



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 11:52 PM GMT

PDB ID : 1YXM  
Title : Crystal structure of peroxisomal trans 2-enoyl CoA reductase  
Authors : Jansson, A.; Ng, S.; Arrowsmith, C.; Sharma, S.; Edwards, A.M.; Von Delft, F.; Sundstrom, M.; Oppermann, U.; Structural Genomics Consortium (SGC)  
Deposited on : 2005-02-22  
Resolution : 1.90 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](mailto: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.

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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

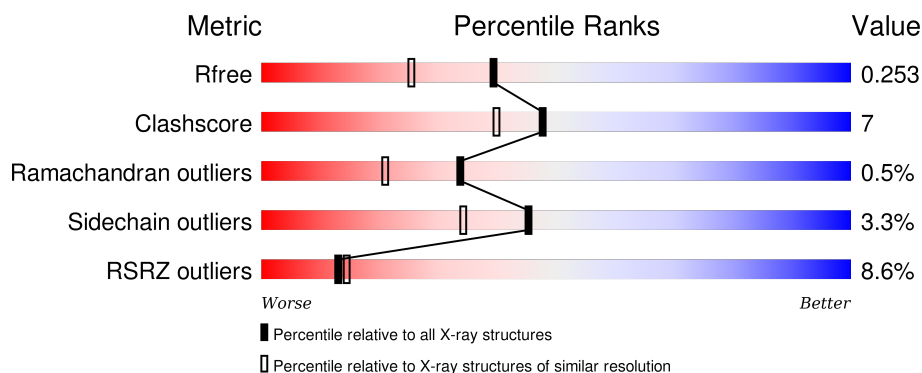
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.90 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	4755 (1.90-1.90)
Clashscore	102246	5398 (1.90-1.90)
Ramachandran outliers	100387	5338 (1.90-1.90)
Sidechain outliers	100360	5339 (1.90-1.90)
RSRZ outliers	91569	4766 (1.90-1.90)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	303	<div> <div>5%</div> <div>86%</div> <div>10%</div> <div>••</div> </div>
1	B	303	<div> <div>3%</div> <div>84%</div> <div>8%</div> <div>• 7%</div> </div>
1	C	303	<div> <div>13%</div> <div>72%</div> <div>13%</div> <div>• 13%</div> </div>
1	D	303	<div> <div>11%</div> <div>79%</div> <div>15%</div> <div>••</div> </div>

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 8697 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 peroxisomal trans 2-enoyl CoA reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	297	Total	C	N	O	S	0	1	0
			2153	1376	366	403	8			
1	B	283	Total	C	N	O	S	0	2	0
			2102	1345	358	391	8			
1	C	264	Total	C	N	O	S	0	0	0
			1892	1210	322	352	8			
1	D	291	Total	C	N	O	S	0	1	0
			2141	1369	363	401	8			

- Molecule 2 is SULFATE ION (three-letter code: SO<sub>4</sub>) (formula: O<sub>4</sub>S).



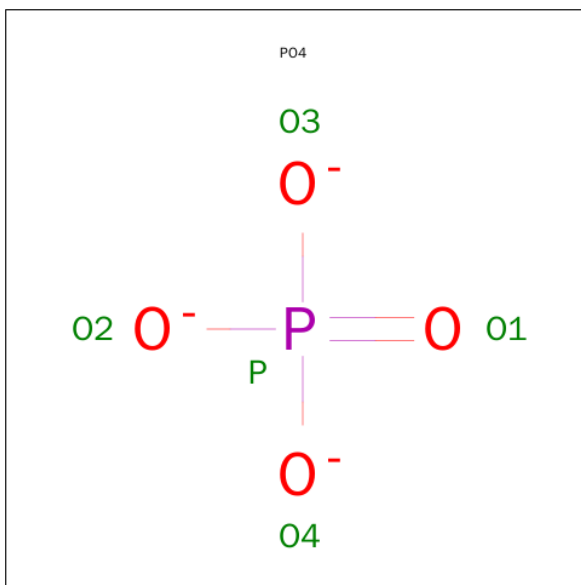
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		

