



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 06:39 AM GMT

PDB ID : 2XTS
Title : CRYSTAL STRUCTURE OF THE SULFANE DEHYDROGENASE SOXCD
FROM PARACOCCLUS PANTOTROPHUS
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Deposited on : 2010-10-12
Resolution : 1.33 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

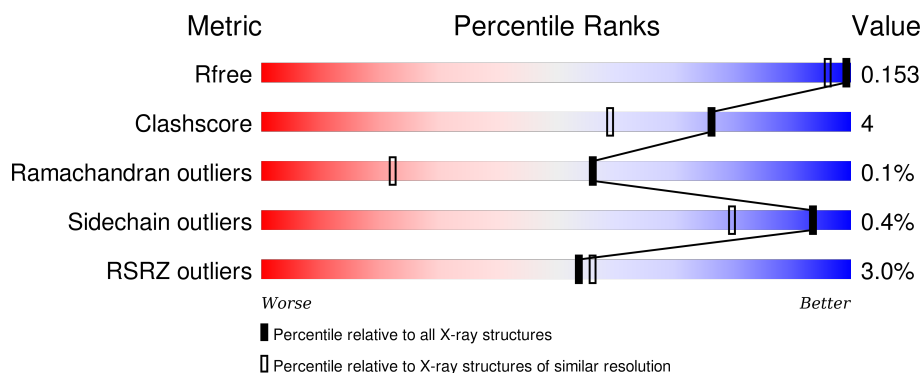
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.33 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	1723 (1.38-1.30)
Clashscore	102246	1806 (1.38-1.30)
Ramachandran outliers	100387	1749 (1.38-1.30)
Sidechain outliers	100360	1749 (1.38-1.30)
RSRZ outliers	91569	1721 (1.38-1.30)

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	390	<div> <div style="width: 91%;"></div> <div style="width: 8%;"></div> <div style="width: 1%;"></div> </div> <div>91% 8% .</div>
1	C	390	<div> <div style="width: 93%;"></div> <div style="width: 7%;"></div> <div style="width: 0%;"></div> </div> <div>93% 7%</div>
2	B	205	<div> <div style="width: 97%;"></div> <div style="width: 7%;"></div> <div style="width: 0%;"></div> </div> <div>97% .</div>
2	D	205	<div> <div style="width: 98%;"></div> <div style="width: 5%;"></div> <div style="width: 0%;"></div> </div> <div>98% .</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 criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
6	GOL	A	1432	-	-	-	X
6	GOL	A	1433	-	-	-	X
6	GOL	A	1434	-	-	-	X
6	GOL	B	1230	-	-	-	X
6	GOL	B	1231	-	-	-	X
6	GOL	C	1432	-	-	-	X
6	GOL	C	1433	-	-	-	X
6	GOL	D	1233	-	-	-	X
6	GOL	D	1234	-	-	-	X
8	CA	B	1229	-	-	-	X
8	CA	D	1232	-	-	-	X

2 Entry composition [i](#)

There are 9 unique types of molecules in this entry. The entry contains 10441 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.

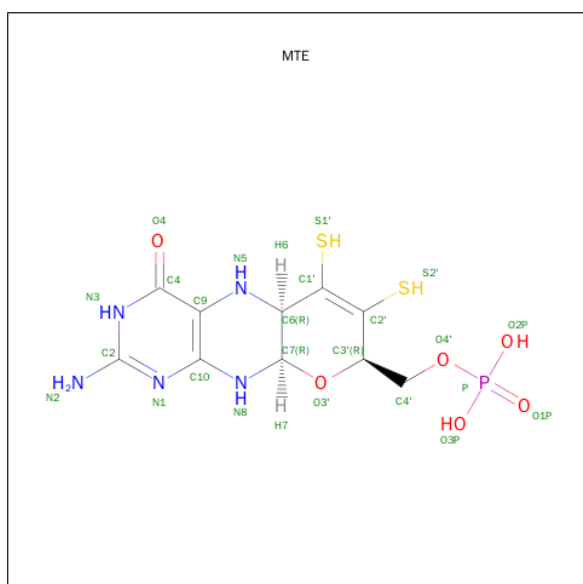
- Molecule 1 is a protein called SULFITE DEHYDROGENASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	389	Total	C	N	O	S	0	9	0
			3100	1976	535	573	16			
1	C	389	Total	C	N	O	S	0	8	0
			3102	1973	539	574	16			

- Molecule 2 is a protein called CYTOCHROME.

