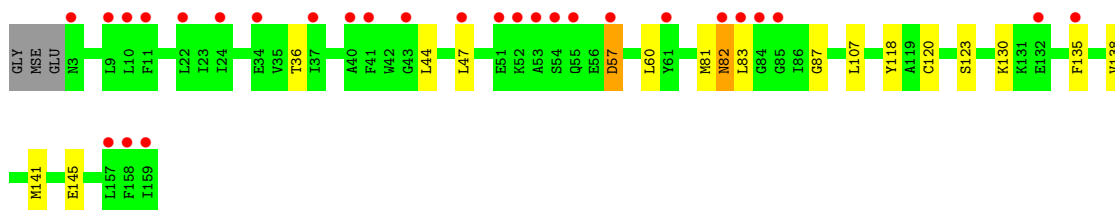

- Molecule 1: Putative sulfurtransferase dsrE

Chain D:

- Molecule 1: Putative sulfurtransferase dsrE

Chain E:

• Molecule 1: Putative sulfurtransferase dsrE

Chain F:

4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	100.42Å 76.50Å 127.65Å 90.00° 93.08° 90.00°	Depositor
Resolution (Å)	29.45 – 1.92 29.45 – 1.92	Depositor EDS
% Data completeness (in resolution range)	98.8 (29.45-1.92) 98.8 (29.45-1.92)	Depositor EDS
R_{merge}	0.03	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.92 (at 1.92Å)	Xtriage
Refinement program	REFMAC 5.5.0110	Depositor
R, R_{free}	0.190 , 0.215 0.194 , 0.218	Depositor DCC
R_{free} test set	3687 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å^2)	39.1	Xtriage
Anisotropy	0.194	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 62.8	EDS
L-test for twinning[2]	$< |L| > = 0.49, < L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	7805	wwPDB-VP
Average B, all atoms (Å^2)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.10% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.
[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: OCS, CL, NA, GOL

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	0.56	0/1307	0.63	0/1734
1	B	0.54	0/1275	0.60	0/1694
1	C	0.57	0/1304	0.64	0/1729
1	D	0.49	0/1283	0.58	0/1704
1	E	0.53	0/1262	0.59	0/1677
1	F	0.46	0/1255	0.57	0/1670
All	All	0.53	0/7686	0.60	0/10208