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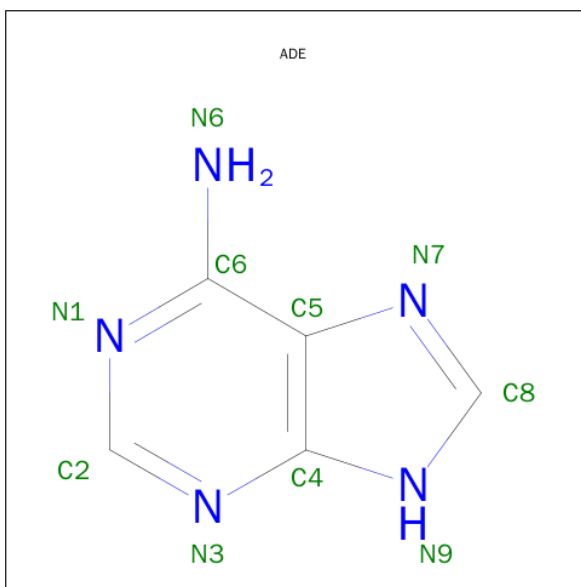
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	D	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is PHOSPHATE ION (three-letter code: PO4) (formula: O<sub>4</sub>P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	O	P	0	0
			5	4	1		

- Molecule 4 is ADENINE (three-letter code: ADE) (formula: C<sub>5</sub>H<sub>5</sub>N<sub>5</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	N	0	0
			10	5	5		

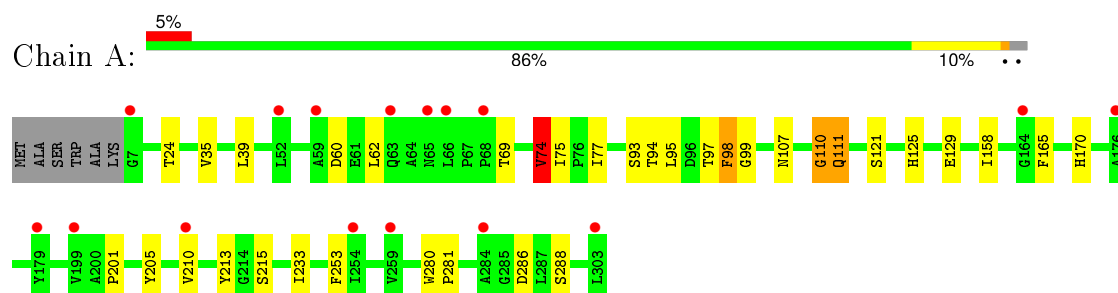
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	101	Total	O	0	0
			101	101		
5	B	96	Total	O	0	0
			96	96		
5	C	70	Total	O	0	0
			70	70		
5	D	107	Total	O	0	0
			107	107		

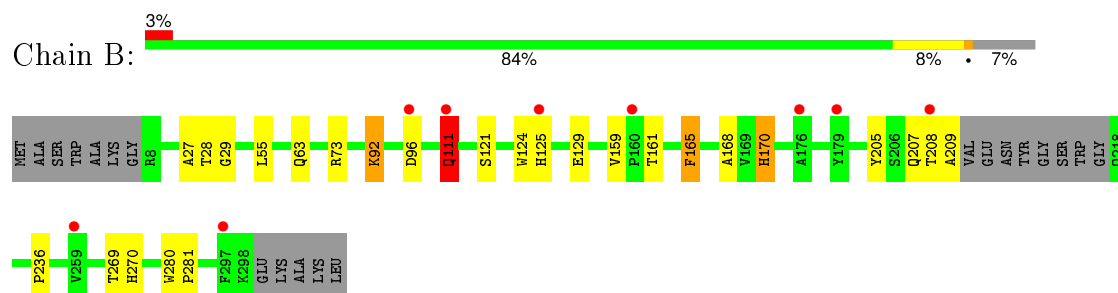
### 3 Residue-property plots [i](#)

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 ( $RSRZ > 2$ ). 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.