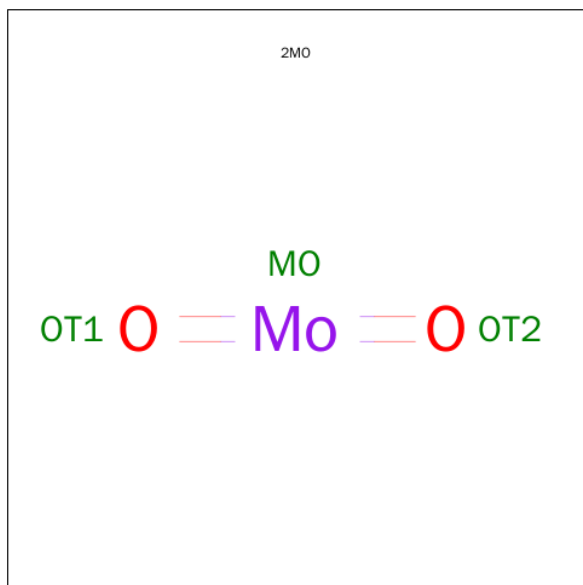
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	204	Total	C	N	O	S	0	2	1
			1533	965	247	314	7			
2	D	204	Total	C	N	O	S	0	3	0
			1548	974	248	318	8			

- Molecule 3 is PHOSPHONIC ACIDMONO-(2-AMINO-5,6-DIMERCAPTO-4-OXO-3,7,8A, 9,10,10A-HEXAHYDRO-4H-8-OXA-1,3,9,10-TETRAAZA-ANTHRACEN-7-YLMETHYL) ESTER (three-letter code: MTE) (formula: C₁₀H₁₄N₅O₆P₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	S	
			24	10	5	6	1	2	
3	C	1	Total	C	N	O	P	S	
			24	10	5	6	1	2	

- Molecule 4 is MOLYBDENUM (IV)OXIDE (three-letter code: 2MO) (formula: MoO₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	Mo	O		
			3	1	2	0	0
4	C	1	Total	Mo	O		
			3	1	2	0	0

- Molecule 5 is COBALT (II) ION (three-letter code: CO) (formula: Co).

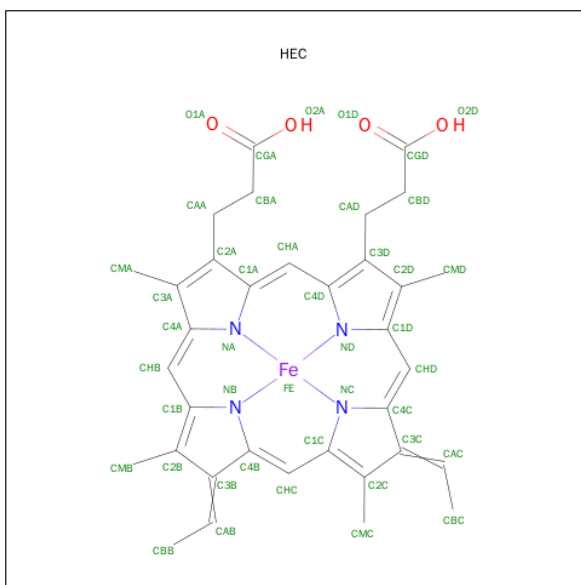
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Co		
			1	1	0	0
5	C	1	Total	Co		
			1	1	0	0