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	1289	0	1306	6	0
1	B	1254	0	1271	10	0
1	C	1273	0	1306	11	0
1	D	1266	0	1267	12	0
1	E	1241	0	1229	12	0
1	F	1245	0	1228	20	0
2	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	1	0	0	0	0
3	A	3	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	3	0	0	0	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0
4	A	6	0	8	0	0
4	B	12	0	16	3	0
4	D	18	0	23	0	0
5	A	40	0	0	0	0
5	B	30	0	0	0	0
5	C	39	0	0	0	0
5	D	29	0	0	0	0
5	E	27	0	0	0	0
5	F	24	0	0	0	0
All	All	7805	0	7654	67	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 (67) 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:C:141[B]:MSE:HG3	1:C:145[B]:GLU:HB3	1.62	0.80
1:B:17:LYS:HZ3	4:B:172[A]:GOL:H12	1.48	0.77
1:B:141[A]:MSE:HE3	1:B:145:GLU:HB3	1.70	0.71
1:E:141[B]:MSE:HE3	1:E:145:GLU:HB3	1.75	0.69
1:A:1:MSE:HE3	1:B:148:LYS:HA	1.75	0.69
1:B:17:LYS:HZ3	4:B:172[A]:GOL:C1	2.13	0.61
1:B:19[A]:LEU:HD12	1:B:106:LEU:HD12	1.83	0.61
1:A:81:MSE:O	1:A:87:GLY:HA3	2.01	0.61
1:B:81:MSE:O	1:B:87:GLY:HA3	2.02	0.59
1:E:132:GLU:H	1:E:132:GLU:CD	2.05	0.59
1:D:19:LEU:HD12	1:D:106:LEU:HD12	1.84	0.58
1:F:107:LEU:HD21	1:F:135[A]:PHE:CZ	2.38	0.58
1:F:141[B]:MSE:HG3	1:F:145[B]:GLU:CB	2.35	0.57
1:F:36:THR:HG23	1:F:118:TYR:CE2	2.40	0.56
1:B:116:LYS:CE	1:B:118:TYR:OH	2.54	0.56
1:E:36:THR:HG23	1:E:118:TYR:CE2	2.40	0.56
1:C:38:PHE:CD1	1:C:141[B]:MSE:SE	3.10	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:81:MSE:O	1:E:83:LEU:N	2.40	0.54
1:B:17:LYS:NZ	4:B:172[A]:GOL:H12	2.22	0.54
1:C:44:LEU:HD11	1:C:123:SER:CB	2.38	0.53
1:C:141[B]:MSE:HG3	1:C:145[B]:GLU:CB	2.36	0.53
1:D:141[A]:MSE:HE3	1:D:145[A]:GLU:HB3	1.91	0.52
1:F:57:ASP:HB3	1:F:130:LYS:NZ	2.24	0.52
1:F:141[B]:MSE:HG3	1:F:145[B]:GLU:HB2	1.90	0.52
1:C:81[B]:MSE:HE1	1:F:83:LEU:CB	2.40	0.52
1:C:36:THR:HG23	1:C:118:TYR:CE2	2.45	0.51
1:D:36:THR:HG23	1:D:118:TYR:CE2	2.45	0.51
1:F:81:MSE:O	1:F:82:ASN:C	2.49	0.51
1:D:78:LEU:HD21	1:D:91:LEU:HD23	1.92	0.49
1:C:44:LEU:HD11	1:C:123:SER:HB2	1.94	0.49
1:A:36:THR:HG23	1:A:118:TYR:CE2	2.47	0.48
1:D:44:LEU:HD11	1:D:123:SER:CB	2.43	0.48
1:D:142[A]:ASP:OD1	1:D:145[A]:GLU:HG3	2.14	0.48
1:F:81:MSE:O	1:F:83:LEU:N	2.47	0.48
1:A:38:PHE:CD1	1:A:141[A]:MSE:SE	3.17	0.47
1:F:47:LEU:HA	1:F:135[A]:PHE:CE2	2.49	0.47
1:B:60:LEU:HD12	1:F:60:LEU:HD12	1.96	0.47
1:E:141[B]:MSE:HE3	1:E:145:GLU:CB	2.44	0.47
1:F:57:ASP:HB3	1:F:130:LYS:HZ1	1.80	0.47
1:F:36:THR:HG23	1:F:118:TYR:CD2	2.51	0.46
1:F:135[A]:PHE:HB2	1:F:138:VAL:HG23	1.99	0.45
1:F:107:LEU:HD21	1:F:135[A]:PHE:HZ	1.80	0.45
1:D:38:PHE:CD1	1:D:141[B]:MSE:SE	3.20	0.45
1:F:44:LEU:HD11	1:F:123:SER:CB	2.47	0.44
1:F:141[B]:MSE:HG3	1:F:145[B]:GLU:HB3	1.99	0.44
1:F:44:LEU:HD11	1:F:123:SER:HB2	2.00	0.43
1:D:44:LEU:HD11	1:D:123:SER:HB3	2.00	0.43
1:E:36:THR:HG23	1:E:118:TYR:CD2	2.52	0.43
1:D:107:LEU:HD21	1:D:135:PHE:HE2	1.83	0.42
1:A:19[A]:LEU:HD23	1:B:41:PHE:CZ	2.54	0.42
1:E:19:LEU:HD12	1:E:106:LEU:HD12	2.02	0.42
1:E:36:THR:HG23	1:E:118:TYR:HE2	1.82	0.42
1:D:78:LEU:HD21	1:D:91:LEU:CD2	2.49	0.42
1:C:44:LEU:HD11	1:C:123:SER:HB3	2.02	0.42
1:C:118:TYR:CD1	1:C:141[A]:MSE:HG3	2.54	0.42
1:F:36:THR:HG23	1:F:118:TYR:HE2	1.84	0.42
1:C:36:THR:HG23	1:C:118:TYR:CD2	2.55	0.42
1:A:36:THR:HG23	1:A:118:TYR:CD2	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:19:LEU:HD21	1:E:95:MSE:CE	2.50	0.42
1:C:38:PHE:HD1	1:C:141[B]:MSE:SE	2.53	0.41
1:F:81:MSE:O	1:F:87:GLY:HA3	2.21	0.41
1:F:141[A]:MSE:SE	1:F:145[A]:GLU:OE1	2.89	0.40
1:E:44:LEU:HD11	1:E:123:SER:CB	2.51	0.40
1:D:81:MSE:O	1:D:87:GLY:HA3	2.22	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	164/160 (102%)	162 (99%)	2 (1%)	0	100	100
1	B	161/160 (101%)	159 (99%)	2 (1%)	0	100	100
1	C	164/160 (102%)	160 (98%)	2 (1%)	2 (1%)	13	4
1	D	163/160 (102%)	160 (98%)	3 (2%)	0	100	100
1	E	161/160 (101%)	153 (95%)	5 (3%)	3 (2%)	8	1
1	F	158/160 (99%)	154 (98%)	3 (2%)	1 (1%)	25	14
All	All	971/960 (101%)	948 (98%)	17 (2%)	6 (1%)	29	14

