



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 28, 2014 – 01:21 AM GMT

PDB ID : 3D4J  
Title : Crystal structure of Human mevalonate diphosphate decarboxylase  
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Deposited on : 2008-05-14  
Resolution : 2.40 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

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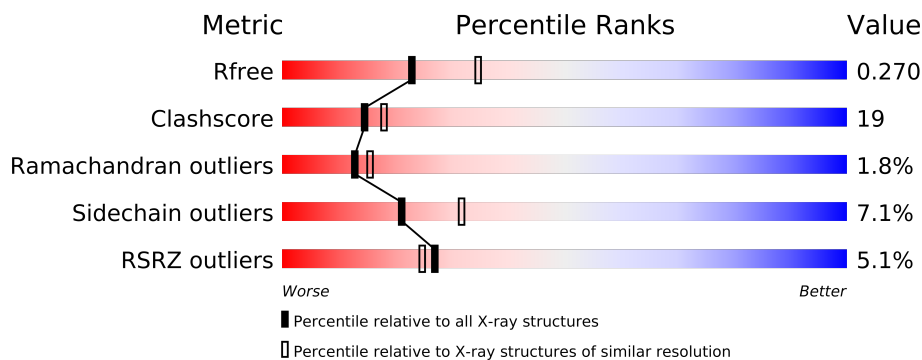
The following versions of software and data (see [references](#)) were used in the production of this report:

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

# 1 Overall quality at a glance



The reported resolution of this entry is 2.40 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	66092	2207 (2.40-2.40)
Clashscore	79885	2789 (2.40-2.40)
Ramachandran outliers	78287	2736 (2.40-2.40)
Sidechain outliers	78261	2737 (2.40-2.40)
RSRZ outliers	66119	2210 (2.40-2.40)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	400	
1	B	400	

## 2 Entry composition

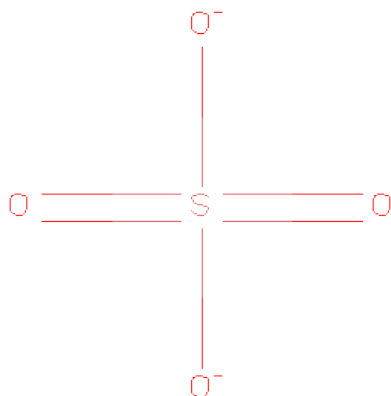
There are 3 unique types of molecules in this entry. The entry contains 5813 atoms, of which 0 are hydrogen and 0 are deuterium.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Diphosphomevalonate decarboxylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	374	Total	C	N	O	S	0	0	0
			2855	1804	504	532	15			
1	B	368	Total	C	N	O	S	0	0	0
			2819	1784	495	525	15			

- 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	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	63	Total 63	O 63	0	0
3	B	66	Total 66	O 66	0	0



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	86.96Å 53.19Å 97.79Å 90.00° 107.25° 90.00°	Depositor
Resolution (Å)	29.45 – 2.40 29.45 – 2.39	Depositor EDS
% Data completeness (in resolution range)	96.4 (29.45-2.40) 96.1 (29.45-2.39)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.06	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.67 (at 2.39Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.218 , 0.274 0.214 , 0.270	Depositor DCC
$R_{free}$ test set	3249 reflections (9.97%)	DCC
Wilson B-factor (Å <sup>2</sup> )	43.2	Xtriage
Anisotropy	0.293	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 33.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.29$	Xtriage
Outliers	0 of 32691 reflections	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	5813	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.96% of the height of the origin peak. No significant pseudotranslation is detected.*

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

## 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

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	0.37	0/2920	0.63	2/3977 (0.1%)
1	B	0.38	0/2883	0.62	1/3926 (0.0%)
All	All	0.37	0/5803	0.63	3/7903 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	57	SER	N-CA-C	5.30	125.32	111.00
1	A	21	ILE	N-CA-C	-5.29	96.72	111.00
1	B	21	ILE	N-CA-C	-5.15	97.10	111.00

There are no chirality outliers.