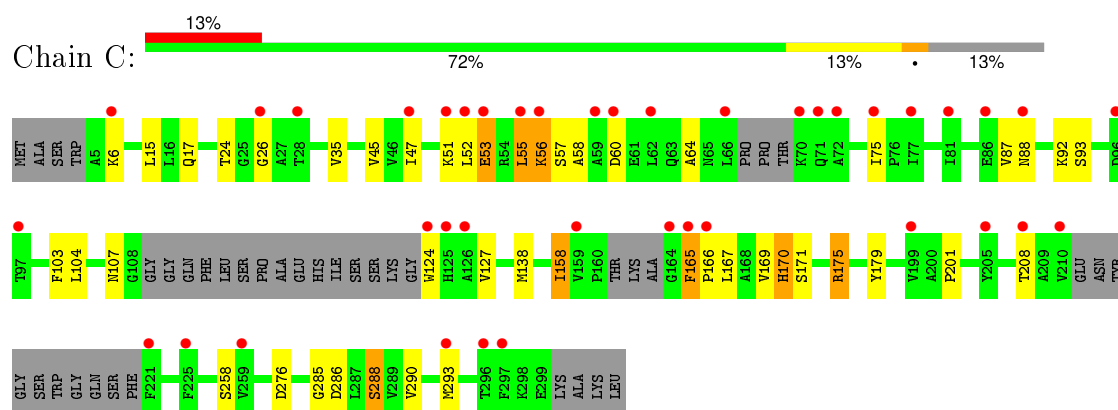
- Molecule 1: peroxisomal trans 2-enoyl CoA reductase



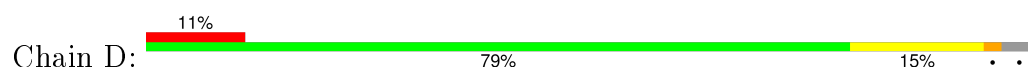
- Molecule 1: peroxisomal trans 2-enoyl CoA reductase



- Molecule 1: peroxisomal trans 2-enoyl CoA reductase



- Molecule 1: peroxisomal trans 2-enoyl CoA reductase





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	78.15Å 119.01Å 119.91Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.00 – 1.90 47.34 – 1.90	Depositor EDS
% Data completeness (in resolution range)	97.5 (47.00-1.90) 97.5 (47.34-1.90)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.05	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.72 (at 1.90Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, $R_{free}$	0.204 , 0.245 0.219 , 0.253	Depositor DCC
$R_{free}$ test set	4438 reflections (5.41%)	DCC
Wilson B-factor (Å <sup>2</sup> )	33.1	Xtriage
Anisotropy	0.113	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 56.6	EDS
Estimated twinning fraction	0.003 for -h,l,k	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.35$	Xtriage
Outliers	0 of 88511 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	8697	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.85% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: PO4, ADE, 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	0.80	1/2200 (0.0%)	0.79	5/2996 (0.2%)
1	B	0.82	0/2152	0.76	1/2926 (0.0%)
1	C	0.75	2/1926 (0.1%)	0.83	5/2617 (0.2%)
1	D	0.89	4/2185 (0.2%)	0.93	6/2972 (0.2%)
All	All	0.82	7/8463 (0.1%)	0.83	17/11511 (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	3
1	B	0	2
1	C	0	3
1	D	3	5
All	All	3	13

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	194	ILE	C-N	-15.25	0.98	1.34
1	D	195	ARG	C-N	9.89	1.56	1.34
1	A	111	GLN	C-N	-8.52	1.14	1.34
1	D	198	CYS	CB-SG	-6.13	1.71	1.82
1	D	195	ARG	CD-NE	-5.84	1.36	1.46
1	C	103	PHE	C-N	-5.58	1.21	1.34
1	C	285	GLY	C-N	-5.33	1.21	1.34