- Molecule 6 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			6	3	3		
6	A	1	Total	C	O	0	0
			6	3	3		
6	A	1	Total	C	O	0	0
			6	3	3		
6	B	1	Total	C	O	0	0
			6	3	3		
6	B	1	Total	C	O	0	0
			6	3	3		
6	C	1	Total	C	O	0	0
			6	3	3		
6	C	1	Total	C	O	0	0
			6	3	3		
6	D	1	Total	C	O	0	0
			6	3	3		
6	D	1	Total	C	O	0	0
			6	3	3		

- Molecule 7 is HEME C (three-letter code: HEC) (formula: $C_{34}H_{34}FeN_4O_4$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	B	1	Total	C	Fe	N	O	
			43	34	1	4	4	
7	D	1	Total	C	Fe	N	O	
			43	34	1	4	4	

- Molecule 8 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	B	2	Total	Ca		
			2	2	0	0
8	D	4	Total	Ca		
			4	4	0	0

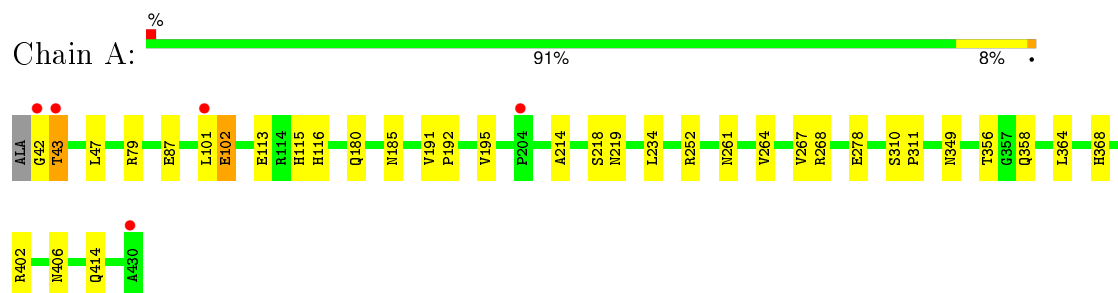
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	304	Total	O		
			304	304	0	0
9	B	172	Total	O		
			172	172	0	0
9	C	309	Total	O		
			309	309	0	0
9	D	171	Total	O		
			171	171	0	0

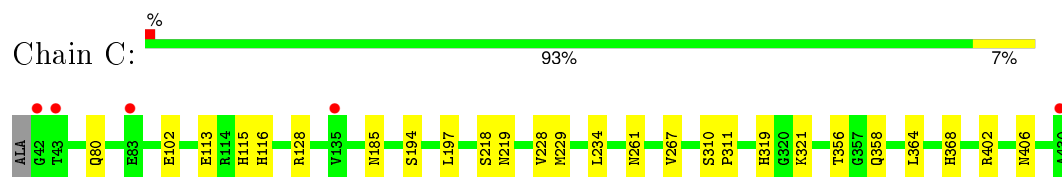
3 Residue-property plots [i](#)

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 ($\text{RSRZ} > 2$). 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.