There are no planarity outliers.

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2855	0	2834	113	0
1	B	2819	0	2797	108	0
2	A	5	0	0	0	0
2	B	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	63	0	0	2	0
3	B	66	0	0	2	0
All	All	5813	0	5631	218	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 19.

All (218) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:140:ARG:HH11	1:B:140:ARG:HB2	1.17	1.04
1:B:109:LYS:HE3	1:B:109:LYS:HA	1.40	1.02
1:A:109:LYS:HE3	1:A:109:LYS:HA	1.46	0.96
1:B:140:ARG:HB2	1:B:140:ARG:NH1	1.82	0.95
1:A:119:PRO:HG2	1:A:122:ALA:HB2	1.51	0.92
1:B:395:LEU:HB3	1:B:396:PRO:HD2	1.55	0.88
1:A:350:LEU:HD22	1:A:354:LEU:HD12	1.63	0.79
1:B:49:LYS:H	1:B:117:ASN:HD21	1.32	0.76
1:B:74:VAL:HA	1:B:79:LEU:HD23	1.66	0.76
1:A:57:SER:HG	1:A:107:SER:N	1.83	0.76
1:A:344:GLN:NE2	1:A:344:GLN:H	1.86	0.74
1:A:340:LEU:HD13	1:A:345:VAL:HG13	1.70	0.72
1:A:10:VAL:HG11	1:A:141:VAL:HG22	1.71	0.72
1:A:179:LYS:NZ	3:A:599:HOH:O	2.23	0.71
1:A:87:ARG:HH11	1:A:110:VAL:HG23	1.55	0.71
1:B:216:ARG:O	1:B:220:GLU:HG2	1.92	0.70
1:A:49:LYS:H	1:A:117:ASN:HD21	1.40	0.69
1:A:335:ASN:N	1:A:335:ASN:HD22	1.89	0.69
1:A:115:VAL:HG12	1:A:389:LEU:HD21	1.74	0.69
1:A:85:GLU:HB3	1:A:151:VAL:HG22	1.74	0.69
1:A:62:GLU:O	1:A:109:LYS:HG3	1.93	0.68
1:A:335:ASN:ND2	1:A:336:GLY:H	1.92	0.68
1:B:62:GLU:HA	1:B:109:LYS:NZ	2.09	0.68
1:B:253:ALA:HB1	1:B:301:ALA:HB2	1.77	0.67
1:A:83:LEU:HA	1:A:86:ILE:HD11	1.77	0.67
1:B:150:GLU:OE1	1:B:179:LYS:HD3	1.94	0.66
1:B:226:ARG:O	1:B:230:GLU:HG3	1.96	0.66
1:A:395:LEU:N	1:A:395:LEU:HD12	2.11	0.66
1:B:109:LYS:CE	1:B:109:LYS:HA	2.23	0.64
1:A:148:LEU:H	1:A:148:LEU:HD13	1.61	0.64
1:A:326:VAL:HG21	1:A:370:ILE:HD11	1.80	0.64
1:A:137:THR:O	1:A:141:VAL:HG23	1.98	0.63
1:B:15:PRO:HB3	1:B:45:GLN:HG3	1.79	0.63

