Full wwPDB X-ray Structure Validation Report (i)

Aug 20, 2023 – 01:08 PM EDT

PDB ID	:	2O2P
Title	:	Crystal structure of the C-terminal domain of rat 10'formyltetrahydrofolate dehydrogenase
Authors	:	Tsybovsky, Y.; Donato, H.; Krupenko, N.I.; Davies, C.; Krupenko, S.A.
Deposited on	:	2006-11-30
Resolution	:	1.70 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
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

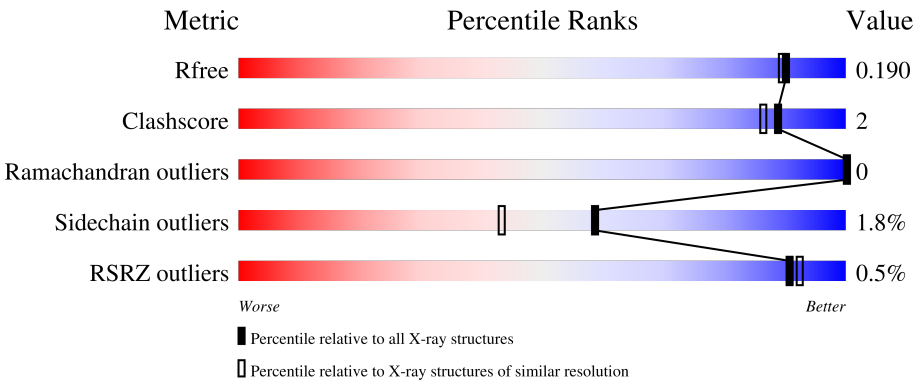
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

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 1.70 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}	130704	4298 (1.70-1.70)
Clashscore	141614	4695 (1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (1.70-1.70)
RSRZ outliers	127900	4222 (1.70-1.70)

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	517	92% • • •
1	B	517	% 91% • •
1	C	517	90% 5% • •
1	D	517	% 90% 6% •

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 17701 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 Formyltetrahydrofolate dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	498	3945	2508	676	739	22	29	24	0
1	B	498	3939	2503	676	738	22	16	24	0
1	C	498	3925	2495	677	731	22	17	21	0
1	D	498	3933	2501	673	737	22	15	22	0

There are 44 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	386	MET	-	initiating methionine	UNP Q5HZB2
A	387	ARG	-	cloning artifact	UNP Q5HZB2
A	388	GLY	-	cloning artifact	UNP Q5HZB2
A	389	SER	-	cloning artifact	UNP Q5HZB2
A	390	HIS	-	expression tag	UNP Q5HZB2
A	391	HIS	-	expression tag	UNP Q5HZB2
A	392	HIS	-	expression tag	UNP Q5HZB2
A	393	HIS	-	expression tag	UNP Q5HZB2
A	394	HIS	-	expression tag	UNP Q5HZB2
A	395	THR	-	cloning artifact	UNP Q5HZB2
A	396	THR	-	cloning artifact	UNP Q5HZB2
B	386	MET	-	initiating methionine	UNP Q5HZB2
B	387	ARG	-	cloning artifact	UNP Q5HZB2
B	388	GLY	-	cloning artifact	UNP Q5HZB2
B	389	SER	-	cloning artifact	UNP Q5HZB2
B	390	HIS	-	expression tag	UNP Q5HZB2
B	391	HIS	-	expression tag	UNP Q5HZB2
B	392	HIS	-	expression tag	UNP Q5HZB2
B	393	HIS	-	expression tag	UNP Q5HZB2
B	394	HIS	-	expression tag	UNP Q5HZB2
B	395	THR	-	cloning artifact	UNP Q5HZB2