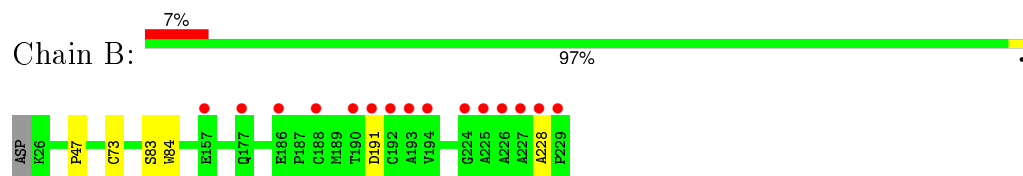
• Molecule 1: SULFITE DEHYDROGENASE



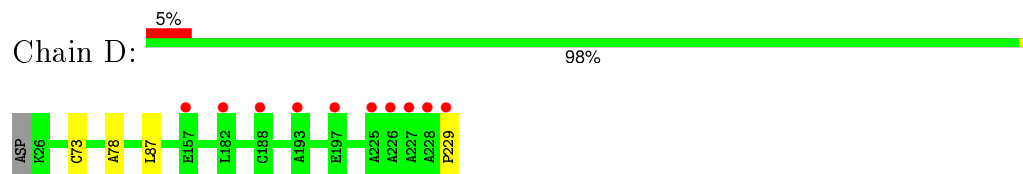
• Molecule 1: SULFITE DEHYDROGENASE



• Molecule 2: CYTOCHROME



• Molecule 2: CYTOCHROME



4 Data and refinement statistics

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, α , β , γ	122.97Å 122.97Å 76.39Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.01 – 1.33 47.90 – 1.33	Depositor EDS
% Data completeness (in resolution range)	96.8 (50.01-1.33) 96.9 (47.90-1.33)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	8.35 (at 1.33Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.107 , 0.111 0.147 , 0.153	Depositor DCC
R_{free} test set	9114 reflections (3.17%)	DCC
Wilson B-factor (Å ²)	9.3	Xtriage
Anisotropy	0.098	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.45 , 54.7	EDS
Estimated twinning fraction	0.008 for -h,-k,l 0.004 for h,-h-k,-l 0.000 for -k,-h,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 288926 reflections	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	10441	wwPDB-VP
Average B, all atoms (Å ²)	11.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.88% 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: GOL, CO, CA, HEC, 2MO, MTE

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	0.53	0/3210	0.75	2/4364 (0.0%)
1	C	0.52	0/3206	0.72	0/4357
2	B	0.47	1/1579 (0.1%)	0.68	0/2163
2	D	0.48	0/1597	0.70	1/2185 (0.0%)
All	All	0.51	1/9592 (0.0%)	0.72	3/13069 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	228	ALA	C-N	-5.10	1.24	1.34

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	79	ARG	NE-CZ-NH1	-10.29	115.16	120.30
1	A	79	ARG	NE-CZ-NH2	6.80	123.70	120.30
2	D	229	PRO	N-CA-CB	5.78	110.24	103.30