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	195	ARG	NE-CZ-NH2	-18.18	111.21	120.30
1	D	195	ARG	O-C-N	-17.14	95.28	122.70
1	D	195	ARG	NE-CZ-NH1	14.56	127.58	120.30
1	C	285	GLY	O-C-N	-10.11	106.53	122.70
1	C	285	GLY	C-N-CA	10.07	146.88	121.70
1	A	110	GLY	O-C-N	-8.39	109.28	122.70
1	D	195	ARG	C-N-CA	7.09	139.42	121.70
1	D	195	ARG	CA-C-N	7.01	132.63	117.20
1	A	110	GLY	C-N-CA	6.52	138.00	121.70
1	C	104	LEU	CB-CG-CD2	6.31	121.73	111.00
1	B	111	GLN	O-C-N	-6.23	112.74	122.70
1	C	285	GLY	CA-C-N	6.13	130.68	117.20
1	C	276	ASP	CB-CG-OD1	5.69	123.42	118.30
1	A	74	VAL	CB-CA-C	-5.45	101.04	111.40
1	D	260	ASP	CB-CG-OD1	5.40	123.16	118.30
1	A	60	ASP	CB-CG-OD2	5.28	123.06	118.30
1	A	110	GLY	CA-C-N	5.08	128.39	117.20

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	D	52	LEU	CA
1	D	53	GLU	CA
1	D	54	ARG	CA

All (13) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	110	GLY	Mainchain
1	A	97	THR	Peptide
1	A	98	PHE	Peptide
1	B	111	GLN	Mainchain
1	B	207	GLN	Peptide
1	C	51	LYS	Peptide
1	C	53	GLU	Peptide
1	C	6	LYS	Peptide
1	D	194	ILE	Mainchain
1	D	195	ARG	Mainchain
1	D	214	GLY	Peptide
1	D	51	LYS	Peptide
1	D	53	GLU	Peptide

## 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	2153	0	2077	16	0
1	B	2102	0	2089	21	0
1	C	1892	0	1838	42	0
1	D	2141	0	2090	49	0
2	A	5	0	0	0	0
2	B	5	0	0	0	0
2	D	10	0	0	0	0
3	B	5	0	0	0	0
4	B	10	0	4	0	0
5	A	101	0	0	1	0
5	B	96	0	0	1	0
5	C	70	0	0	2	0
5	D	107	0	0	4	0
All	All	8697	0	8098	122	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 7.