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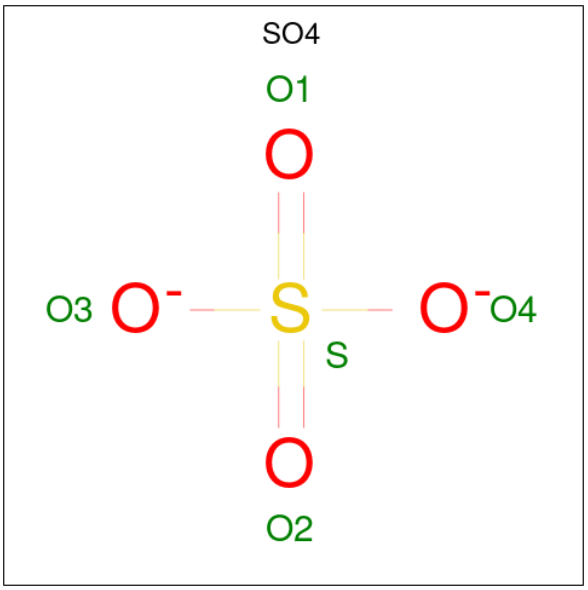
Chain	Residue	Modelled	Actual	Comment	Reference
B	396	THR	-	cloning artifact	UNP Q5HZB2
C	386	MET	-	initiating methionine	UNP Q5HZB2
C	387	ARG	-	cloning artifact	UNP Q5HZB2
C	388	GLY	-	cloning artifact	UNP Q5HZB2
C	389	SER	-	cloning artifact	UNP Q5HZB2
C	390	HIS	-	expression tag	UNP Q5HZB2
C	391	HIS	-	expression tag	UNP Q5HZB2
C	392	HIS	-	expression tag	UNP Q5HZB2
C	393	HIS	-	expression tag	UNP Q5HZB2
C	394	HIS	-	expression tag	UNP Q5HZB2
C	395	THR	-	cloning artifact	UNP Q5HZB2
C	396	THR	-	cloning artifact	UNP Q5HZB2
D	386	MET	-	initiating methionine	UNP Q5HZB2
D	387	ARG	-	cloning artifact	UNP Q5HZB2
D	388	GLY	-	cloning artifact	UNP Q5HZB2
D	389	SER	-	cloning artifact	UNP Q5HZB2
D	390	HIS	-	expression tag	UNP Q5HZB2
D	391	HIS	-	expression tag	UNP Q5HZB2
D	392	HIS	-	expression tag	UNP Q5HZB2
D	393	HIS	-	expression tag	UNP Q5HZB2
D	394	HIS	-	expression tag	UNP Q5HZB2
D	395	THR	-	cloning artifact	UNP Q5HZB2
D	396	THR	-	cloning artifact	UNP Q5HZB2

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
2	A	1	5	4	1	0	0
			Total	O	S		
2	A	1	5	4	1	0	0
			Total	O	S		
2	A	1	5	4	1	0	0
			Total	O	S		
2	A	1	5	4	1	0	0
			Total	O	S		
2	A	1	5	4	1	0	0
			Total	O	S		
2	A	1	5	4	1	0	0
			Total	O	S		
2	A	1	5	4	1	0	0
			Total	O	S		
2	A	1	5	4	1	0	0
			Total	O	S		
2	B	1	5	4	1	0	0
			Total	O	S		
2	B	1	5	4	1	0	0
			Total	O	S		
2	B	1	5	4	1	0	0
			Total	O	S		
2	B	1	5	4	1	0	0
			Total	O	S		
2	B	1	5	4	1	0	0
			Total	O	S		
2	B	1	5	4	1	0	0
			Total	O	S		
2	B	1	5	4	1	0	0
			Total	O	S		
2	B	1	5	4	1	0	0
			Total	O	S		
2	C	1	5	4	1	0	0
			Total	O	S		
2	C	1	5	4	1	0	0
			Total	O	S		
2	C	1	5	4	1	0	0
			Total	O	S		
2	C	1	5	4	1	0	0
			Total	O	S		
2	C	1	5	4	1	0	0
			Total	O	S		
2	C	1	5	4	1	0	0