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	3100	0	3047	34	0
1	C	3102	0	3039	26	0
2	B	1533	0	1434	9	0
2	D	1548	0	1444	6	0
3	A	24	0	10	2	0
3	C	24	0	10	2	0
4	A	3	0	0	0	0
4	C	3	0	0	0	0
5	A	1	0	0	0	0
5	C	1	0	0	0	0
6	A	18	0	24	1	0
6	B	12	0	16	0	0
6	C	12	0	16	0	0
6	D	12	0	16	1	0
7	B	43	0	31	7	0
7	D	43	0	31	6	0
8	B	2	0	0	0	0
8	D	4	0	0	0	0
9	A	304	0	0	1	0
9	B	172	0	0	0	0
9	C	309	0	0	2	0
9	D	171	0	0	0	0
All	All	10441	0	9118	71	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 (71) 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)
2:D:73:CYS:SG	7:D:500:HEC:CAC	2.11	1.37
2:B:73:CYS:SG	7:B:500:HEC:CAC	2.16	1.33
2:D:73:CYS:SG	7:D:500:HEC:HAC	1.85	1.08
2:B:73:CYS:SG	7:B:500:HEC:HAC	2.01	1.00
1:C:228:VAL:HG12	1:C:229:MET:HE3	1.41	0.99
1:A:358:GLN:HE22	1:C:358:GLN:HE22	1.18	0.91
1:A:42:GLY:O	1:A:43:THR:HG22	1.76	0.85
1:A:180:GLN:HE22	1:A:414:GLN:HE21	1.23	0.84
1:C:228:VAL:HG12	1:C:229:MET:CE	2.07	0.84
1:A:87:GLU:OE2	2:B:83:SER:C	2.23	0.76
1:C:197:LEU:HD12	1:C:229:MET:HE1	1.67	0.75
1:A:87:GLU:OE2	2:B:84:TRP:N	2.23	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:73:CYS:HG	7:D:500:HEC:HAC	1.58	0.68
1:A:356:THR:OG1	1:A:368:HIS:HD2	1.76	0.68
1:C:356:THR:OG1	1:C:368:HIS:HD2	1.77	0.67
1:C:228:VAL:CG1	1:C:229:MET:HE3	2.22	0.66
2:D:73:CYS:SG	7:D:500:HEC:CBC	2.84	0.66
2:B:73:CYS:SG	7:B:500:HEC:CBC	2.82	0.66
1:A:87:GLU:HG3	1:A:87:GLU:O	1.96	0.65
1:A:47[B]:LEU:HD22	1:C:128:ARG:NH2	2.13	0.64
1:C:116:HIS:HD2	3:C:500:MTE:O4	1.81	0.64
1:A:402:ARG:HD3	1:A:406:ASN:ND2	2.14	0.63
1:A:116:HIS:HD2	3:A:500:MTE:O4	1.82	0.62
1:C:102:GLU:OE2	1:C:368:HIS:HE1	1.83	0.61
2:B:73:CYS:SG	7:B:500:HEC:C3C	2.88	0.61
1:A:102:GLU:OE1	1:A:368:HIS:HE1	1.84	0.60
2:D:73:CYS:SG	7:D:500:HEC:C3C	2.89	0.60
1:A:234:LEU:CD1	1:A:267[B]:VAL:HG11	2.36	0.56
1:A:87:GLU:CG	1:A:87:GLU:O	2.54	0.56
1:A:219:ASN:HD21	1:A:261:ASN:HD21	1.54	0.56
1:A:43:THR:HG23	1:A:43:THR:O	2.05	0.56
1:C:234:LEU:CD1	1:C:267[A]:VAL:HG11	2.38	0.54
1:C:229:MET:HE2	1:C:229:MET:HA	1.90	0.54
1:A:349:ASN:ND2	2:B:191:ASP:H	2.06	0.54
1:C:402:ARG:HD3	1:C:406:ASN:ND2	2.24	0.52
1:C:113:GLU:OE1	1:C:115:HIS:HE1	1.93	0.51
1:C:219:ASN:HD21	1:C:261:ASN:HD21	1.59	0.51
1:A:113:GLU:OE1	1:A:115:HIS:HE1	1.94	0.50
1:A:116:HIS:HE1	9:A:2184:HOH:O	1.93	0.50
1:A:185:ASN:ND2	1:A:364:LEU:H	2.10	0.49
1:C:197:LEU:HD12	1:C:229:MET:CE	2.41	0.49
7:B:500:HEC:HMB1	7:B:500:HEC:HBB3	1.94	0.49
1:C:116:HIS:HE1	9:C:2185:HOH:O	1.95	0.49
1:C:234:LEU:HD11	1:C:267[A]:VAL:CG1	2.42	0.48
1:A:191:VAL:CG1	1:A:195[B]:VAL:CG1	2.92	0.48
1:C:185:ASN:ND2	1:C:364:LEU:H	2.13	0.46
1:C:234:LEU:CD1	1:C:267[A]:VAL:CG1	2.93	0.46
1:C:116:HIS:CD2	3:C:500:MTE:O4	2.67	0.46
1:A:180:GLN:HE22	1:A:414:GLN:NE2	2.01	0.46
1:C:319:HIS:HE1	9:C:2216:HOH:O	1.99	0.46
7:D:500:HEC:HMB1	7:D:500:HEC:HBB3	1.97	0.45
1:A:219:ASN:HD21	1:A:261:ASN:ND2	2.14	0.45
1:C:310[A]:SER:HA	1:C:311:PRO:C	2.37	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:234:LEU:HD11	1:A:267[B]:VAL:CG1	2.47	0.45
1:C:219:ASN:HD21	1:C:261:ASN:ND2	2.15	0.44
1:A:278[B]:GLU:HG3	2:B:47:PRO:HG2	1.99	0.44
2:B:73:CYS:HG	7:B:500:HEC:HAC	1.79	0.44
1:A:116:HIS:CD2	3:A:500:MTE:O4	2.68	0.44
1:A:264:VAL:O	1:A:267[A]:VAL:HG22	2.17	0.44
1:A:234:LEU:CD1	1:A:267[B]:VAL:CG1	2.95	0.44
1:A:310[A]:SER:HA	1:A:311:PRO:C	2.38	0.43
1:C:194:SER:HA	1:C:229:MET:HE1	2.01	0.42
2:D:78:ALA:HB1	2:D:87:LEU:HB2	2.02	0.42
1:A:101:LEU:O	6:A:1433:GOL:H31	2.19	0.42
1:A:252:ARG:HA	1:A:267[A]:VAL:HG23	2.02	0.41
7:B:500:HEC:HBC3	7:B:500:HEC:HMC1	2.03	0.41
1:C:80:GLN:OE1	6:D:1233:GOL:H32	2.21	0.41
1:A:180:GLN:NE2	1:A:414:GLN:HE21	2.03	0.41
1:A:47[B]:LEU:HD22	1:C:128:ARG:CZ	2.50	0.40
1:A:192:PRO:HG2	1:A:195[A]:VAL:HG23	2.04	0.40
1:A:214:ALA:HA	1:A:268:ARG:HD3	2.03	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	396/390 (102%)	386 (98%)	9 (2%)	1 (0%)	46	18
1	C	395/390 (101%)	387 (98%)	8 (2%)	0	100	100
2	B	204/205 (100%)	197 (97%)	7 (3%)	0	100	100
2	D	205/205 (100%)	198 (97%)	7 (3%)	0	100	100
All	All	1200/1190 (101%)	1168 (97%)	31 (3%)	1 (0%)	56	22

