Full wwPDB X-ray Structure Validation Report ⓘ

Feb 4, 2024 – 09:27 AM EST

PDB ID	:	1RVG
Title	:	crystal structure of class II fructose-bisphosphate aldolase from Thermus aquaticus in complex with Y
Authors	:	Izard, T.; Sygusch, J.
Deposited on	:	2003-12-13
Resolution	:	2.00 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 ⓘ 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 ⓘ) were used in the production of this report:

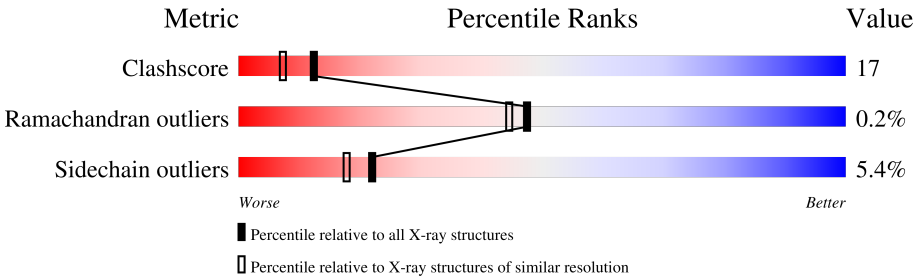
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.00 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))
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)

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%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	305	72% 24%
1	B	305	73% 24%
1	C	305	72% 25%
1	D	305	69% 30%

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
2	SO4	A	1604	-	-	X	-

2 Entry composition (i)

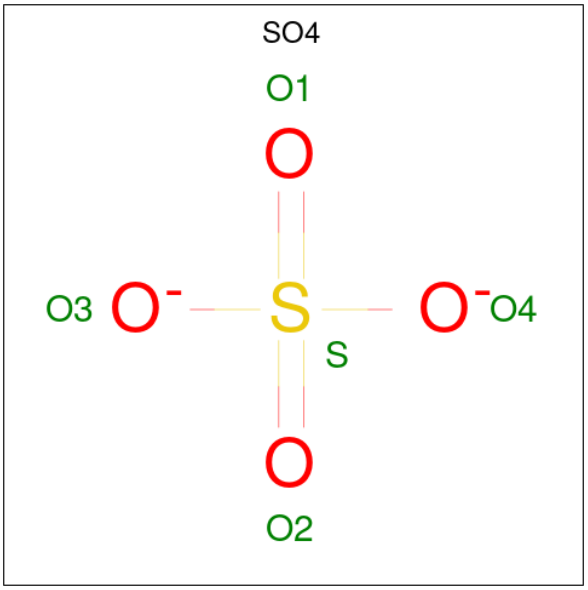
There are 6 unique types of molecules in this entry. The entry contains 10382 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 fructose-1,6-bisphosphate aldolase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	299	Total	C	N	O	S	40	10	0
			2356	1478	429	442	7			
1	B	305	Total	C	N	O	S	0	0	0
			2329	1464	421	437	7			
1	C	305	Total	C	N	O	S	0	0	0
			2329	1464	421	437	7			
1	D	305	Total	C	N	O	S	0	0	0
			2329	1464	421	437	7			

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



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

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

- Molecule 3 is COBALT (II) ION (three-letter code: CO) (formula: Co).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	2	Total Co 2 2	0	0
3	B	1	Total Co 1 1	0	0
3	C	1	Total Co 1 1	0	0
3	D	1	Total Co 1 1	0	0

- Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total Na 1 1	0	0
4	B	1	Total Na 1 1	0	0
4	C	1	Total Na 1 1	0	0
4	D	1	Total Na 1 1	0	0

- Molecule 5 is YTTRIUM (III) ION (three-letter code: YT3) (formula: Y).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total Y 1 1	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	266	Total O 266 266	0	0
6	B	240	Total O 240 240	0	0
6	C	258	Total O 258 258	0	0
6	D	210	Total O 210 210	0	0

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. 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. 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.

Note EDS was not executed.

• Molecule 1: fructose-1,6-bisphosphate aldolase

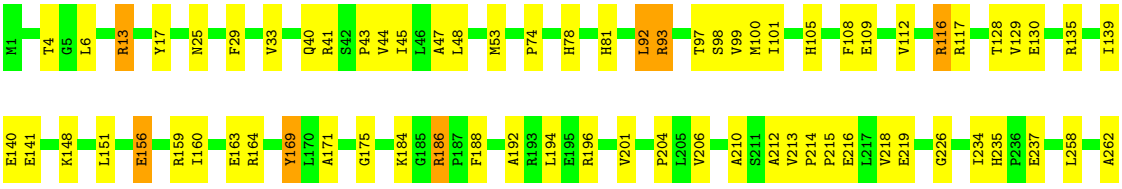
Chain A:

• Molecule 1: fructose-1,6-bisphosphate aldolase

Chain B:

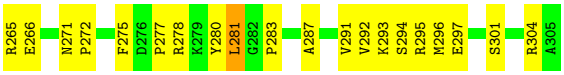
• Molecule 1: fructose-1,6-bisphosphate aldolase

Chain C:



• Molecule 1: fructose-1,6-bisphosphate aldolase

Chain D:



4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	99.86Å 57.55Å 138.62Å 90.00° 90.26° 90.00°	Depositor
Resolution (Å)	40.00 – 2.00	Depositor
% Data completeness (in resolution range)	91.9 (40.00-2.00)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.225 , 0.259	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	10382	wwPDB-VP
Average B, all atoms (Å^2)	31.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NA, YT3, CO, 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	0.42	3/2393 (0.1%)	0.61	1/3224 (0.0%)
1	B	0.32	0/2365	0.57	0/3190
1	C	0.34	0/2365	0.59	0/3190
1	D	0.31	0/2365	0.56	0/3190
All	All	0.35	3/9488 (0.0%)	0.58	1/12794 (0.0%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	182	LYS	CD-CE	7.83	1.70	1.51
1	A	182	LYS	CB-CG	-6.21	1.35	1.52
1	A	182	LYS	CE-NZ	-5.81	1.34	1.49

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	182	LYS	CD-CE-NZ	-5.93	98.06	111.70

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	2356	0	2383	80	0
1	B	2329	0	2372	84	0
1	C	2329	0	2372	84	0
1	D	2329	0	2372	90	0
2	A	15	0	0	3	0
2	B	15	0	0	0	0
2	C	15	0	0	0	0
2	D	10	0	0	0	0
3	A	2	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
5	A	1	0	0	0	0
6	A	266	0	0	6	0
6	B	240	0	0	8	0
6	C	258	0	0	11	0
6	D	210	0	0	10	0
All	All	10382	0	9499	318	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 17.