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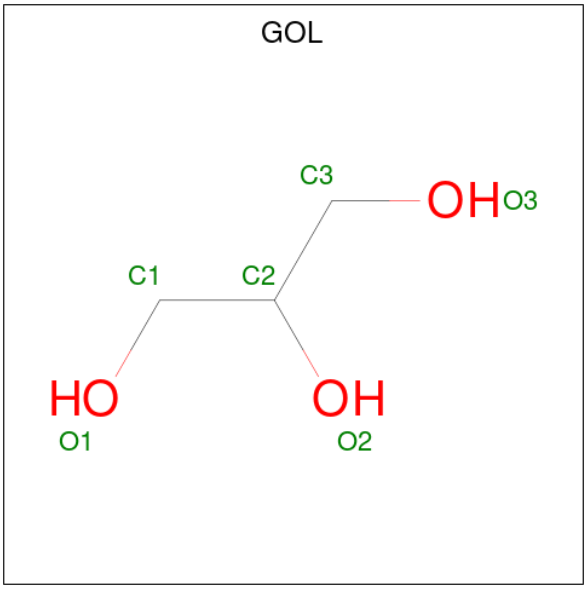
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	C	1	Total O S 5 4 1	0	0
2	D	1	Total O S 5 4 1	0	0
2	D	1	Total O S 5 4 1	0	0
2	D	1	Total O S 5 4 1	0	0
2	D	1	Total O S 5 4 1	0	0
2	D	1	Total O S 5 4 1	0	0

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 4 is water.

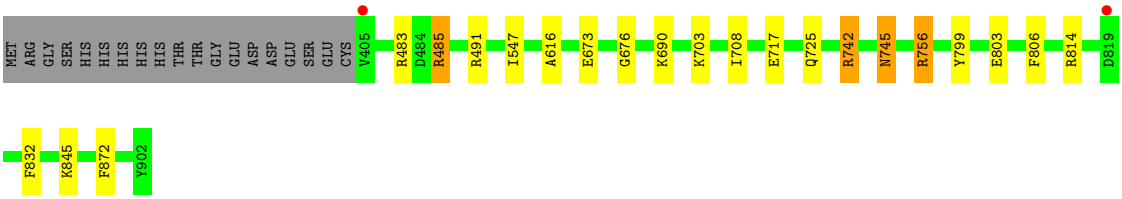
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	457	457	457	0	6
			Total	O		
4	B	418	418	418	0	6
			Total	O		
4	C	490	490	490	0	6
			Total	O		
4	D	430	430	430	0	5

3 Residue-property plots (i)

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.

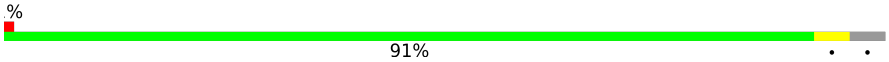
• Molecule 1: Formyltetrahydrofolate dehydrogenase

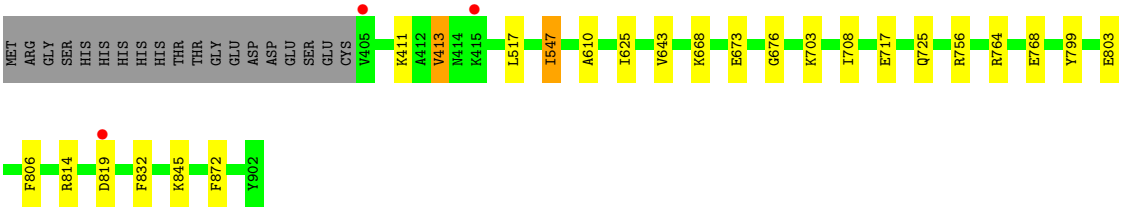
Chain A:



• Molecule 1: Formyltetrahydrofolate dehydrogenase

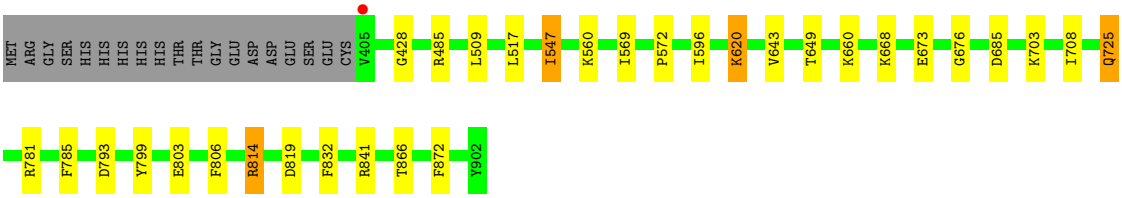
Chain B:





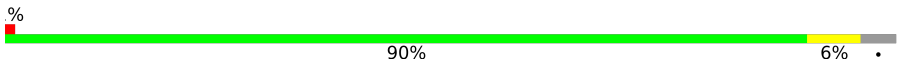
• Molecule 1: Formyltetrahydrofolate dehydrogenase

Chain C:



• Molecule 1: Formyltetrahydrofolate dehydrogenase

Chain D:



K703
Q725
K735
N745
R756
R764
E768
R781
F785
Y799
E803
F806
D819
F832
I895
Y902

4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	259.50Å 194.40Å 97.30Å 90.00° 108.90° 90.00°	Depositor
Resolution (Å)	50.00 – 1.70 49.91 – 1.70	Depositor EDS
% Data completeness (in resolution range)	97.5 (50.00-1.70) 97.4 (49.91-1.70)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	0.09	Depositor
$< I/\sigma(I) >$ [1]	2.46 (at 1.70Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.174 , 0.189 0.176 , 0.190	Depositor DCC
R_{free} test set	24236 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å^2)	17.7	Xtriage
Anisotropy	0.145	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 48.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	17701	wwPDB-VP
Average B, all atoms (Å^2)	19.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.70% 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, 0.333 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: SO4, 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	0.88	5/4114 (0.1%)	0.67	7/5560 (0.1%)
1	B	0.70	2/4114 (0.0%)	0.65	2/5560 (0.0%)
1	C	0.64	4/4088 (0.1%)	0.68	4/5525 (0.1%)
1	D	0.58	2/4095 (0.0%)	0.63	1/5535 (0.0%)
All	All	0.71	13/16411 (0.1%)	0.66	14/22180 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	756[A]	ARG	CD-NE	26.29	1.91	1.46
1	A	756[B]	ARG	CD-NE	26.29	1.91	1.46
1	B	725[A]	GLN	CG-CD	-20.95	1.02	1.51
1	B	725[B]	GLN	CG-CD	-20.95	1.02	1.51
1	A	725[A]	GLN	CG-CD	18.41	1.93	1.51
1	A	725[B]	GLN	CG-CD	18.41	1.93	1.51
1	C	725[A]	GLN	CG-CD	10.26	1.74	1.51
1	C	725[B]	GLN	CG-CD	10.26	1.74	1.51
1	D	725[A]	GLN	CG-CD	9.39	1.72	1.51
1	D	725[B]	GLN	CG-CD	9.39	1.72	1.51
1	C	620[A]	LYS	CE-NZ	7.88	1.68	1.49
1	C	620[B]	LYS	CE-NZ	7.88	1.68	1.49
1	A	690	LYS	CG-CD	-5.21	1.34	1.52

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	756[A]	ARG	CD-NE-CZ	10.78	138.70	123.60
1	A	756[B]	ARG	CD-NE-CZ	10.78	138.70	123.60
1	B	725[A]	GLN	CB-CG-CD	9.39	136.02	111.60
1	B	725[B]	GLN	CB-CG-CD	9.39	136.02	111.60
1	C	814	ARG	NE-CZ-NH2	-7.67	116.47	120.30
1	C	485	ARG	NE-CZ-NH2	-6.95	116.83	120.30
1	A	725[A]	GLN	CB-CG-CD	-6.37	95.03	111.60
1	A	725[B]	GLN	CB-CG-CD	-6.37	95.03	111.60
1	C	485	ARG	NE-CZ-NH1	5.97	123.28	120.30
1	C	814	ARG	NE-CZ-NH1	5.82	123.21	120.30
1	A	756[A]	ARG	CG-CD-NE	-5.54	100.16	111.80
1	A	756[B]	ARG	CG-CD-NE	-5.54	100.16	111.80
1	D	485	ARG	NE-CZ-NH2	-5.26	117.67	120.30
1	A	485	ARG	NE-CZ-NH2	-5.08	117.76	120.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	756[A]	ARG	Sidechain
1	A	756[B]	ARG	Sidechain