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	43	THR

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	330/321 (103%)	328 (99%)	2 (1%)	90	70
1	C	329/321 (102%)	327 (99%)	2 (1%)	90	70
2	B	165/165 (100%)	165 (100%)	0	100	100
2	D	166/165 (101%)	166 (100%)	0	100	100
All	All	990/972 (102%)	986 (100%)	4 (0%)	93	80

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

Mol	Chain	Res	Type
1	A	102	GLU
1	A	218	SER
1	C	218	SER
1	C	321	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	115	HIS
1	A	116	HIS
1	A	185	ASN
1	A	219	ASN
1	A	319	HIS
1	A	334	ASN
1	A	349	ASN
1	A	368	HIS
1	A	406	ASN
1	A	414	GLN
1	C	115	HIS
1	C	116	HIS

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Mol	Chain	Res	Type
1	C	185	ASN
1	C	219	ASN
1	C	319	HIS
1	C	334	ASN
1	C	358	GLN
1	C	368	HIS
1	C	406	ASN

5.3.3 RNA ⓘ

There are no RNA molecules 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 ⓘ

Of 23 ligands modelled in this entry, 8 are monoatomic - leaving 15 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	$\# Z > 2$
6	GOL	A	1432	-	5,5,5	0.49	0	5,5,5	0.70	0
6	GOL	A	1433	-	5,5,5	0.85	0	5,5,5	0.70	0
6	GOL	A	1434	-	5,5,5	0.28	0	5,5,5	0.81	0
3	MTE	A	500	4	19,26,26	1.17	2 (10%)	19,40,40	2.03	7 (36%)
4	2MO	A	501	1,3	0,2,2	0.00	-	0,1,1	0.00	-
6	GOL	B	1230	-	5,5,5	0.41	0	5,5,5	0.24	0
6	GOL	B	1231	-	5,5,5	0.31	0	5,5,5	0.79	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	HEC	B	500	2	24,50,50	2.11	3 (12%)	19,82,82	2.38	4 (21%)
6	GOL	C	1432	-	5,5,5	0.72	0	5,5,5	1.15	0
6	GOL	C	1433	-	5,5,5	0.68	0	5,5,5	0.90	0
3	MTE	C	500	4	19,26,26	1.19	2 (10%)	19,40,40	1.80	4 (21%)
4	2MO	C	501	1,3	0,2,2	0.00	-	0,1,1	0.00	-
6	GOL	D	1233	-	5,5,5	0.63	0	5,5,5	1.29	1 (20%)
6	GOL	D	1234	-	5,5,5	0.36	0	5,5,5	0.23	0
7	HEC	D	500	2	24,50,50	2.49	4 (16%)	19,82,82	2.43	5 (26%)