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	82[A]	ASN
1	E	82[B]	ASN
1	E	83	LEU
1	C	83	LEU
1	F	82	ASN
1	C	53	ALA

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	136/129 (105%)	136 (100%)	0	100	100
1	B	130/129 (101%)	130 (100%)	0	100	100
1	C	135/129 (105%)	134 (99%)	1 (1%)	84	83
1	D	130/129 (101%)	128 (98%)	2 (2%)	65	61
1	E	125/129 (97%)	122 (98%)	3 (2%)	49	41
1	F	126/129 (98%)	125 (99%)	1 (1%)	81	81
All	All	782/774 (101%)	775 (99%)	7 (1%)	81	78

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	98	GLU
1	D	66	SER
1	D	86	ILE
1	E	132	GLU
1	E	142[A]	ASP
1	E	142[B]	ASP
1	F	57	ASP

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

Mol	Chain	Res	Type
1	A	55	GLN

5.3.3   RNA ⓘ

There are no RNA molecules in this entry.

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

6 non-standard protein/DNA/RNA residues 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	#$|Z| > 2$
1	OCS	E	120	1	7,8,9	0.83	0	6,11,13	1.93	2 (33%)
1	OCS	D	120	1	7,8,9	1.06	0	6,11,13	2.39	3 (50%)
1	OCS	F	120	1	7,8,9	0.87	0	6,11,13	1.89	2 (33%)
1	OCS	B	120	1	7,8,9	1.03	0	6,11,13	2.39	2 (33%)
1	OCS	C	120	1	7,8,9	1.27	0	6,11,13	2.37	2 (33%)
1	OCS	A	120	1	7,8,9	0.98	0	6,11,13	2.45	2 (33%)

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
1	OCS	E	120	1	-	4/4/7/9	-
1	OCS	D	120	1	-	4/4/7/9	-
1	OCS	F	120	1	-	4/4/7/9	-
1	OCS	B	120	1	-	4/4/7/9	-
1	OCS	C	120	1	-	4/4/7/9	-
1	OCS	A	120	1	-	4/4/7/9	-

There are no bond length outliers.

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	120	OCS	OD3-SG-CB	4.68	112.50	106.94
1	A	120	OCS	OD3-SG-CB	4.53	112.32	106.94
1	D	120	OCS	OD1-SG-CB	4.03	111.73	106.94
1	B	120	OCS	OD3-SG-CB	3.76	111.41	106.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	E	120	OCS	OD2-SG-CB	3.63	111.52	105.74
1	B	120	OCS	OD1-SG-CB	3.52	111.13	106.94
1	C	120	OCS	OD1-SG-CB	2.86	110.33	106.94
1	A	120	OCS	OD1-SG-CB	2.79	110.25	106.94
1	F	120	OCS	OD2-SG-CB	2.77	110.15	105.74
1	F	120	OCS	OD3-SG-CB	2.70	110.14	106.94
1	D	120	OCS	OD3-SG-CB	2.61	110.04	106.94
1	E	120	OCS	OD3-SG-CB	2.46	109.86	106.94
1	D	120	OCS	OD2-SG-CB	2.36	109.50	105.74

There are no chirality outliers.