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:340:LEU:HD13	1:A:345:VAL:CG1	2.29	0.62
1:A:343:LEU:HD22	1:A:373:THR:HA	1.82	0.60
1:B:390:LEU:HB2	1:B:394:GLY:HA2	1.82	0.60
1:A:135:ALA:O	1:A:139:ALA:HB2	2.02	0.60
1:B:17:ASN:HD21	1:B:161:ARG:HH21	1.48	0.60
1:B:35:ILE:HG13	1:B:36:ASN:HD22	1.66	0.60
1:A:122:ALA:O	1:A:309:ASN:ND2	2.35	0.59
1:A:287:LEU:HD11	1:A:358:LEU:HD13	1.84	0.59
1:B:61:THR:O	1:B:62:GLU:CG	2.51	0.59
1:A:373:THR:OG1	1:A:374:GLN:N	2.32	0.59
1:B:319:VAL:HG23	1:B:320:ALA:N	2.18	0.58
1:B:124:LEU:HB2	3:B:550:HOH:O	2.04	0.58
1:B:60:PHE:CE2	1:B:64:ARG:HD2	2.39	0.58
1:A:60:PHE:HB2	1:A:109:LYS:HB3	1.86	0.58
1:A:11:THR:CG2	1:A:382:LEU:HD12	2.34	0.58
1:B:390:LEU:CB	1:B:394:GLY:HA2	2.34	0.58
1:A:122:ALA:O	1:A:201:VAL:HG22	2.04	0.58
1:A:70:ARG:H	1:A:70:ARG:HD2	1.68	0.57
1:A:177:ASP:OD2	1:A:179:LYS:HB2	2.04	0.57
1:B:287:LEU:HD12	1:B:358:LEU:HD22	1.86	0.57
1:A:226:ARG:O	1:A:230:GLU:HG3	2.05	0.56
1:B:350:LEU:HD22	1:B:354:LEU:HD23	1.87	0.56
1:B:166:GLY:N	1:B:189:GLU:HG3	2.20	0.56
1:A:91:ARG:N	1:A:91:ARG:HD2	2.19	0.56
1:A:198:LEU:HD22	1:A:372:VAL:HG22	1.86	0.56
1:B:86:ILE:HD11	1:B:144:VAL:HG21	1.87	0.56
1:A:287:LEU:HD12	1:A:358:LEU:HD22	1.88	0.56
1:A:294:HIS:ND1	1:A:354:LEU:HD23	2.21	0.56
1:B:74:VAL:HA	1:B:79:LEU:CD2	2.36	0.55
1:A:216:ARG:O	1:A:220:GLU:HG3	2.07	0.55
1:A:109:LYS:CE	1:A:109:LYS:HA	2.29	0.55
1:B:189:GLU:H	1:B:189:GLU:CD	2.08	0.55
1:A:18:ILE:HG21	1:A:311:VAL:HG11	1.87	0.55
1:A:86:ILE:HG23	1:A:151:VAL:HG11	1.89	0.54
1:B:239:GLU:HG3	1:B:242:ARG:HH11	1.72	0.54
1:B:56:ILE:O	1:B:56:ILE:HG23	2.07	0.54
1:A:253:ALA:HB1	1:A:301:ALA:HB2	1.89	0.54
1:A:45:GLN:HA	1:A:48:LEU:O	2.07	0.54
1:A:67:LEU:C	1:A:69:GLY:H	2.09	0.54
1:A:66:TRP:CG	1:A:395:LEU:HD21	2.42	0.54
1:A:14:ALA:HB3	1:A:133:CYS:HB2	1.89	0.54
1:A:140:ARG:CZ	1:A:140:ARG:HB2	2.37	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:117:ASN:ND2	1:B:117:ASN:H	2.06	0.53
1:B:108:CYS:N	1:B:142:TYR:HE2	2.07	0.53
1:A:391:GLY:C	1:A:393:ASP:H	2.12	0.53
1:A:53:THR:OG1	1:A:389:LEU:HB2	2.09	0.52