All (318) 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:140:GLU:OE1	1:C:160:ILE:CD1	1.83	1.26
1:C:140:GLU:O	1:C:141:GLU:HG2	1.46	1.15
1:C:186:ARG:H	1:C:186:ARG:HD3	1.04	1.10
1:C:139:ILE:HD12	1:C:140:GLU:OE1	1.54	1.07
1:C:140:GLU:OE1	1:C:160:ILE:HD13	1.46	1.06
1:A:207[A]:LEU:HD22	1:A:210:ALA:HB2	1.47	0.97
1:A:176:THR:HG21	1:A:207[A]:LEU:HD21	1.48	0.94
1:D:212:ALA:O	1:D:214:PRO:HD3	1.67	0.94
1:B:176:THR:HG21	1:B:207:LEU:HD21	1.50	0.93
1:A:106:GLU:HG2	1:A:110:THR:HG21	1.48	0.92
1:D:103:LYS:HG3	1:D:114:GLU:HG2	1.52	0.92
1:C:186:ARG:HD3	1:C:186:ARG:N	1.88	0.87
1:A:40:GLN:HE21	1:A:40:GLN:HA	1.40	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:210:ALA:HA	1:C:234:ILE:HD13	1.61	0.82
1:A:43:PRO:HB3	1:A:74:PRO:HG2	1.62	0.81
1:C:139:ILE:CD1	1:C:140:GLU:OE1	2.28	0.81
1:A:179[B]:GLY:O	1:A:182:LYS:HE3	1.81	0.81
1:D:40:GLN:HE21	1:D:40:GLN:HA	1.46	0.81
1:C:140:GLU:O	1:C:141:GLU:CG	2.30	0.80
1:B:186:ARG:H	1:B:186:ARG:HH11	1.29	0.79
1:A:179[A]:GLY:O	1:A:182:LYS:HE3	1.83	0.78
1:C:212:ALA:O	1:C:214:PRO:HD3	1.82	0.78
1:C:43:PRO:HB3	1:C:74:PRO:HG2	1.62	0.78
1:A:106:GLU:HG2	1:A:110:THR:CG2	2.13	0.77
1:B:43:PRO:HB3	1:B:74:PRO:HG2	1.66	0.77
1:B:295:ARG:HH11	1:B:295:ARG:HG2	1.52	0.75
1:D:93:ARG:HD3	6:D:1777:HOH:O	1.85	0.74
1:D:106:GLU:HG2	1:D:110:THR:HG21	1.71	0.73
1:B:188:PHE:C	1:B:189:ILE:HD12	2.08	0.72
1:A:272:PRO:HA	1:B:265:ARG:NH2	2.04	0.72
1:C:235:HIS:CE1	1:C:237:GLU:HG3	2.24	0.72
1:D:106:GLU:HG2	1:D:110:THR:CG2	2.20	0.71
1:B:295:ARG:HG2	1:B:295:ARG:NH1	2.05	0.71
1:A:236:PRO:O	1:A:240:LYS:HG3	1.91	0.70
1:D:181:TYR:HH	1:D:188:PHE:HE2	1.38	0.69
1:D:169:TYR:HB3	1:D:204:PRO:HG2	1.75	0.69
1:A:106:GLU:HG3	6:A:2035:HOH:O	1.92	0.69
1:B:40:GLN:HE21	1:B:40:GLN:HA	1.57	0.68
1:D:249:LYS:NZ	1:D:251:ASN:HD21	1.92	0.68
1:C:262:ALA:O	1:C:266:GLU:HG3	1.94	0.67
1:B:135:ARG:HG3	1:B:135:ARG:HH11	1.59	0.67
1:D:214:PRO:O	1:D:218:VAL:HG23	1.95	0.67
1:A:86:GLU:CD	1:A:86:GLU:H	1.99	0.66
1:A:25:ASN:ND2	1:B:278:ARG:HH11	1.93	0.66
1:B:234:ILE:HD12	1:B:234:ILE:H	1.59	0.66
1:A:265:ARG:NH2	1:B:272:PRO:HA	2.11	0.66
1:A:25:ASN:HD21	1:B:278:ARG:HH11	1.42	0.65
1:B:148:LYS:HA	1:B:151:LEU:HD11	1.78	0.65
1:B:151:LEU:HD22	1:B:181:TYR:HA	1.76	0.65
1:C:25:ASN:ND2	1:D:278:ARG:HD3	2.12	0.65
1:C:116:ARG:HD3	1:C:116:ARG:O	1.97	0.64
1:B:169:TYR:HB3	1:B:204:PRO:HG2	1.78	0.64
1:C:186:ARG:H	1:C:186:ARG:CD	1.92	0.64
1:B:289:LYS:HE3	6:B:1907:HOH:O	1.98	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:210:ALA:HA	1:B:234:ILE:HD13	1.81	0.63
1:A:235:HIS:CD2	1:A:237:GLU:H	2.18	0.62
1:C:140:GLU:C	1:C:141:GLU:HG2	2.17	0.62
1:C:140:GLU:OE1	1:C:160:ILE:HD12	1.92	0.62
1:C:140:GLU:OE1	1:C:160:ILE:HD11	1.92	0.62
1:D:11:LYS:HE2	6:D:1786:HOH:O	1.99	0.61
1:B:135:ARG:HG2	1:B:151:LEU:HA	1.81	0.61
1:D:43:PRO:HB3	1:D:74:PRO:HG2	1.82	0.61
1:C:278:ARG:HD3	1:D:25:ASN:ND2	2.16	0.61