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	3945	0	3954	10	0
1	B	3939	0	3945	14	0
1	C	3925	0	3934	20	0
1	D	3933	0	3940	18	0
2	A	40	0	0	0	0
2	B	40	0	0	0	0
2	C	35	0	0	0	0
2	D	25	0	0	1	0
3	A	6	0	8	0	0
3	B	6	0	8	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	6	0	8	1	0
3	D	6	0	8	0	0
4	A	457	0	0	1	0
4	B	418	0	0	4	0
4	C	490	0	0	1	0
4	D	430	0	0	3	0
All	All	17701	0	15805	60	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 2.

All (60) 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:841[B]:ARG:HG2	1:C:841[B]:ARG:HH11	1.12	1.12
1:C:799:TYR:CE2	1:C:803[A]:GLU:HG3	2.15	0.81
1:B:799:TYR:CE2	1:B:803[B]:GLU:HG3	2.18	0.79
1:A:799:TYR:CE2	1:A:803[A]:GLU:HG3	2.20	0.77
4:B:3437:HOH:O	1:C:560[A]:LYS:HG2	1.83	0.77
1:C:793:ASP:OD2	1:C:814:ARG:NH2	2.19	0.75
1:B:768[B]:GLU:HG3	4:B:3442:HOH:O	1.84	0.74
1:A:717:GLU:OE2	1:A:814:ARG:HD3	1.88	0.74
1:D:768[B]:GLU:HG3	4:D:3455:HOH:O	1.92	0.70
1:D:428:GLY:HA3	1:D:620[B]:LYS:HD2	1.75	0.67
1:D:799:TYR:CE2	1:D:803[A]:GLU:HG3	2.30	0.65
1:C:841[B]:ARG:HG2	1:C:841[B]:ARG:NH1	1.92	0.62
1:D:781[B]:ARG:HD2	1:D:785:PHE:CD2	2.38	0.58
1:C:428:GLY:HA3	1:C:620[B]:LYS:HG3	1.88	0.56
1:B:676:GLY:HA2	1:B:832[A]:PHE:CD1	2.41	0.55
1:A:491:ARG:HD2	1:A:616:ALA:O	2.07	0.55
1:B:717:GLU:OE2	1:B:814:ARG:HD3	2.07	0.55
1:C:620[B]:LYS:HE3	4:C:3504:HOH:O	2.07	0.54
1:A:485:ARG:NH2	4:A:3464:HOH:O	2.39	0.51
1:D:692:VAL:O	1:D:696:MET:HG2	2.11	0.51
1:D:428:GLY:HA3	1:D:620[A]:LYS:HG2	1.93	0.50
1:B:610:ALA:HB2	1:B:625:ILE:HD12	1.94	0.50
1:C:781[B]:ARG:HD2	1:C:785:PHE:CD2	2.48	0.49
1:A:676:GLY:HA2	1:A:832[A]:PHE:CD1	2.48	0.49
1:B:411:LYS:HE3	1:B:413:VAL:HG11	1.94	0.49
1:C:866:THR:OG1	3:C:2003:GOL:H11	2.14	0.48
1:D:491[B]:ARG:HH12	1:D:498:GLN:HE22	1.62	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:756:ARG:NH2	4:D:3378:HOH:O	2.47	0.47
1:B:708:ILE:CG2	1:B:872[A]:PHE:HE1	2.27	0.47
1:B:799:TYR:CZ	1:B:803[B]:GLU:HG3	2.49	0.47
1:C:660:LYS:HG3	1:D:660:LYS:HG3	1.97	0.47
1:C:547:ILE:H	1:C:547:ILE:HD13	1.81	0.46
1:D:676:GLY:HA2	1:D:832[A]:PHE:CD1	2.51	0.46
1:B:764:ARG:O	1:B:768[B]:GLU:HG2	2.16	0.45
1:C:676:GLY:HA2	1:C:832[A]:PHE:CD1	2.51	0.45
1:C:685:ASP:O	1:C:841[A]:ARG:HD2	2.16	0.45
1:B:768[B]:GLU:CG	4:B:3442:HOH:O	2.54	0.45
1:B:547:ILE:H	1:B:547:ILE:HD13	1.82	0.44