All (24) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	120	OCS	N-CA-CB-SG
1	A	120	OCS	CA-CB-SG-OD1
1	A	120	OCS	CA-CB-SG-OD3
1	B	120	OCS	N-CA-CB-SG
1	B	120	OCS	CA-CB-SG-OD1
1	B	120	OCS	CA-CB-SG-OD2
1	B	120	OCS	CA-CB-SG-OD3
1	C	120	OCS	N-CA-CB-SG
1	C	120	OCS	CA-CB-SG-OD1
1	C	120	OCS	CA-CB-SG-OD2
1	C	120	OCS	CA-CB-SG-OD3
1	D	120	OCS	N-CA-CB-SG
1	D	120	OCS	CA-CB-SG-OD1
1	D	120	OCS	CA-CB-SG-OD2
1	D	120	OCS	CA-CB-SG-OD3
1	E	120	OCS	N-CA-CB-SG
1	E	120	OCS	CA-CB-SG-OD1
1	E	120	OCS	CA-CB-SG-OD2
1	E	120	OCS	CA-CB-SG-OD3
1	F	120	OCS	N-CA-CB-SG
1	F	120	OCS	CA-CB-SG-OD1
1	F	120	OCS	CA-CB-SG-OD2
1	F	120	OCS	CA-CB-SG-OD3
1	A	120	OCS	CA-CB-SG-OD2

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 18 ligands modelled in this entry, 12 are monoatomic - leaving 6 for Mogul analysis.

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	#$|Z| > 2$
4	GOL	A	175	-	5,5,5	0.47	0	5,5,5	0.13	0
4	GOL	D	173[A]	3	5,5,5	0.40	0	5,5,5	0.23	0
4	GOL	D	173[B]	3	5,5,5	0.39	0	5,5,5	0.49	0
4	GOL	D	174	-	5,5,5	0.34	0	5,5,5	0.34	0
4	GOL	B	172[A]	3	5,5,5	0.35	0	5,5,5	0.72	0
4	GOL	B	172[B]	3	5,5,5	0.40	0	5,5,5	0.66	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
4	GOL	A	175	-	-	2/4/4/4	-
4	GOL	D	173[A]	3	-	1/4/4/4	-
4	GOL	D	173[B]	3	-	2/4/4/4	-
4	GOL	D	174	-	-	2/4/4/4	-
4	GOL	B	172[A]	3	-	0/4/4/4	-
4	GOL	B	172[B]	3	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	172[B]	GOL	O1-C1-C2-C3
4	B	172[B]	GOL	O1-C1-C2-O2
4	A	175	GOL	C1-C2-C3-O3
4	D	173[A]	GOL	O1-C1-C2-C3
4	D	173[B]	GOL	C1-C2-C3-O3
4	D	174	GOL	C1-C2-C3-O3
4	D	173[B]	GOL	O2-C2-C3-O3
4	D	174	GOL	O2-C2-C3-O3
4	A	175	GOL	O2-C2-C3-O3

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	172[A]	GOL	3	0

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(Å²)	Q<0.9
1	A	150/160 (93%)	1.29	36 (24%)	0	0	34, 49, 74, 84	0
1	B	148/160 (92%)	1.03	24 (16%)	1	2	34, 48, 72, 80	0
1	C	148/160 (92%)	1.01	17 (11%)	4	5	33, 46, 70, 78	0
1	D	150/160 (93%)	0.98	22 (14%)	2	2	39, 52, 72, 87	0
1	E	148/160 (92%)	1.34	37 (25%)	0	0	40, 52, 74, 82	0
1	F	148/160 (92%)	1.29	28 (18%)	1	1	40, 55, 72, 76	0
All	All	892/960 (92%)	1.15	164 (18%)	1	1	33, 51, 73, 87	0