1:B:135:ARG:HG3	1:B:135:ARG:NH1	2.16	0.60
1:A:235:HIS:CD2	1:A:237:GLU:HB2	2.35	0.60
1:B:189:ILE:HD12	1:B:189:ILE:N	2.16	0.60
1:A:17:TYR:CZ	1:A:304:ARG:HG2	2.36	0.60
1:C:140:GLU:CD	1:C:160:ILE:CD1	2.67	0.60
1:C:277:PRO:O	1:C:281:LEU:HB2	2.02	0.60
1:D:235:HIS:CE1	1:D:237:GLU:HB2	2.36	0.60
1:D:11:LYS:HE3	1:D:17:TYR:OH	2.01	0.60
1:B:148:LYS:O	1:B:151:LEU:HD12	2.02	0.60
1:D:249:LYS:HZ3	1:D:251:ASN:HD21	1.49	0.59
1:B:230:GLU:OE2	1:B:230:GLU:HA	2.02	0.59
1:C:151:LEU:CD1	1:C:184:LYS:HG2	2.32	0.59
1:D:210:ALA:CB	1:D:234:ILE:HD12	2.32	0.59
1:C:139:ILE:HD11	1:C:160:ILE:HD12	1.84	0.58
1:A:199:ARG:HH11	1:A:199:ARG:HB2	1.67	0.58
1:D:224:SER:HB2	1:D:265:ARG:HB2	1.85	0.58
1:C:40:GLN:HE21	1:C:40:GLN:HA	1.68	0.58
1:A:25:ASN:ND2	1:B:278:ARG:HD3	2.18	0.58
1:B:234:ILE:HD12	1:B:234:ILE:N	2.18	0.58
1:C:13:ARG:HD3	6:C:1836:HOH:O	2.04	0.58
1:C:101:ILE:HG22	6:C:1797:HOH:O	2.03	0.57
1:C:212:ALA:HB3	1:C:295:ARG:HH12	1.69	0.57
1:B:189:ILE:HD11	1:B:234:ILE:HG23	1.86	0.57
1:C:291:VAL:O	1:C:295:ARG:HG2	2.05	0.57
1:B:146:ASP:OD2	1:B:147:GLU:N	2.36	0.57
1:D:277:PRO:O	1:D:281:LEU:HB2	2.04	0.57
1:A:301:SER:O	1:A:304:ARG:HB2	2.04	0.57
1:D:210:ALA:HB1	1:D:234:ILE:HD12	1.86	0.56
1:D:294:SER:O	1:D:297:GLU:HB3	2.05	0.56
1:A:182:LYS:CD	1:A:182:LYS:N	2.66	0.56
1:A:250:ILE:HD12	1:A:250:ILE:N	2.20	0.56
1:B:186:ARG:H	1:B:186:ARG:HD3	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:164:ARG:HD2	6:D:1895:HOH:O	2.05	0.56
1:A:253:ASP:OD1	1:A:257:ARG:HD2	2.06	0.56
1:B:30:LEU:HD11	1:B:46:LEU:HD13	1.86	0.56
1:A:204:PRO:HD3	6:A:1848:HOH:O	2.06	0.56
1:B:72:ARG:NH1	6:B:1938:HOH:O	2.38	0.56
1:D:212:ALA:C	1:D:214:PRO:HD3	2.27	0.56
1:D:235:HIS:CE1	1:D:237:GLU:H	2.24	0.56
1:B:231:ALA:HB1	6:B:1900:HOH:O	2.06	0.56
1:A:211:SER:HB2	1:A:255:ASP:CG	2.27	0.55
1:D:218:VAL:HG21	1:D:231:ALA:HB2	1.88	0.55
1:D:117:ARG:HD3	6:D:1834:HOH:O	2.07	0.55
1:A:25:ASN:HD21	1:B:278:ARG:NH1	2.03	0.54
1:B:186:ARG:HH11	1:B:186:ARG:N	2.03	0.54
1:A:40:GLN:HA	1:A:40:GLN:NE2	2.16	0.54
1:D:105:HIS:HB2	6:D:1875:HOH:O	2.08	0.53
1:B:137:ALA:HB3	1:B:139:ILE:HG12	1.91	0.53
1:C:280:TYR:CD1	1:C:281:LEU:HD13	2.43	0.53
1:B:149:ASP:HA	1:B:193:ARG:NH2	2.24	0.53
1:B:234:ILE:H	1:B:234:ILE:CD1	2.21	0.53
1:A:277:PRO:HA	1:A:280:TYR:CE2	2.44	0.53
1:B:230:GLU:OE1	1:D:180:ALA:HB1	2.08	0.52
1:A:277:PRO:O	1:A:281:LEU:HB2	2.09	0.52
1:B:295:ARG:HH11	1:B:295:ARG:CG	2.20	0.52
1:A:40:GLN:HE21	1:A:40:GLN:CA	2.18	0.52
1:C:148:LYS:HE2	6:C:1918:HOH:O	2.08	0.52
1:C:212:ALA:HB3	1:C:295:ARG:NH1	2.25	0.52
1:A:108:PHE:O	1:A:112:VAL:HG23	2.09	0.52
1:C:287:ALA:O	1:C:291:VAL:HG23	2.09	0.52
1:D:263:LEU:HD22	1:D:287:ALA:HB2	1.92	0.51
1:A:277:PRO:HA	1:A:280:TYR:CZ	2.44	0.51
1:D:25:ASN:HD22	1:D:52:ALA:HA	1.76	0.51
1:D:250:ILE:HD12	1:D:250:ILE:N	2.26	0.51
1:D:211:SER:HB2	1:D:255:ASP:OD2	2.11	0.51