1:A:62:GLU:HA	1:A:109:LYS:HD3	1.90	0.52
1:A:241:ALA:O	1:A:245:ARG:HG3	2.09	0.52
1:A:338:THR:O	1:A:341:LYS:HE3	2.09	0.51
1:A:123:GLY:HA2	1:A:309:ASN:HD22	1.75	0.51
1:B:250:PRO:O	1:B:254:GLN:HG3	2.10	0.51
1:B:13:THR:HA	1:B:50:THR:O	2.10	0.51
1:B:286:HIS:HB3	1:B:290:ARG:CZ	2.41	0.51
1:B:394:GLY:C	1:B:395:LEU:HD12	2.31	0.51
1:A:34:PRO:HD3	1:A:170:TRP:CZ2	2.46	0.51
1:A:335:ASN:C	1:A:337:ASP:H	2.13	0.50
1:A:211:SER:O	1:A:215:MET:HG2	2.12	0.50
1:B:85:GLU:O	1:B:89:LEU:HD23	2.10	0.50
1:A:394:GLY:HA2	3:A:623:HOH:O	2.11	0.50
1:B:62:GLU:C	1:B:109:LYS:HE2	2.32	0.50
1:A:198:LEU:HB2	1:A:312:ILE:HB	1.94	0.50
1:A:119:PRO:CG	1:A:122:ALA:HB2	2.32	0.50
1:A:393:ASP:OD1	1:A:394:GLY:N	2.41	0.50
1:B:110:VAL:HG12	1:B:111:HIS:N	2.26	0.50
1:A:66:TRP:C	1:A:67:LEU:HD22	2.32	0.49
1:B:131:TYR:CD2	1:B:155:GLY:HA3	2.46	0.49
1:A:131:TYR:CD2	1:A:155:GLY:HA3	2.47	0.49
1:B:202:VAL:HG11	1:B:280:ILE:HB	1.93	0.49
1:A:11:THR:HG21	1:A:382:LEU:HD12	1.94	0.49
1:B:74:VAL:O	1:B:74:VAL:HG22	2.12	0.49
1:B:18:ILE:HG21	1:B:311:VAL:HG11	1.93	0.49
1:A:65:ILE:HD12	1:A:79:LEU:HD13	1.95	0.49
1:A:49:LYS:H	1:A:117:ASN:ND2	2.09	0.49
1:B:73:ASP:O	1:B:76:GLN:HG3	2.13	0.48
1:B:34:PRO:HD3	1:B:170:TRP:CZ2	2.49	0.48
1:A:86:ILE:HG13	1:A:87:ARG:N	2.28	0.48
1:A:228:ARG:O	1:A:232:VAL:HB	2.13	0.48
1:B:14:ALA:HB3	1:B:133:CYS:HB2	1.95	0.48
1:B:61:THR:O	1:B:62:GLU:HG2	2.13	0.48
1:B:202:VAL:CG1	1:B:203:SER:N	2.77	0.48
1:B:148:LEU:N	1:B:148:LEU:HD22	2.29	0.48
1:B:202:VAL:HG12	1:B:203:SER:N	2.29	0.47
1:A:240:MET:O	1:A:244:ILE:HG13	2.13	0.47
1:B:325:ALA:HA	1:B:350:LEU:HD11	1.95	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:65:ILE:HA	1:B:112:VAL:O	2.14	0.47
1:B:395:LEU:HB3	1:B:396:PRO:CD	2.32	0.47
1:A:156:SER:HB3	1:A:159:ALA:HB2	1.95	0.47
1:A:205:GLU:HG2	1:A:206:LYS:N	2.28	0.47
1:B:61:THR:HG22	1:B:62:GLU:HG2	1.97	0.47
1:B:189:GLU:HG2	1:B:377:PRO:HA	1.96	0.47
1:B:35:ILE:HG13	1:B:36:ASN:ND2	2.29	0.47
1:B:319:VAL:CG2	1:B:320:ALA:N	2.77	0.47
1:A:205:GLU:HG2	1:A:206:LYS:H	1.80	0.47
1:A:74:VAL:HG12	1:A:74:VAL:O	2.15	0.47