1:A:745:ASN:C	1:A:745:ASN:HD22	2.21	0.44
1:B:411:LYS:HE3	1:B:413:VAL:CG1	2.48	0.44
1:C:708:ILE:CG2	1:C:872[A]:PHE:HE1	2.31	0.44
1:B:756[A]:ARG:NH2	4:B:3332:HOH:O	2.50	0.43
1:D:561:LYS:HD3	1:D:895:ILE:HG12	2.00	0.43
1:C:643:VAL:O	1:C:668:LYS:HE3	2.18	0.43
1:D:610:ALA:HB2	1:D:625:ILE:HD12	2.00	0.43
1:D:735:LYS:H	1:D:745:ASN:HD21	1.66	0.43
1:D:768[B]:GLU:CG	4:D:3455:HOH:O	2.59	0.42
1:A:708:ILE:CG2	1:A:872[A]:PHE:HE1	2.32	0.42
1:C:572:PRO:HD3	1:C:649:THR:HB	2.01	0.42
1:B:643:VAL:O	1:B:668:LYS:HE3	2.19	0.42
1:C:569:ILE:HD11	1:C:596:ILE:HG12	2.01	0.42
1:D:517:LEU:HD11	1:D:701:PHE:CZ	2.55	0.41
1:A:483:ARG:HB3	1:D:548:ASN:HD21	1.84	0.41
1:A:799:TYR:CZ	1:A:803[A]:GLU:HG3	2.56	0.41
1:A:742:ARG:HD3	1:A:742:ARG:HA	1.80	0.41
1:D:669:LYS:NZ	2:D:3026:SO4:O2	2.34	0.41
1:D:764:ARG:O	1:D:768[B]:GLU:HG2	2.20	0.41
1:C:547:ILE:H	1:C:547:ILE:CD1	2.35	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	520/517 (101%)	509 (98%)	11 (2%)	0	100	100
1	B	520/517 (101%)	506 (97%)	14 (3%)	0	100	100
1	C	517/517 (100%)	504 (98%)	13 (2%)	0	100	100
1	D	518/517 (100%)	505 (98%)	13 (2%)	0	100	100
All	All	2075/2068 (100%)	2024 (98%)	51 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	432/426 (101%)	425 (98%)	7 (2%)	62	48
1	B	432/426 (101%)	424 (98%)	8 (2%)	57	41
1	C	429/426 (101%)	420 (98%)	9 (2%)	53	36
1	D	430/426 (101%)	424 (99%)	6 (1%)	67	53
All	All	1723/1704 (101%)	1693 (98%)	30 (2%)	59	46

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	547	ILE
1	A	673	GLU
1	A	703	LYS
1	A	742	ARG
1	A	745	ASN
1	A	806	PHE
1	A	845	LYS
1	B	413	VAL
1	B	517	LEU
1	B	547	ILE

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Mol	Chain	Res	Type
1	B	673	GLU
1	B	703	LYS
1	B	806	PHE
1	B	819	ASP
1	B	845	LYS
1	C	509	LEU
1	C	517	LEU
1	C	547	ILE
1	C	673	GLU
1	C	703	LYS
1	C	725[A]	GLN
1	C	725[B]	GLN
1	C	806	PHE
1	C	819	ASP
1	D	418	LEU
1	D	547	ILE
1	D	673	GLU
1	D	703	LYS
1	D	745	ASN
1	D	806	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (24) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	457	GLN
1	A	600	GLN
1	A	706	ASN
1	A	745	ASN
1	A	750	ASN
1	A	797	HIS
1	B	457	GLN
1	B	706	ASN
1	B	797	HIS
1	C	407	ASN
1	C	457	GLN
1	C	600	GLN
1	C	706	ASN
1	C	750	ASN
1	C	797	HIS
1	D	407	ASN
1	D	457	GLN
1	D	498	GLN