All (164) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	84	GLY	9.6
1	C	86	ILE	9.0
1	F	83	LEU	8.1
1	D	51	GLU	8.0
1	E	84	GLY	7.9
1	B	86	ILE	7.7
1	A	53	ALA	7.6
1	F	82	ASN	7.5
1	E	83	LEU	7.1
1	E	54	SER	7.1
1	F	3	ASN	6.0
1	E	56	GLU	5.6
1	D	86	ILE	5.6
1	C	83	LEU	5.5
1	B	53	ALA	5.4
1	A	86	ILE	5.4
1	A	54	SER	5.4
1	F	157	LEU	5.3
1	C	85	GLY	5.2

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WORLDWIDE
wwPDB
PROTEIN DATA BANK

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Mol	Chain	Res	Type	RSRZ
1	D	0	GLY	5.2
1	E	158	PHE	5.1
1	F	10	LEU	5.1
1	C	54	SER	5.1
1	C	82	ASN	5.1
1	A	159	ILE	5.0
1	A	82	ASN	4.9
1	A	158	PHE	4.8
1	E	85	GLY	4.8
1	E	53	ALA	4.8
1	A	10	LEU	4.8
1	A	84	GLY	4.8
1	B	158	PHE	4.7
1	D	135	PHE	4.7
1	C	159	ILE	4.7
1	E	82[A]	ASN	4.7
1	E	10	LEU	4.7
1	E	9	LEU	4.6
1	F	158	PHE	4.6
1	D	157	LEU	4.5
1	A	57	ASP	4.5
1	E	55	GLN	4.5
1	E	51	GLU	4.4
1	A	83	LEU	4.3
1	A	51	GLU	4.3
1	E	159	ILE	4.2
1	F	85	GLY	4.2
1	A	11	PHE	4.2
1	A	40	ALA	4.2
1	A	157	LEU	4.2
1	B	54	SER	4.1
1	B	9	LEU	4.1
1	C	55	GLN	4.0
1	B	52	LYS	4.0
1	B	159	ILE	3.9
1	C	158	PHE	3.8
1	E	157	LEU	3.8
1	D	158	PHE	3.8
1	B	157	LEU	3.8
1	E	50	PRO	3.6
1	D	159	ILE	3.6
1	E	86	ILE	3.6

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Mol	Chain	Res	Type	RSRZ
1	F	135[A]	PHE	3.6
1	F	159	ILE	3.5
1	E	52	LYS	3.4
1	F	53	ALA	3.4
1	C	84	GLY	3.4
1	E	135	PHE	3.4
1	A	8	LEU	3.4
1	B	85	GLY	3.3
1	D	53	ALA	3.3
1	A	61	TYR	3.3
1	E	47	LEU	3.2
1	A	9	LEU	3.2
1	C	134	LEU	3.2
1	A	0	GLY	3.2
1	F	57	ASP	3.2
1	B	11	PHE	3.1
1	B	37	ILE	3.1
1	F	54	SER	3.1
1	A	56	GLU	3.1
1	E	132	GLU	3.1
1	A	39	CYS	3.1
1	A	52	LYS	3.1
1	C	157	LEU	3.0
1	D	9	LEU	3.0
1	A	136	PRO	3.0
1	E	11	PHE	2.9
1	E	130[A]	LYS	2.9
1	A	60	LEU	2.9
1	D	85	GLY	2.8
1	F	22	LEU	2.8
1	B	57	ASP	2.8
1	F	52	LYS	2.8
1	F	40	ALA	2.8
1	B	41	PHE	2.7
1	D	50	PRO	2.7
1	B	10	LEU	2.7
1	F	9	LEU	2.7
1	E	37	ILE	2.7
1	F	11	PHE	2.7
1	B	44	LEU	2.7
1	A	20	ALA	2.6
1	F	51	GLU	2.6