All (122) 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:D:52:LEU:CA	1:D:53:GLU:HG3	1.65	1.26
1:C:52:LEU:HB3	1:C:53:GLU:HA	1.30	1.12
1:D:52:LEU:N	1:D:53:GLU:HA	1.49	1.09
1:C:52:LEU:HD23	1:C:55:LEU:H	1.15	1.08
1:B:208:THR:HG23	5:B:4085:HOH:O	1.51	1.08
1:D:52:LEU:H	1:D:53:GLU:CA	1.65	1.08
1:D:52:LEU:H	1:D:53:GLU:HA	0.89	1.01
1:C:52:LEU:HD21	1:C:56:LYS:H	1.22	1.01
1:C:52:LEU:CD2	1:C:55:LEU:N	2.24	1.00
1:D:52:LEU:HA	1:D:53:GLU:HG3	1.00	0.99
1:C:124:TRP:HE1	1:D:133:THR:HG22	1.26	0.99
1:C:52:LEU:HD23	1:C:55:LEU:N	1.81	0.95
1:D:52:LEU:HA	1:D:53:GLU:CG	1.95	0.95
1:C:52:LEU:HD21	1:C:56:LYS:N	1.82	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:52:LEU:CD2	1:C:55:LEU:H	1.88	0.85
1:D:154:ILE:HB	1:D:196:ILE:HG12	1.65	0.78
1:C:52:LEU:HD22	1:C:53:GLU:O	1.83	0.77
1:D:50:ARG:O	1:D:78:GLN:HG3	1.84	0.77
1:B:29:GLY:H	1:B:209:ALA:HA	1.49	0.77
1:C:52:LEU:CB	1:C:53:GLU:HA	2.13	0.76
1:D:52:LEU:CA	1:D:53:GLU:CG	2.58	0.74
1:C:60:ASP:O	1:C:64:ALA:HB2	1.88	0.73
1:B:125[B]:HIS:NE2	1:B:129:GLU:HG3	2.02	0.73
1:D:277:HIS:HD2	1:D:279:ASN:H	1.38	0.70
1:D:50:ARG:O	1:D:78:GLN:CG	2.40	0.69
1:D:52:LEU:H	1:D:53:GLU:CB	2.07	0.67
1:D:52:LEU:N	1:D:53:GLU:HG3	2.10	0.66
1:C:52:LEU:CD2	1:C:55:LEU:CA	2.74	0.66
1:D:52:LEU:N	1:D:53:GLU:CA	2.29	0.64
1:C:55:LEU:O	1:C:56:LYS:C	2.35	0.64
1:B:63:GLN:HE22	1:B:73:ARG:HA	1.62	0.64
1:D:109:GLY:HA3	1:D:131:ASN:OD1	1.98	0.64
1:D:289:VAL:HG12	1:D:293:MET:HE3	1.77	0.64
1:A:39:LEU:HD11	1:A:74:VAL:HG22	1.80	0.63
1:B:205:TYR:O	1:B:236:PRO:HD3	1.98	0.63
1:D:51:LYS:HA	1:D:52:LEU:HB3	1.81	0.63
1:D:49:SER:HB3	1:D:55:LEU:HG	1.82	0.61
1:C:52:LEU:CD2	1:C:56:LYS:N	2.61	0.61
1:C:52:LEU:HB3	1:C:53:GLU:CA	2.17	0.61
1:C:169:VAL:CG1	1:D:181:LEU:HD13	2.32	0.60
1:C:17:GLN:NE2	5:C:356:HOH:O	2.25	0.60
1:C:26:GLY:HA3	1:C:47:ILE:HG23	1.85	0.59
1:D:51:LYS:CA	1:D:52:LEU:HB3	2.34	0.58
1:D:182:THR:HG23	1:D:196:ILE:HG22	1.85	0.58
1:B:111:GLN:HE22	1:B:165:PHE:HE2	1.51	0.57
1:C:52:LEU:HD22	1:C:55:LEU:N	2.17	0.57
1:C:88:ASN:O	1:C:92:LYS:HG3	2.05	0.57
1:B:92:LYS:HE2	1:B:96:ASP:OD1	2.06	0.56
1:C:52:LEU:HD21	1:C:55:LEU:CA	2.34	0.56
1:D:289:VAL:HG12	1:D:293:MET:CE	2.36	0.55
1:C:169:VAL:CG1	1:D:181:LEU:CD1	2.85	0.55
1:D:19:GLN:NE2	5:D:2085:HOH:O	2.39	0.55
1:D:52:LEU:N	1:D:53:GLU:CG	2.70	0.54
1:B:125[B]:HIS:CD2	1:B:129:GLU:HG3	2.42	0.54
1:B:92:LYS:O	1:B:92:LYS:HE3	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:269:THR:HA	1:D:269:THR:HA	1.89	0.53
1:B:125[B]:HIS:NE2	1:B:129:GLU:CG	2.71	0.53
1:D:277:HIS:CD2	1:D:279:ASN:H	2.23	0.53
1:D:46:VAL:HG22	1:D:75:ILE:CG1	2.38	0.53
1:C:124:TRP:NE1	1:D:133:THR:HG22	2.10	0.53
1:A:210:VAL:HG12	1:A:213:TYR:HB2	1.90	0.53
1:C:290:VAL:HA	1:C:293:MET:HE2	1.91	0.52
1:D:117:GLU:HG3	1:D:118:HIS:CD2	2.45	0.52