1:B:205:GLU:O	1:B:206:LYS:C	2.53	0.46
1:B:390:LEU:O	1:B:390:LEU:HD12	2.14	0.46
1:A:344:GLN:H	1:A:344:GLN:CD	2.18	0.46
1:B:61:THR:O	1:B:62:GLU:HG3	2.14	0.46
1:B:60:PHE:CD2	1:B:61:THR:N	2.84	0.46
1:A:85:GLU:O	1:A:89:LEU:HB2	2.15	0.46
1:A:335:ASN:CG	1:A:336:GLY:H	2.18	0.46
1:B:86:ILE:HG23	1:B:87:ARG:N	2.30	0.46
1:A:14:ALA:CB	1:A:133:CYS:HB2	2.45	0.46
1:A:110:VAL:HG12	1:A:111:HIS:N	2.30	0.46
1:B:73:ASP:C	1:B:75:GLY:H	2.19	0.46
1:A:198:LEU:CD2	1:A:372:VAL:HG13	2.46	0.46
1:A:30:GLU:OE2	1:A:30:GLU:HA	2.16	0.46
1:B:249:PHE:CZ	1:B:314:THR:HA	2.51	0.46
1:B:85:GLU:O	1:B:88:CYS:HB3	2.15	0.46
1:A:150:GLU:O	1:A:154:ARG:HG2	2.15	0.45
1:B:62:GLU:HA	1:B:109:LYS:HZ1	1.81	0.45
1:A:124:LEU:CD1	1:A:306:ALA:H	2.28	0.45
1:B:17:ASN:HD22	1:B:40:SER:HB2	1.80	0.45
1:A:124:LEU:HD12	1:A:306:ALA:H	1.82	0.45
1:B:51:THR:HB	1:B:115:VAL:HG12	1.98	0.45
1:B:110:VAL:CG1	1:B:111:HIS:N	2.80	0.45
1:A:267:CYS:HB3	1:A:274:ILE:HB	1.99	0.45
1:B:253:ALA:CB	1:B:301:ALA:HB2	2.47	0.45
1:B:124:LEU:O	1:B:126:SER:N	2.41	0.45
1:A:87:ARG:HH11	1:A:110:VAL:CG2	2.27	0.44
1:A:282:TRP:CH2	1:B:268:LEU:HD13	2.51	0.44
1:A:70:ARG:N	1:A:70:ARG:HD2	2.33	0.44
1:B:53:THR:HB	1:B:389:LEU:HB2	1.99	0.44
1:A:115:VAL:HG22	1:A:116:ASN:N	2.32	0.44
1:A:124:LEU:O	1:A:126:SER:N	2.51	0.44
1:B:39:LEU:HD13	1:B:240:MET:HG3	2.00	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:44:HIS:HA	1:B:376:GLY:HA3	2.00	0.44
1:A:44:HIS:HA	1:A:376:GLY:HA3	2.00	0.44
1:B:278:ASN:O	1:B:281:SER:HB2	2.18	0.44
1:A:287:LEU:HD13	1:A:360:MET:SD	2.58	0.43
1:B:200:LEU:HD12	1:B:284:ILE:HD13	2.00	0.43
1:B:86:ILE:CD1	1:B:144:VAL:HG21	2.48	0.43
1:A:86:ILE:HG13	1:A:87:ARG:H	1.84	0.43
1:A:67:LEU:O	1:A:69:GLY:N	2.51	0.43
1:B:178:GLY:HA2	3:B:560:HOH:O	2.18	0.43
1:B:89:LEU:HB3	1:B:144:VAL:HG13	2.01	0.43
1:B:24:TRP:CD2	1:B:263:PHE:HE1	2.37	0.43
1:A:205:GLU:O	1:A:206:LYS:C	2.56	0.43
1:A:86:ILE:HG23	1:A:151:VAL:CG1	2.47	0.43
1:B:205:GLU:OE2	1:B:205:GLU:HA	2.19	0.43
1:A:154:ARG:HH11	1:A:154:ARG:HG3	1.83	0.43
1:A:44:HIS:HB3	1:A:47:GLN:NE2	2.34	0.43