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Mol	Chain	Res	Type	RSRZ
1	D	56	GLU	2.6
1	F	24	ILE	2.6
1	A	44	LEU	2.6
1	C	9	LEU	2.5
1	E	142[A]	ASP	2.5
1	B	40	ALA	2.5
1	C	56	GLU	2.5
1	B	84	GLY	2.5
1	B	47	LEU	2.5
1	D	83	LEU	2.5
1	F	34	GLU	2.5
1	E	20	ALA	2.4
1	A	45	LEU	2.4
1	F	132	GLU	2.4
1	E	22	LEU	2.4
1	A	38	PHE	2.4
1	B	3	ASN	2.4
1	C	47	LEU	2.4
1	C	11	PHE	2.4
1	E	21[A]	SER	2.4
1	A	85	GLY	2.4
1	E	30	GLU	2.4
1	B	61	TYR	2.3
1	D	52	LYS	2.3
1	E	24	ILE	2.3
1	A	124	VAL	2.3
1	D	37	ILE	2.3
1	F	55	GLN	2.3
1	D	71	ARG	2.3
1	F	61	TYR	2.3
1	D	55	GLN	2.2
1	A	126	ILE	2.2
1	D	68	LEU	2.2
1	C	51[A]	GLU	2.2
1	F	41	PHE	2.2
1	A	135[A]	PHE	2.2
1	A	55	GLN	2.2
1	E	18	ALA	2.2
1	A	50	PRO	2.1
1	E	8	LEU	2.1
1	B	96	LYS	2.1
1	A	41	PHE	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	65	PHE	2.1
1	C	61	TYR	2.1
1	F	43	GLY	2.1
1	E	38	PHE	2.1
1	B	71[A]	ARG	2.1
1	F	37	ILE	2.1
1	E	68	LEU	2.1
1	D	11	PHE	2.1
1	E	19	LEU	2.1
1	F	47	LEU	2.1
1	A	122	LEU	2.0
1	D	10	LEU	2.0
1	D	47	LEU	2.0
1	D	54	SER	2.0
1	B	38	PHE	2.0
1	E	156	GLN	2.0
1	B	60	LEU	2.0
1	E	32	GLU	2.0
1	E	145	GLU	2.0

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

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. 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	B-factors(Å^2)	Q<0.9
1	OCS	B	120	9/10	0.91	0.14	41,42,56,56	0
1	OCS	D	120	9/10	0.93	0.14	45,47,59,60	0
1	OCS	C	120	9/10	0.94	0.12	37,40,52,53	0
1	OCS	A	120	9/10	0.94	0.12	45,47,56,58	0
1	OCS	E	120	9/10	0.95	0.11	49,50,59,60	0
1	OCS	F	120	9/10	0.96	0.09	48,49,58,59	0

6.3 Carbohydrates ⓘ

There are no monosaccharides 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. 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	B-factors(Å^2)	Q<0.9
4	GOL	D	173[A]	6/6	0.80	0.39	48,49,51,51	6
4	GOL	D	173[B]	6/6	0.80	0.39	43,45,46,47	6
4	GOL	B	172[A]	6/6	0.84	0.33	49,51,52,52	6
4	GOL	B	172[B]	6/6	0.84	0.33	43,47,47,47	6
4	GOL	D	174	6/6	0.85	0.18	71,73,74,74	0
3	NA	E	168	1/1	0.90	0.12	51,51,51,51	0
4	GOL	A	175	6/6	0.91	0.44	63,64,65,65	0
3	NA	C	169	1/1	0.94	0.08	56,56,56,56	0
3	NA	A	164	1/1	0.95	0.13	56,56,56,56	0
3	NA	F	163	1/1	0.95	0.36	65,65,65,65	0
3	NA	D	165	1/1	0.96	0.21	46,46,46,46	0
3	NA	B	162	1/1	0.97	0.19	57,57,57,57	0
3	NA	D	167	1/1	0.97	0.09	43,43,43,43	0
3	NA	D	171	1/1	0.98	0.11	38,38,38,38	0
3	NA	A	166	1/1	0.98	0.06	36,36,36,36	0
3	NA	A	170	1/1	0.98	0.10	32,32,32,32	0
2	CL	A	161	1/1	0.99	0.05	34,34,34,34	0
2	CL	D	160	1/1	0.99	0.06	39,39,39,39	0

6.5 Other polymers ⓘ

There are no such residues in this entry.