1:D:280:TRP:CD2	1:D:281:PRO:HD2	2.45	0.52
1:A:77:ILE:HD13	1:A:93:SER:OG	2.10	0.51
1:D:73:ARG:NH1	5:D:2075:HOH:O	2.42	0.51
1:C:60:ASP:O	1:C:64:ALA:CB	2.56	0.50
1:D:46:VAL:HG22	1:D:75:ILE:HD11	1.92	0.50
1:C:52:LEU:CB	1:C:53:GLU:CA	2.86	0.49
1:C:55:LEU:O	1:C:58:ALA:N	2.39	0.49
1:A:95:LEU:O	1:A:99:GLY:CA	2.59	0.49
1:C:52:LEU:HD22	1:C:53:GLU:C	2.33	0.48
1:B:63:GLN:NE2	1:B:73:ARG:HA	2.29	0.48
1:C:166:PRO:O	1:C:167:LEU:HB2	2.13	0.48
1:B:280:TRP:CD2	1:B:281:PRO:HD2	2.48	0.48
1:A:125:HIS:O	1:A:129:GLU:HB2	2.14	0.47
1:A:94:THR:O	1:A:98:PHE:HB2	2.15	0.47
1:C:124:TRP:CE3	1:C:170:HIS:HB3	2.49	0.47
1:A:95:LEU:O	1:A:99:GLY:HA2	2.15	0.47
1:C:55:LEU:O	1:C:57:SER:N	2.47	0.46
1:B:27:ALA:HB2	1:B:55:LEU:HD23	1.97	0.46
1:D:63:GLN:HG2	5:D:2089:HOH:O	2.16	0.46
1:A:286:ASP:CA	5:A:405:HOH:O	2.64	0.46
1:A:35:VAL:HG11	1:A:62:LEU:HD13	1.98	0.45
1:B:124:TRP:CE3	1:B:170:HIS:HB3	2.51	0.45
1:A:75:ILE:HD13	1:A:98:PHE:CZ	2.51	0.45
1:D:26:GLY:HA3	1:D:47:ILE:HG23	1.99	0.45
1:D:51:LYS:O	1:D:55:LEU:HB2	2.17	0.45
1:B:208:THR:O	1:B:209:ALA:HB2	2.17	0.44
1:D:50:ARG:O	1:D:78:GLN:NE2	2.51	0.44
1:D:84:GLU:OE2	1:D:140:LYS:NZ	2.50	0.44
1:D:117:GLU:OE2	5:D:2066:HOH:O	2.21	0.44
1:C:286:ASP:OD2	1:C:288:SER:OG	2.34	0.44
1:A:205:TYR:HB2	1:A:233:ILE:HD12	2.00	0.44
1:A:280:TRP:CD2	1:A:281:PRO:HD2	2.53	0.44
1:C:165:PHE:CD1	1:C:171:SER:OG	2.65	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:57:SER:O	1:D:61:GLU:HB2	2.18	0.43
1:A:158:ILE:O	1:A:201:PRO:HD2	2.18	0.43
1:B:270:HIS:HE1	1:D:272:TYR:O	2.02	0.43
1:D:280:TRP:CG	1:D:281:PRO:HD2	2.53	0.43
1:B:280:TRP:CG	1:B:281:PRO:HD2	2.54	0.42
1:D:24:THR:O	1:D:107:ASN:HB3	2.18	0.42
1:B:28:THR:HB	1:B:209:ALA:HA	2.00	0.42
1:C:158:ILE:HB	1:C:175:ARG:HG3	2.00	0.42
1:C:35:VAL:HG13	1:C:45:VAL:HG11	2.01	0.42
1:D:179:TYR:CZ	1:D:183:LYS:HE2	2.54	0.42
1:C:24:THR:O	1:C:107:ASN:HB3	2.20	0.42
1:C:127:VAL:HG21	1:C:170:HIS:CD2	2.54	0.42
1:B:165:PHE:CD1	1:B:168:ALA:HB3	2.55	0.42
1:A:24:THR:O	1:A:107:ASN:HB3	2.19	0.42
1:A:95:LEU:O	1:A:99:GLY:HA3	2.21	0.41
1:C:208:THR:CG2	5:C:373:HOH:O	2.68	0.41
1:B:159:VAL:O	1:B:161:THR:HG23	2.19	0.41
1:C:158:ILE:O	1:C:201:PRO:HD2	2.19	0.41
1:D:35:VAL:CG1	1:D:62:LEU:HD13	2.51	0.41
1:D:83:ASN:OD1	1:D:86:GLU:HG3	2.21	0.41
1:A:205:TYR:HB2	1:A:233:ILE:CD1	2.51	0.41
1:C:165:PHE:O	1:C:166:PRO:C	2.57	0.41
1:D:51:LYS:HA	1:D:52:LEU:CB	2.49	0.40
1:C:87:VAL:HG13	1:C:138:MET:SD	2.61	0.40
1:C:179:TYR:CE1	1:C:258:SER:HB2	2.57	0.40
1:D:52:LEU:H	1:D:53:GLU:CG	2.32	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	296/303 (98%)	284 (96%)	11 (4%)	1 (0%)	46	35
1	B	281/303 (93%)	271 (96%)	10 (4%)	0	100	100
1	C	254/303 (84%)	240 (94%)	11 (4%)	3 (1%)	16	5
1	D	288/303 (95%)	276 (96%)	10 (4%)	2 (1%)	26	14
All	All	1119/1212 (92%)	1071 (96%)	42 (4%)	6 (0%)	34	21