1:A:75:GLY:O	1:A:76:GLN:C	2.56	0.43
1:A:335:ASN:ND2	1:A:336:GLY:N	2.65	0.42
1:B:211:SER:O	1:B:215:MET:HG2	2.19	0.42
1:A:109:LYS:HE3	1:A:109:LYS:CA	2.32	0.42
1:B:170:TRP:C	1:B:170:TRP:CD1	2.93	0.42
1:B:135:ALA:O	1:B:139:ALA:HB2	2.20	0.42
1:B:61:THR:C	1:B:62:GLU:HG2	2.39	0.42
1:A:300:VAL:HG12	1:A:301:ALA:N	2.35	0.42
1:A:9:ALA:HA	1:A:55:VAL:HG22	2.02	0.42
1:B:166:GLY:HA2	1:B:375:VAL:CG1	2.50	0.42
1:A:253:ALA:CB	1:A:301:ALA:HB2	2.49	0.42
1:A:83:LEU:HA	1:A:86:ILE:CD1	2.49	0.42
1:B:32:VAL:HG12	1:B:32:VAL:O	2.20	0.42
1:B:119:PRO:CG	1:B:369:TYR:OH	2.67	0.42
1:A:182:ILE:C	1:A:182:ILE:HD12	2.39	0.42
1:B:67:LEU:C	1:B:67:LEU:HD23	2.40	0.42
1:A:268:LEU:O	1:B:261:ASN:HB3	2.20	0.42
1:B:52:THR:HB	1:B:133:CYS:SG	2.60	0.42
1:A:26:LYS:NZ	1:A:215:MET:SD	2.93	0.41
1:B:73:ASP:OD2	1:B:75:GLY:N	2.50	0.41
1:B:148:LEU:H	1:B:148:LEU:HD22	1.84	0.41
1:B:36:ASN:HB2	1:B:233:VAL:HG11	2.02	0.41
1:A:286:HIS:O	1:A:290:ARG:HG2	2.19	0.41
1:A:335:ASN:N	1:A:335:ASN:ND2	2.60	0.41
1:B:16:VAL:HG12	1:B:129:ALA:HB2	2.02	0.41
1:A:268:LEU:HD13	1:B:282:TRP:CH2	2.55	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:189:GLU:HG2	1:A:376:GLY:C	2.41	0.41
1:B:384:ASP:HA	1:B:385:PRO:HD3	1.81	0.41
1:B:27:ARG:HD3	1:B:34:PRO:O	2.21	0.41
1:A:67:LEU:N	1:A:67:LEU:HD22	2.36	0.41
1:A:148:LEU:HD13	1:A:148:LEU:N	2.33	0.41
1:B:353:GLU:CD	1:B:353:GLU:H	2.24	0.41
1:B:395:LEU:CB	1:B:396:PRO:HD2	2.36	0.41
1:B:74:VAL:HG23	1:B:79:LEU:HD21	2.03	0.41
1:B:287:LEU:HD13	1:B:360:MET:SD	2.61	0.41
1:B:62:GLU:HA	1:B:109:LYS:HZ3	1.84	0.40
1:A:64:ARG:HD2	1:A:71:GLU:OE2	2.21	0.40
1:B:194:GLU:H	1:B:194:GLU:CD	2.25	0.40
1:A:13:THR:HA	1:A:50:THR:O	2.21	0.40
1:B:86:ILE:HA	1:B:89:LEU:HD23	2.04	0.40
1:B:86:ILE:C	1:B:88:CYS:N	2.74	0.40
1:B:285:ILE:HG23	1:B:302:TYR:CZ	2.56	0.40
1:B:57:SER:O	1:B:59:ASP:N	2.54	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	370/400 (92%)	335 (90%)	28 (8%)	7 (2%)	12	14
1	B	362/400 (90%)	330 (91%)	26 (7%)	6 (2%)	14	17
All	All	732/800 (92%)	665 (91%)	54 (7%)	13 (2%)	13	15