1:B:171:ALA:HA	1:B:206:VAL:HB	1.93	0.51
1:B:110:THR:O	1:B:114:GLU:HG2	2.11	0.51
1:C:235:HIS:HE1	1:C:237:GLU:HG3	1.72	0.51
1:C:234:ILE:HD12	1:C:234:ILE:N	2.25	0.51
1:D:223:ALA:HB3	6:D:1795:HOH:O	2.10	0.51
1:D:40:GLN:HA	1:D:40:GLN:NE2	2.21	0.51
1:A:139:ILE:HG13	1:A:175:GLY:HA2	1.92	0.50
1:A:235:HIS:HD2	1:A:237:GLU:HB2	1.74	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:141:GLU:O	1:B:141:GLU:HG2	2.12	0.50
1:C:212:ALA:C	1:C:214:PRO:HD3	2.30	0.50
1:B:186:ARG:HD3	1:B:186:ARG:N	2.26	0.50
1:A:56:GLY:HA3	1:A:60:LEU:HB2	1.93	0.50
1:C:210:ALA:HA	1:C:234:ILE:CD1	2.38	0.50
1:D:93:ARG:O	1:D:93:ARG:HG3	2.11	0.50
1:C:93:ARG:HD3	6:C:1846:HOH:O	2.12	0.50
1:B:186:ARG:H	1:B:186:ARG:CD	2.22	0.49
1:D:222:ARG:HA	1:D:226:GLY:O	2.11	0.49
1:A:171:ALA:HA	1:A:206:VAL:HB	1.93	0.49
1:C:192:ALA:O	1:C:196:ARG:HG3	2.12	0.49
1:D:30:LEU:HD11	1:D:46:LEU:HD13	1.93	0.49
1:D:222:ARG:HG3	1:D:222:ARG:HH11	1.78	0.49
1:D:179:GLY:O	1:D:182:LYS:HB2	2.12	0.49
1:C:280:TYR:CE1	1:C:281:LEU:HD13	2.48	0.49
1:D:277:PRO:HA	1:D:280:TYR:CZ	2.47	0.49
1:C:13:ARG:NH2	1:C:201:VAL:O	2.43	0.49
1:A:101:ILE:HG23	1:A:101:ILE:O	2.13	0.49
1:A:136:LEU:HB2	6:A:2006:HOH:O	2.13	0.48
1:C:156:GLU:OE1	1:C:159:ARG:NH1	2.46	0.48
1:D:6:LEU:HB3	1:D:128:THR:HG21	1.95	0.48
1:B:230:GLU:OE2	1:D:135:ARG:NH2	2.46	0.48
1:C:6:LEU:HB3	1:C:128:THR:HG21	1.95	0.48
1:C:78:HIS:HA	1:C:98:SER:O	2.13	0.48
1:A:101:ILE:HB	1:A:118:VAL:HG21	1.96	0.48
1:D:181:TYR:OH	1:D:188:PHE:HE2	1.95	0.48
1:D:23:ASN:HA	1:D:47:ALA:O	2.12	0.48
1:B:151:LEU:HD13	1:B:181:TYR:HD2	1.79	0.48
1:B:176:THR:HG21	1:B:207:LEU:CD2	2.34	0.48
1:A:35:GLU:O	1:A:39:GLU:HG3	2.14	0.47
1:A:132[A]:GLU:HG3	1:A:171:ALA:HB3	1.96	0.47
1:C:305:ALA:HB3	6:C:1890:HOH:O	2.15	0.47
1:B:182:LYS:O	1:B:184:LYS:HG3	2.13	0.47
1:A:17:TYR:CE1	1:A:304:ARG:HG2	2.49	0.47
1:A:47:ALA:C	1:A:48:LEU:HD12	2.34	0.47
1:A:109:GLU:OE2	1:A:164:ARG:NH2	2.47	0.47
1:A:234:ILE:HD12	1:A:234:ILE:N	2.29	0.47
1:B:262:ALA:O	1:B:266:GLU:HG3	2.14	0.47
1:D:56:GLY:HA3	1:D:60:LEU:HB2	1.96	0.47
1:A:86:GLU:CD	1:A:86:GLU:N	2.66	0.47
1:A:106:GLU:CG	1:A:110:THR:HG21	2.34	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:48:LEU:HD23	1:D:60:LEU:HD13	1.97	0.47
1:A:53:MET:HE2	6:A:1992:HOH:O	2.14	0.47
1:D:228:ILE:HG12	1:D:229:GLY:N	2.29	0.47
1:A:182:LYS:HZ2	1:A:233:GLY:HA2	1.80	0.47
1:D:40:GLN:HE21	1:D:40:GLN:CA	2.23	0.47
1:A:182:LYS:N	1:A:182:LYS:HD2	2.30	0.47
1:A:292:VAL:O	1:A:296:MET:HG3	2.15	0.47
1:C:109:GLU:HG2	6:C:1774:HOH:O	2.14	0.46
1:D:263:LEU:CD2	1:D:287:ALA:HB2	2.45	0.46
1:B:6:LEU:HB3	1:B:128:THR:HG21	1.96	0.46
1:C:92:LEU:HD13	1:C:99:VAL:HG11	1.97	0.46
1:D:85:TYR:CE1	1:D:117:ARG:HG2	2.50	0.46
1:B:189:ILE:HD11	1:B:234:ILE:CG2	2.45	0.46
1:D:148:LYS:HZ2	1:D:188:PHE:HE2	1.56	0.46
1:D:25:ASN:ND2	1:D:52:ALA:HA	2.30	0.46
1:D:103:LYS:CG	1:D:114:GLU:HG2	2.35	0.46
1:D:283:PRO:HB2	6:D:1745:HOH:O	2.15	0.46