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	56	LYS
1	D	53	GLU
1	C	55	LEU
1	A	111	GLN
1	C	158	ILE
1	D	158	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	215/245 (88%)	207 (96%)	8 (4%)	41	29
1	B	221/245 (90%)	217 (98%)	4 (2%)	66	61
1	C	191/245 (78%)	184 (96%)	7 (4%)	41	29
1	D	219/245 (89%)	210 (96%)	9 (4%)	37	25
All	All	846/980 (86%)	818 (97%)	28 (3%)	45	34

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	69	THR
1	A	74	VAL
1	A	121	SER
1	A	165	PHE
1	A	170	HIS

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Mol	Chain	Res	Type
1	A	215	SER
1	A	253	PHE
1	A	288	SER
1	B	92	LYS
1	B	121	SER
1	B	165	PHE
1	B	170	HIS
1	C	15	LEU
1	C	75	ILE
1	C	93	SER
1	C	165	PHE
1	C	170	HIS
1	C	175	ARG
1	C	288	SER
1	D	50	ARG
1	D	52	LEU
1	D	53	GLU
1	D	55	LEU
1	D	57	SER
1	D	74	VAL
1	D	113	LEU
1	D	165	PHE
1	D	170	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	131	ASN
1	B	63	GLN
1	B	111	GLN
1	B	180	ASN
1	B	270	HIS
1	D	80	ASN
1	D	118	HIS
1	D	150	HIS
1	D	277	HIS

### 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 ⓘ

6 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	A	304	-	4,4,4	0.27	0	6,6,6	0.45	0
3	PO4	B	3001	-	4,4,4	0.29	0	6,6,6	0.26	0
2	SO4	B	4001	-	4,4,4	0.57	0	6,6,6	0.43	0
4	ADE	B	4002	-	8,11,11	1.68	2 (25%)	4,15,15	6.21	2 (50%)
2	SO4	D	1001	-	4,4,4	0.28	0	6,6,6	0.49	0
2	SO4	D	2001	-	4,4,4	0.38	0	6,6,6	0.62	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
2	SO4	A	304	-	-	0/0/0/0	0/0/0/0
3	PO4	B	3001	-	-	0/0/0/0	0/0/0/0
2	SO4	B	4001	-	-	0/0/0/0	0/0/0/0
4	ADE	B	4002	-	-	0/0/0/0	0/2/2/2
2	SO4	D	1001	-	-	0/0/0/0	0/0/0/0
2	SO4	D	2001	-	-	0/0/0/0	0/0/0/0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	4002	ADE	C4-N9	2.01	1.38	1.34
4	B	4002	ADE	C2-N3	3.77	1.38	1.32

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	4002	ADE	N3-C2-N1	-12.11	119.62	128.89
4	B	4002	ADE	C4-C5-N7	-2.48	107.20	109.48

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	297/303 (98%)	0.53	16 (5%) 29 33	22, 34, 53, 59	1 (0%)
1	B	283/303 (93%)	0.41	9 (3%) 51 54	20, 33, 48, 53	0
1	C	264/303 (87%)	0.91	40 (15%) 3 3	24, 38, 56, 60	0
1	D	291/303 (96%)	0.67	33 (11%) 7 7	25, 37, 55, 60	1 (0%)
All	All	1135/1212 (93%)	0.62	98 (8%) 13 14	20, 35, 53, 60	2 (0%)