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Mol	Chain	Res	Type
1	D	548	ASN
1	D	600	GLN
1	D	706	ASN
1	D	745	ASN
1	D	750	ASN
1	D	797	HIS

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

32 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	$\#\|Z\| > 2$
2	SO4	B	3004	-	4,4,4	0.16	0	6,6,6	0.14	0
2	SO4	D	3012	-	4,4,4	0.13	0	6,6,6	0.10	0
2	SO4	B	3024	-	4,4,4	0.26	0	6,6,6	0.39	0
2	SO4	A	3017	-	4,4,4	0.14	0	6,6,6	0.13	0
2	SO4	C	3019	-	4,4,4	0.15	0	6,6,6	0.16	0
2	SO4	A	3001	-	4,4,4	0.12	0	6,6,6	0.13	0
2	SO4	A	3025	-	4,4,4	0.12	0	6,6,6	0.39	0
2	SO4	A	3011	-	4,4,4	0.14	0	6,6,6	0.08	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	SO4	A	3014	-	4,4,4	0.13	0	6,6,6	0.16	0
3	GOL	C	2003	-	5,5,5	0.30	0	5,5,5	0.41	0
2	SO4	B	3009	-	4,4,4	0.15	0	6,6,6	0.05	0
2	SO4	B	3005	-	4,4,4	0.13	0	6,6,6	0.23	0
2	SO4	A	3006	-	4,4,4	0.14	0	6,6,6	0.30	0
2	SO4	D	3008	-	4,4,4	0.12	0	6,6,6	0.21	0
2	SO4	C	3010	-	4,4,4	0.14	0	6,6,6	0.10	0
2	SO4	C	3022	-	4,4,4	0.12	0	6,6,6	0.44	0
2	SO4	B	3021	-	4,4,4	0.15	0	6,6,6	0.13	0
2	SO4	B	3015	-	4,4,4	0.17	0	6,6,6	0.17	0
2	SO4	B	3018	-	4,4,4	0.16	0	6,6,6	0.22	0
2	SO4	D	3016	-	4,4,4	0.15	0	6,6,6	0.16	0
2	SO4	D	3023	-	4,4,4	0.15	0	6,6,6	0.11	0
2	SO4	C	3028	-	4,4,4	0.18	0	6,6,6	0.29	0
2	SO4	A	3002	-	4,4,4	0.16	0	6,6,6	0.19	0
3	GOL	B	2002	-	5,5,5	0.32	0	5,5,5	0.31	0
2	SO4	C	3007	-	4,4,4	0.14	0	6,6,6	0.36	0
2	SO4	A	3020	-	4,4,4	0.20	0	6,6,6	0.14	0
3	GOL	D	2004	-	5,5,5	0.32	0	5,5,5	0.34	0
3	GOL	A	2001	-	5,5,5	0.34	0	5,5,5	0.36	0
2	SO4	B	3003	-	4,4,4	0.16	0	6,6,6	0.19	0
2	SO4	C	3013	-	4,4,4	0.13	0	6,6,6	0.16	0
2	SO4	C	3027	-	4,4,4	0.14	0	6,6,6	0.37	0
2	SO4	D	3026	-	4,4,4	0.18	0	6,6,6	0.50	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	GOL	A	2001	-	-	2/4/4/4	-
3	GOL	D	2004	-	-	0/4/4/4	-
3	GOL	C	2003	-	-	2/4/4/4	-
3	GOL	B	2002	-	-	4/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	2001	GOL	C1-C2-C3-O3
3	B	2002	GOL	C1-C2-C3-O3
3	B	2002	GOL	O2-C2-C3-O3
3	C	2003	GOL	C1-C2-C3-O3
3	A	2001	GOL	O2-C2-C3-O3
3	C	2003	GOL	O2-C2-C3-O3
3	B	2002	GOL	O1-C1-C2-O2
3	B	2002	GOL	O1-C1-C2-C3