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	122	ALA
1	A	125	ALA
1	A	335	ASN

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Mol	Chain	Res	Type
1	B	125	ALA
1	B	145	GLU
1	A	334	SER
1	A	393	ASP
1	B	206	LYS
1	B	57	SER
1	B	58	LYS
1	B	394	GLY
1	A	68	ASN
1	A	32	VAL

### 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	305/327 (93%)	279 (92%)	26 (8%)	15	23
1	B	303/327 (93%)	286 (94%)	17 (6%)	30	45
All	All	608/654 (93%)	565 (93%)	43 (7%)	21	32

All (43) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	22	LYS
1	A	23	TYR
1	A	39	LEU
1	A	57	SER
1	A	62	GLU
1	A	89	LEU
1	A	91	ARG
1	A	109	LYS
1	A	117	ASN
1	A	118	PHE
1	A	140	ARG
1	A	145	GLU
1	A	148	LEU
1	A	209	THR
1	A	242	ARG

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Mol	Chain	Res	Type
1	A	255	LEU
1	A	263	PHE
1	A	268	LEU
1	A	318	THR
1	A	334	SER
1	A	335	ASN
1	A	343	LEU
1	A	344	GLN
1	A	389	LEU
1	A	393	ASP
1	A	395	LEU
1	B	15	PRO
1	B	17	ASN
1	B	23	TYR
1	B	108	CYS
1	B	109	LYS
1	B	117	ASN
1	B	148	LEU
1	B	184	ARG
1	B	192	TRP
1	B	226	ARG
1	B	255	LEU
1	B	263	PHE
1	B	290	ARG
1	B	318	THR
1	B	337	ASP
1	B	380	GLN
1	B	390	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	36	ASN
1	A	45	GLN
1	A	47	GLN
1	A	111	HIS
1	A	117	ASN
1	A	254	GLN
1	A	335	ASN
1	A	344	GLN
1	A	374	GLN
1	B	17	ASN

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Mol	Chain	Res	Type
1	B	36	ASN
1	B	45	GLN
1	B	76	GLN
1	B	117	ASN
1	B	254	GLN
1	B	295	HIS
1	B	355	GLN

### 5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

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

### 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

### 5.6 Ligand geometry ⓘ

2 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	401	-	4,4,4	0.19	0	6,6,6	0.20	0
2	SO4	B	402	-	4,4,4	0.12	0	6,6,6	0.32	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	401	-	-	0/0/0/0	0/0/0/0
2	SO4	B	402	-	-	0/0/0/0	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	374/400 (93%)	0.38	18 (4%) 29 27	27, 47, 84, 94	0
1	B	368/400 (92%)	0.10	20 (5%) 25 23	27, 44, 76, 99	0
All	All	742/800 (92%)	0.24	38 (5%) 27 25	27, 45, 82, 99	0

All (38) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	59	ASP	5.0
1	B	124	LEU	4.4
1	A	124	LEU	4.4
1	B	56	ILE	3.9
1	B	108	CYS	3.9
1	A	338	THR	3.6
1	B	205	GLU	3.4
1	A	56	ILE	3.4
1	B	62	GLU	3.4
1	B	119	PRO	3.3
1	B	9	ALA	3.1
1	B	70	ARG	3.0
1	A	142	TYR	3.0
1	B	396	PRO	3.0
1	A	70	ARG	3.0
1	B	145	GLU	2.9
1	B	120	THR	2.7
1	B	55	VAL	2.7
1	A	57	SER	2.7
1	B	57	SER	2.7
1	B	59	ASP	2.6
1	B	58	LYS	2.5
1	B	206	LYS	2.5
1	A	335	ASN	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	391	GLY	2.4
1	A	120	THR	2.3
1	B	61	THR	2.3
1	A	73	ASP	2.3
1	A	108	CYS	2.2
1	A	260	SER	2.2
1	A	19	ALA	2.1
1	A	386	CYS	2.1
1	A	60	PHE	2.1
1	B	146	SER	2.1
1	A	301	ALA	2.1
1	A	303	THR	2.0
1	B	395	LEU	2.0
1	A	133	CYS	2.0

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

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

## 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 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	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
2	SO4	B	402	5/5	0.11	-0.91	38,39,43,43	0
2	SO4	A	401	5/5	0.10	-1.33	36,37,39,40	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.