All (98) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	52	LEU	7.0
1	C	296	THR	6.9
1	A	52	LEU	6.3
1	D	57	SER	6.2
1	D	50	ARG	5.7
1	C	72	ALA	5.4
1	A	68	PRO	5.3
1	C	210	VAL	5.3
1	A	303	LEU	5.0
1	D	112	PHE	4.8
1	C	59	ALA	4.7
1	C	52	LEU	4.6
1	C	297	PHE	4.4
1	C	70	LYS	4.4
1	A	66	LEU	4.3
1	C	221	PHE	4.2
1	C	60	ASP	4.2
1	C	208	THR	4.0
1	D	66	LEU	3.8
1	D	77	ILE	3.8
1	D	55	LEU	3.7

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Mol	Chain	Res	Type	RSRZ
1	A	59	ALA	3.6
1	D	60	ASP	3.6
1	C	165	PHE	3.6
1	D	108	GLY	3.5
1	A	65	ASN	3.5
1	D	267	LEU	3.4
1	D	83	ASN	3.4
1	A	7	GLY	3.3
1	C	225	PHE	3.2
1	D	64	ALA	3.2
1	B	259	VAL	3.2
1	B	179	TYR	3.1
1	D	54	ARG	3.1
1	A	179	TYR	3.1
1	C	77	ILE	3.1
1	D	111	GLN	3.0
1	B	96	ASP	3.0
1	C	293	MET	3.0
1	A	284	ALA	3.0
1	D	59	ALA	2.9
1	D	75	ILE	2.9
1	D	196	ILE	2.9
1	D	303	LEU	2.9
1	C	159	VAL	2.8
1	C	125	HIS	2.8
1	D	259	VAL	2.8
1	D	91	VAL	2.8
1	A	210	VAL	2.8
1	C	53	GLU	2.8
1	B	176	ALA	2.7
1	D	58	ALA	2.7
1	C	26	GLY	2.7
1	D	98	PHE	2.7
1	C	96	ASP	2.6
1	C	71	GLN	2.6
1	D	72	ALA	2.6
1	C	86	GLU	2.6
1	C	51	LYS	2.6
1	C	56	LYS	2.6
1	C	259	VAL	2.6
1	C	166	PRO	2.5
1	D	73	ARG	2.5

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Mol	Chain	Res	Type	RSRZ
1	C	66	LEU	2.5
1	B	111	GLN	2.5
1	D	163	ALA	2.5
1	C	55	LEU	2.5
1	B	297	PHE	2.4
1	B	125[A]	HIS	2.4
1	A	259	VAL	2.4
1	D	79	CYS	2.4
1	C	28	THR	2.4
1	B	208	THR	2.4
1	D	78	GLN	2.3
1	C	62	LEU	2.3
1	C	81	ILE	2.3
1	A	199	VAL	2.3
1	C	88	ASN	2.3
1	A	164	GLY	2.3
1	C	75	ILE	2.3
1	C	126	ALA	2.3
1	C	205	TYR	2.3
1	D	65	ASN	2.2
1	A	63	GLN	2.2
1	C	97	THR	2.2
1	C	124	TRP	2.2
1	A	176	ALA	2.2
1	D	90	LEU	2.2
1	D	146	TRP	2.2
1	D	136	PHE	2.2
1	B	160	PRO	2.1
1	D	99	GLY	2.1
1	A	254	ILE	2.1
1	C	199	VAL	2.1
1	C	164	GLY	2.1
1	C	6	LYS	2.0
1	C	47	ILE	2.0
1	D	27	ALA	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 [i](#)

There are no carbohydrates in this entry.

### 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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( $\text{\AA}^2$ )	Q<0.9
4	ADE	B	4002	10/10	0.85	0.18	1.78	47,48,49,49	0
2	SO4	A	304	5/5	0.95	0.15	-0.05	53,56,56,56	0
2	SO4	D	2001	5/5	0.96	0.12	-0.51	60,60,64,64	0
2	SO4	D	1001	5/5	0.95	0.09	-1.12	50,53,57,59	0
2	SO4	B	4001	5/5	0.98	0.08	-1.54	33,35,38,39	0
3	PO4	B	3001	5/5	0.85	0.28	-	56,56,57,57	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.