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
6	GOL	A	1432	-	-	0/4/4/4	0/0/0/0
6	GOL	A	1433	-	-	0/4/4/4	0/0/0/0
6	GOL	A	1434	-	-	0/4/4/4	0/0/0/0
3	MTE	A	500	4	-	0/6/34/34	0/3/3/3
4	2MO	A	501	1,3	-	0/0/0/0	0/0/0/0
6	GOL	B	1230	-	-	0/4/4/4	0/0/0/0
6	GOL	B	1231	-	-	0/4/4/4	0/0/0/0
7	HEC	B	500	2	-	0/6/54/54	0/0/8/8
6	GOL	C	1432	-	-	0/4/4/4	0/0/0/0
6	GOL	C	1433	-	-	0/4/4/4	0/0/0/0
3	MTE	C	500	4	-	0/6/34/34	0/3/3/3
4	2MO	C	501	1,3	-	0/0/0/0	0/0/0/0
6	GOL	D	1233	-	-	0/4/4/4	0/0/0/0
6	GOL	D	1234	-	-	0/4/4/4	0/0/0/0
7	HEC	D	500	2	-	0/6/54/54	0/0/8/8

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	D	500	HEC	C3B-C2B	-8.13	1.32	1.40
7	D	500	HEC	C3C-C2C	-6.90	1.33	1.40
7	B	500	HEC	C3C-C2C	-6.10	1.34	1.40
7	B	500	HEC	C3B-C2B	-5.97	1.34	1.40
3	C	500	MTE	O3'-C7	-2.33	1.40	1.43
3	C	500	MTE	C7-C6	-2.28	1.51	1.53
3	A	500	MTE	C4-N3	2.03	1.36	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	D	500	HEC	C4B-NB	2.13	1.39	1.36
3	A	500	MTE	C9-C10	2.74	1.47	1.41
7	D	500	HEC	C3D-C2D	2.94	1.46	1.37
7	B	500	HEC	C3D-C2D	3.50	1.48	1.37

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	B	500	HEC	CBB-CAB-C3B	-7.86	109.88	127.35
7	D	500	HEC	CBB-CAB-C3B	-7.79	110.05	127.35
7	D	500	HEC	CMB-C2B-C1B	-4.36	121.15	128.36
7	B	500	HEC	CMB-C2B-C1B	-3.44	122.67	128.36
7	B	500	HEC	CBC-CAC-C3C	-3.05	120.56	127.35
3	A	500	MTE	O4'-P-O1P	-2.52	100.74	107.14
7	B	500	HEC	CMC-C2C-C1C	-2.23	124.67	128.36
7	D	500	HEC	CAA-C2A-C1A	-2.22	124.60	127.01
7	D	500	HEC	CMC-C2C-C1C	-2.09	124.91	128.36
3	A	500	MTE	N3-C2-N1	-2.08	122.13	125.53
7	D	500	HEC	CBC-CAC-C3C	-2.04	122.81	127.35
3	A	500	MTE	C9-N5-C6	-2.01	113.25	118.65
3	C	500	MTE	C4-C9-C10	2.23	116.58	114.56
3	C	500	MTE	C9-C10-N8	2.41	120.86	118.34
3	A	500	MTE	O3P-P-O2P	2.58	117.20	107.38
6	D	1233	GOL	O3-C3-C2	2.64	122.97	110.18
3	A	500	MTE	C2-N1-C10	2.87	120.99	114.54
3	C	500	MTE	O3P-P-O2P	2.92	118.49	107.38
3	A	500	MTE	C9-C10-N8	3.66	122.17	118.34
3	A	500	MTE	C4-N3-C2	4.73	122.51	115.94
3	C	500	MTE	C4-N3-C2	4.89	122.72	115.94

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6 monomers are involved in 19 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	1433	GOL	1	0
3	A	500	MTE	2	0
7	B	500	HEC	7	0
3	C	500	MTE	2	0
6	D	1233	GOL	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	D	500	HEC	6	0