1:B:182:LYS:HD3	1:B:183:GLY:N	2.30	0.46
1:C:140:GLU:CD	1:C:160:ILE:HD11	2.34	0.46
1:A:235:HIS:HD2	1:A:237:GLU:CB	2.29	0.46
1:A:273:LYS:HG3	1:B:227:GLU:HB2	1.98	0.46
1:B:106:GLU:HG2	1:B:110:THR:CG2	2.45	0.46
1:C:151:LEU:HD11	1:C:184:LYS:HG2	1.97	0.46
1:A:25:ASN:ND2	1:A:52:ALA:HA	2.31	0.46
1:C:265:ARG:HH21	1:D:272:PRO:HA	1.80	0.46
1:A:182:LYS:HG2	1:A:234:ILE:HD12	1.98	0.46
1:B:109:GLU:HB2	6:B:1749:HOH:O	2.16	0.46
1:D:262:ALA:O	1:D:266:GLU:HG3	2.16	0.46
1:A:10:LYS:NZ	6:A:2000:HOH:O	2.48	0.46
1:D:260:PHE:CE2	1:D:264:ILE:HD11	2.51	0.46
1:A:257:ARG:HB3	1:B:275:PHE:O	2.16	0.45
1:B:78:HIS:CE1	1:B:100:MET:HB2	2.51	0.45
1:D:186:ARG:O	1:D:188:PHE:HD2	1.99	0.45
1:D:292:VAL:O	1:D:296:MET:HG3	2.16	0.45
1:A:9:LEU:HD11	1:A:249:LYS:HD2	1.98	0.45
1:A:216:GLU:H	1:A:216:GLU:CD	2.19	0.45
1:B:81:HIS:CG	1:B:100:MET:HE3	2.51	0.45
1:B:135:ARG:HD3	1:B:136:LEU:N	2.31	0.45
1:C:263:LEU:HD22	1:C:287:ALA:HB2	1.98	0.45
1:C:274:GLU:OE2	1:C:279:LYS:HG3	2.16	0.45
1:D:130:GLU:HB2	1:D:169:TYR:CD1	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:199:ARG:HB2	1:A:199:ARG:NH1	2.31	0.45
1:D:103:LYS:HG3	1:D:114:GLU:CG	2.36	0.45
1:D:103:LYS:HE3	1:D:114:GLU:HG2	1.99	0.45
1:A:136:LEU:HD11	1:A:208[A]:HIS:HB2	1.97	0.45
1:B:185:GLY:HA2	6:B:1922:HOH:O	2.17	0.45
1:D:261:THR:O	1:D:265:ARG:HG3	2.16	0.45
1:C:175:GLY:HA3	1:C:188:PHE:O	2.16	0.45
1:B:40:GLN:HA	1:B:40:GLN:NE2	2.29	0.45
1:B:139:ILE:C	1:B:141:GLU:H	2.20	0.45
1:B:250:ILE:N	1:B:250:ILE:HD12	2.32	0.45
1:D:211:SER:HA	6:D:1803:HOH:O	2.17	0.45
1:C:135:ARG:HD3	6:C:1830:HOH:O	2.17	0.44
1:D:295:ARG:HA	1:D:295:ARG:NE	2.32	0.44
1:C:81:HIS:HA	1:C:100:MET:SD	2.57	0.44
1:D:22:PHE:HB3	1:D:256:LEU:HD11	1.98	0.44
1:B:35:GLU:O	1:B:39:GLU:HG3	2.17	0.44
1:A:25:ASN:HD22	1:A:52:ALA:HA	1.82	0.44
1:C:13:ARG:HA	6:C:1729:HOH:O	2.17	0.44
1:C:105:HIS:CD2	1:C:105:HIS:H	2.36	0.44
1:C:215:PRO:HA	1:C:218:VAL:HG22	1.98	0.44
1:C:263:LEU:CD2	1:C:287:ALA:HB2	2.48	0.44
1:B:136:LEU:HD11	1:B:142:HIS:HD2	1.82	0.44
1:A:35:GLU:HG3	6:A:1916:HOH:O	2.16	0.44
1:A:288:VAL:O	1:A:292:VAL:HG23	2.18	0.44
1:A:265:ARG:HH21	1:B:272:PRO:HA	1.83	0.43
1:C:17:TYR:CE2	1:C:304:ARG:HG3	2.54	0.43
1:B:6:LEU:CB	1:B:128:THR:HG21	2.48	0.43
1:B:295:ARG:HA	1:B:295:ARG:HD3	1.76	0.43
1:D:28:GLU:CD	1:D:28:GLU:H	2.22	0.43
1:A:171:ALA:HB1	1:A:208[A]:HIS:HD2	1.83	0.43
1:A:182:LYS:HB2	1:A:232:ALA:O	2.19	0.43
1:C:25:ASN:HD22	1:D:278:ARG:HD3	1.81	0.43
1:A:209[A]:GLY:HA2	2:A:1604:SO4:O3	2.18	0.43
1:B:216:GLU:OE1	1:B:216:GLU:O	2.37	0.43
1:C:171:ALA:HA	1:C:206:VAL:HB	2.00	0.43
1:C:265:ARG:NH2	1:D:272:PRO:HA	2.34	0.43
1:A:135:ARG:HD2	2:A:1609:SO4:O3	2.19	0.42
1:A:209[B]:GLY:HA2	2:A:1604:SO4:O3	2.19	0.42
1:D:36:ALA:HB1	1:D:293:LYS:HG3	2.01	0.42
1:D:291:VAL:O	1:D:295:ARG:HG2	2.18	0.42
1:A:214:PRO:HA	1:A:215:PRO:HD3	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:108:PHE:O	1:B:112:VAL:HG23	2.18	0.42