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	2003	GOL	1	0
2	D	3026	SO4	1	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 (i)

6.1 Protein, DNA and RNA chains (i)

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	498/517 (96%)	-0.53	2 (0%)	92	93	9, 17, 26, 35	20 (4%)
1	B	498/517 (96%)	-0.47	3 (0%)	89	91	10, 18, 28, 39	17 (3%)
1	C	498/517 (96%)	-0.54	1 (0%)	95	95	9, 15, 23, 35	18 (3%)
1	D	498/517 (96%)	-0.49	3 (0%)	89	91	9, 18, 27, 38	19 (3%)
All	All	1992/2068 (96%)	-0.51	9 (0%)	91	92	9, 17, 26, 39	74 (3%)

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	405	VAL	7.8
1	B	405	VAL	7.3
1	A	405	VAL	6.3
1	C	405	VAL	5.3
1	B	819	ASP	2.8
1	B	415	LYS	2.3
1	D	415	LYS	2.3
1	D	819	ASP	2.3
1	A	819	ASP	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 monosaccharides 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. 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
2	SO4	A	3017	5/5	0.81	0.18	38,39,40,40	5
3	GOL	D	2004	6/6	0.81	0.13	49,50,51,52	0
2	SO4	B	3024	5/5	0.83	0.15	27,34,35,36	5
2	SO4	A	3011	5/5	0.83	0.25	79,79,80,80	5
3	GOL	C	2003	6/6	0.84	0.14	47,49,49,50	0
2	SO4	B	3009	5/5	0.84	0.18	96,96,96,96	0
2	SO4	A	3020	5/5	0.85	0.15	26,28,29,29	5
3	GOL	A	2001	6/6	0.86	0.12	47,48,49,49	0
2	SO4	C	3019	5/5	0.86	0.14	33,36,36,36	5
2	SO4	D	3012	5/5	0.86	0.14	77,77,77,77	5
2	SO4	A	3025	5/5	0.88	0.15	24,33,33,34	5
2	SO4	D	3026	5/5	0.89	0.14	20,31,31,32	5
2	SO4	B	3018	5/5	0.90	0.14	32,33,34,35	5
2	SO4	C	3010	5/5	0.90	0.16	64,64,64,65	5
2	SO4	D	3016	5/5	0.91	0.11	34,34,35,35	5
2	SO4	A	3006	5/5	0.92	0.14	33,35,36,37	5
3	GOL	B	2002	6/6	0.92	0.14	51,52,52,52	0
2	SO4	C	3022	5/5	0.92	0.12	26,27,29,29	5
2	SO4	C	3027	5/5	0.92	0.11	20,29,30,30	5
2	SO4	D	3008	5/5	0.93	0.10	35,35,37,38	5
2	SO4	C	3007	5/5	0.93	0.13	35,36,37,38	5
2	SO4	D	3023	5/5	0.94	0.13	38,39,39,39	5
2	SO4	B	3005	5/5	0.94	0.14	41,42,43,43	5
2	SO4	C	3028	5/5	0.94	0.10	30,31,34,34	5
2	SO4	C	3013	5/5	0.94	0.10	34,34,35,36	5
2	SO4	A	3014	5/5	0.94	0.11	29,30,31,31	5
2	SO4	B	3015	5/5	0.94	0.10	32,32,33,33	5
2	SO4	B	3021	5/5	0.97	0.08	38,39,39,39	5
2	SO4	A	3001	5/5	0.97	0.09	28,28,29,29	5
2	SO4	A	3002	5/5	0.97	0.10	23,24,24,25	5
2	SO4	B	3003	5/5	0.98	0.09	22,22,22,23	5
2	SO4	B	3004	5/5	0.99	0.07	25,25,26,26	5

6.5 Other polymers (i)

There are no such residues in this entry.