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	389/390 (99%)	0.38	5 (1%) 79 82	6, 9, 17, 30	2 (0%)
1	C	389/390 (99%)	0.37	5 (1%) 79 82	6, 9, 17, 28	0
2	B	204/205 (99%)	0.58	15 (7%) 17 17	7, 12, 21, 27	0
2	D	204/205 (99%)	0.52	10 (4%) 33 33	7, 12, 19, 29	0
All	All	1186/1190 (99%)	0.43	35 (2%) 54 56	6, 10, 18, 30	2 (0%)

All (35) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	42	GLY	8.8
2	B	229	PRO	7.3
2	D	228	ALA	7.2
2	B	228	ALA	6.4
2	B	227	ALA	6.1
2	B	193	ALA	5.9
2	D	229	PRO	5.4
2	B	226	ALA	5.3
1	C	42	GLY	5.3
2	D	227	ALA	4.3
1	A	43	THR	4.0
2	D	226	ALA	4.0
2	B	188	CYS	3.3
2	D	188	CYS	3.1
2	B	186	GLU	3.0
2	B	224	GLY	3.0
1	C	43	THR	3.0
2	B	191	ASP	3.0
1	C	135	VAL	3.0
2	B	225	ALA	2.8
2	D	225	ALA	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	430	ALA	2.7
2	B	190	THR	2.6
2	B	192	CYS	2.5
2	D	193	ALA	2.4
2	B	177	GLN	2.4
2	D	182	LEU	2.4
1	C	430	ALA	2.4
2	B	157	GLU	2.4
2	B	194[A]	VAL	2.2
1	A	204	PRO	2.1
2	D	157	GLU	2.1
1	C	83	GLU	2.1
1	A	101	LEU	2.0
2	D	197[A]	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, 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
6	GOL	A	1434	6/6	0.93	0.29	25.17	5,6,6,7	0
6	GOL	C	1433	6/6	0.86	0.29	15.28	5,6,6,7	0
6	GOL	B	1231	6/6	0.97	0.23	13.65	4,5,6,7	0
6	GOL	C	1432	6/6	0.96	0.21	11.66	0,4,4,5	0
6	GOL	A	1433	6/6	0.88	0.26	11.12	5,6,6,7	0
6	GOL	D	1234	6/6	0.87	0.31	7.98	4,6,7,7	0
6	GOL	B	1230	6/6	0.86	0.25	7.14	4,6,6,7	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
6	GOL	D	1233	6/6	0.91	0.34	6.32	0,5,5,7	0
6	GOL	A	1432	6/6	0.97	0.24	6.26	4,5,5,5	0
8	CA	B	1229	1/1	0.98	0.19	3.46	5,5,5,5	1
8	CA	D	1232	1/1	0.97	0.20	3.22	5,5,5,5	1
7	HEC	D	500	43/43	0.99	0.08	-0.41	1,2,3,3	0
7	HEC	B	500	43/43	0.99	0.08	-1.27	1,2,3,3	0
5	CO	A	1431	1/1	1.00	0.07	-1.83	2,2,2,2	1
4	2MO	C	501	3/3	1.00	0.08	-2.15	2,2,3,3	0
4	2MO	A	501	3/3	1.00	0.08	-2.72	2,2,3,3	0
3	MTE	A	500	24/24	0.99	0.04	-4.47	0,2,2,2	0
3	MTE	C	500	24/24	0.99	0.04	-4.58	1,1,2,6	0
5	CO	C	1431	1/1	1.00	0.05	-5.01	2,2,2,2	1
8	CA	D	1231	1/1	0.98	0.22	-	5,5,5,5	1
8	CA	B	1228	1/1	0.99	0.21	-	5,5,5,5	1
8	CA	D	1230	1/1	0.99	0.19	-	4,4,4,4	1
8	CA	D	1229	1/1	0.99	0.13	-	4,4,4,4	1

6.5 Other polymers [i](#)

There are no such residues in this entry.