1:B:135:ARG:HD3	1:B:150:ALA:O	2.20	0.42
1:D:101:ILE:HB	1:D:118:VAL:HG21	2.00	0.42
1:D:222:ARG:HG3	1:D:222:ARG:NH1	2.34	0.42
1:A:182:LYS:HD3	1:A:232:ALA:O	2.20	0.42
1:D:101:ILE:HG23	1:D:101:ILE:O	2.19	0.42
1:A:235:HIS:HA	1:A:236:PRO:HD3	1.95	0.42
1:B:106:GLU:HG2	1:B:110:THR:HG21	2.00	0.42
1:C:100:MET:HG2	1:C:130:GLU:O	2.20	0.42
1:C:204:PRO:HD3	6:C:1748:HOH:O	2.19	0.42
1:D:271:ASN:HA	6:D:1913:HOH:O	2.18	0.42
1:A:15:GLU:HA	1:A:15:GLU:OE1	2.18	0.42
1:A:177[A]:SER:O	1:A:182:LYS:HE2	2.19	0.42
1:B:176:THR:HB	1:B:209:GLY:O	2.20	0.42
1:B:116:ARG:HH21	1:B:119:VAL:HG11	1.85	0.42
1:C:213:VAL:HG12	1:C:218:VAL:CG1	2.49	0.42
1:D:188:PHE:CD1	1:D:189:ILE:N	2.88	0.42
1:B:101:ILE:HG23	1:B:101:ILE:O	2.20	0.42
1:C:226:GLY:HA2	1:D:272:PRO:O	2.20	0.42
1:C:258:LEU:HD23	1:D:275:PHE:CG	2.54	0.42
1:D:218:VAL:O	1:D:222:ARG:HG2	2.20	0.42
1:B:189:ILE:CD1	1:B:234:ILE:HG23	2.50	0.41
1:C:47:ALA:C	1:C:48:LEU:HD12	2.40	0.41
1:A:10:LYS:O	1:A:14:GLU:HB2	2.20	0.41
1:A:214:PRO:HB2	1:A:216:GLU:OE1	2.20	0.41
1:B:199:ARG:HG3	1:B:199:ARG:HH11	1.84	0.41
1:C:277:PRO:HA	1:C:280:TYR:CZ	2.55	0.41
1:B:23:ASN:HA	1:B:47:ALA:O	2.21	0.41
1:B:230:GLU:HG3	1:B:230:GLU:O	2.20	0.41
1:C:44:VAL:HG22	1:C:45:ILE:N	2.35	0.41
1:C:130:GLU:HB2	1:C:169:TYR:CD1	2.56	0.41
1:D:6:LEU:CB	1:D:128:THR:HG21	2.51	0.41
1:B:90:ARG:HD2	6:B:1790:HOH:O	2.20	0.41
1:C:41:ARG:HD2	6:C:1811:HOH:O	2.19	0.41
1:D:148:LYS:NZ	1:D:188:PHE:CE2	2.80	0.41
1:D:213:VAL:HG12	1:D:218:VAL:HG22	2.01	0.41
1:B:277:PRO:HA	1:B:280:TYR:CZ	2.55	0.41
1:C:29:PHE:O	1:C:33:VAL:HG23	2.20	0.41
1:C:186:ARG:HG3	6:C:1951:HOH:O	2.19	0.41
1:C:273:LYS:HA	1:D:227:GLU:O	2.20	0.41
1:D:301:SER:HA	1:D:304:ARG:HG3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:81[A]:HIS:ND1	1:A:102:ASP:OD1	2.45	0.41
1:C:108:PHE:O	1:C:112:VAL:HG23	2.21	0.41
1:D:48:LEU:CD2	1:D:60:LEU:HD13	2.50	0.41
1:B:162:MET:SD	1:B:170:LEU:HB2	2.61	0.41
1:B:41:ARG:HD2	6:B:1750:HOH:O	2.20	0.41
1:C:4:THR:HA	1:C:97:THR:HB	2.03	0.41
1:C:6:LEU:CB	1:C:128:THR:HG21	2.51	0.41
1:D:17:TYR:CE2	1:D:304:ARG:HD2	2.56	0.41
1:C:92:LEU:CD1	1:C:99:VAL:HG11	2.51	0.41
1:C:109:GLU:CD	1:C:164:ARG:HH22	2.23	0.41
1:A:218:VAL:HG13	1:A:228:ILE:HG21	2.04	0.40
1:B:117:ARG:HD3	6:B:1891:HOH:O	2.21	0.40
1:C:281:LEU:HB3	1:D:55:TYR:OH	2.21	0.40
1:C:17:TYR:CE2	1:C:304:ARG:CG	3.04	0.40
1:B:130:GLU:HB2	1:B:169:TYR:CE1	2.56	0.40
1:C:151:LEU:HD13	1:C:184:LYS:HG2	2.01	0.40
1:D:47:ALA:C	1:D:48:LEU:HD12	2.42	0.40
1:D:90:ARG:NH2	6:D:1863:HOH:O	2.55	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	305/305 (100%)	295 (97%)	9 (3%)	1 (0%)	41	37
1	B	303/305 (99%)	284 (94%)	18 (6%)	1 (0%)	41	37
1	C	303/305 (99%)	298 (98%)	5 (2%)	0	100	100
1	D	303/305 (99%)	291 (96%)	12 (4%)	0	100	100
All	All	1214/1220 (100%)	1168 (96%)	44 (4%)	2 (0%)	47	44

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	140	GLU
1	B	139	ILE

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	239/237 (101%)	226 (95%)	13 (5%)	22	18
1	B	237/237 (100%)	224 (94%)	13 (6%)	21	17
1	C	237/237 (100%)	221 (93%)	16 (7%)	16	11
1	D	237/237 (100%)	228 (96%)	9 (4%)	33	31
All	All	950/948 (100%)	899 (95%)	51 (5%)	22	18

All (51) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	40	GLN
1	A	53	MET
1	A	60	LEU
1	A	79	LEU
1	A	140	GLU
1	A	156	GLU
1	A	169	TYR
1	A	182	LYS
1	A	237	GLU
1	A	281	LEU
1	A	297	GLU
1	A	304	ARG
1	B	1	MET
1	B	40	GLN
1	B	60	LEU
1	B	129	VAL
1	B	135	ARG
1	B	136	LEU
1	B	151	LEU

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Mol	Chain	Res	Type
1	B	169	TYR
1	B	186	ARG
1	B	194	LEU
1	B	207	LEU
1	B	211	SER
1	B	295	ARG
1	C	13	ARG
1	C	53	MET
1	C	92	LEU
1	C	93	ARG
1	C	116	ARG
1	C	117	ARG
1	C	129	VAL
1	C	156	GLU
1	C	163	GLU
1	C	169	TYR
1	C	186	ARG
1	C	194	LEU
1	C	216	GLU
1	C	219	GLU
1	C	281	LEU
1	C	304	ARG
1	D	1	MET
1	D	40	GLN
1	D	53	MET
1	D	60	LEU
1	D	79	LEU
1	D	92	LEU
1	D	93	ARG
1	D	169	TYR
1	D	281	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	25	ASN
1	A	40	GLN
1	A	235	HIS
1	B	40	GLN
1	B	142	HIS
1	B	208	HIS
1	C	25	ASN

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Mol	Chain	Res	Type
1	C	40	GLN
1	C	105	HIS
1	D	25	ASN
1	D	40	GLN
1	D	251	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 monosaccharides in this entry.

5.6 Ligand geometry

Of 21 ligands modelled in this entry, 10 are monoatomic - leaving 11 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	$\#\|Z\| > 2$
2	SO4	C	1605	-	4,4,4	0.25	0	6,6,6	0.09	0
2	SO4	A	1603	-	4,4,4	0.26	0	6,6,6	0.07	0
2	SO4	A	1604	-	4,4,4	0.26	0	6,6,6	0.10	0
2	SO4	D	1608	-	4,4,4	0.24	0	6,6,6	0.05	0
2	SO4	B	1602	-	4,4,4	0.24	0	6,6,6	0.05	0
2	SO4	A	1609	-	4,4,4	0.26	0	6,6,6	0.09	0
2	SO4	D	1607	-	4,4,4	0.27	0	6,6,6	0.09	0
2	SO4	C	1611	-	4,4,4	0.27	0	6,6,6	0.06	0
2	SO4	B	1601	-	4,4,4	0.24	0	6,6,6	0.15	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	SO4	B	1610	-	4,4,4	0.25	0	6,6,6	0.04	0
2	SO4	C	1606	-	4,4,4	0.27	0	6,6,6	0.08	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.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1604	SO4	2	0
2	A	1609	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

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.