Full wwPDB X-ray Structure Validation Report (i)

Mar 9, 2024 – 03:06 PM EST

PDB ID	:	3WKU
Title	:	Crystal structure of the anaerobic DesB-gallate complex
Authors	:	Sugimoto, K.; Senda, M.; Kasai, D.; Fukuda, M.; Masai, E.; Senda, T.
Deposited on	:	2013-10-31
Resolution	:	2.70 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:

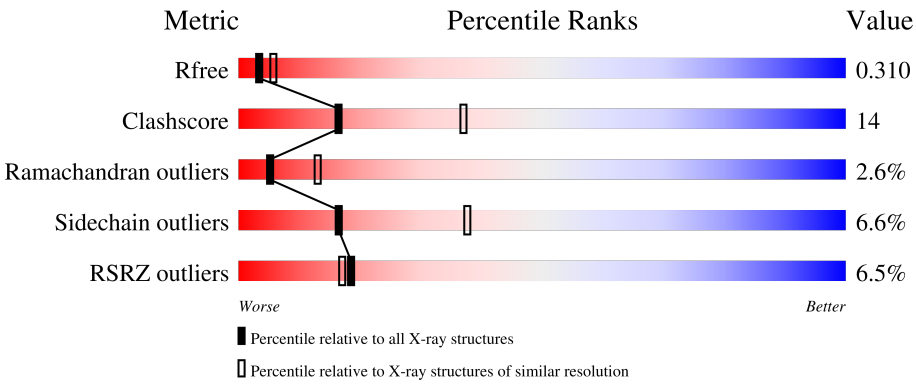
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.70 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	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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	418	12%; 62%; 31%; 5% •
1	B	418	68%; 26%; • •

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 6466 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.

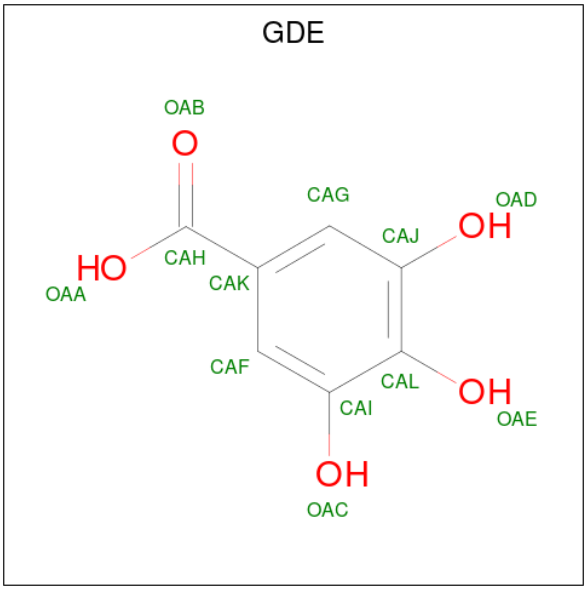
- Molecule 1 is a protein called Gallate dioxygenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	407	3229	2074	554	587	14	0	0	0
1	B	405	3220	2068	553	585	14	0	0	0

- Molecule 2 is FE (III) ION (three-letter code: FE) (formula: Fe).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Fe		
2	A	1	1	1	0	0
2	B	1	2	2	0	1

- Molecule 3 is 3,4,5-trihydroxybenzoic acid (three-letter code: GDE) (formula: $C_7H_6O_5$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
3	A	1	12	7	5	0	0

- Molecule 4 is water.

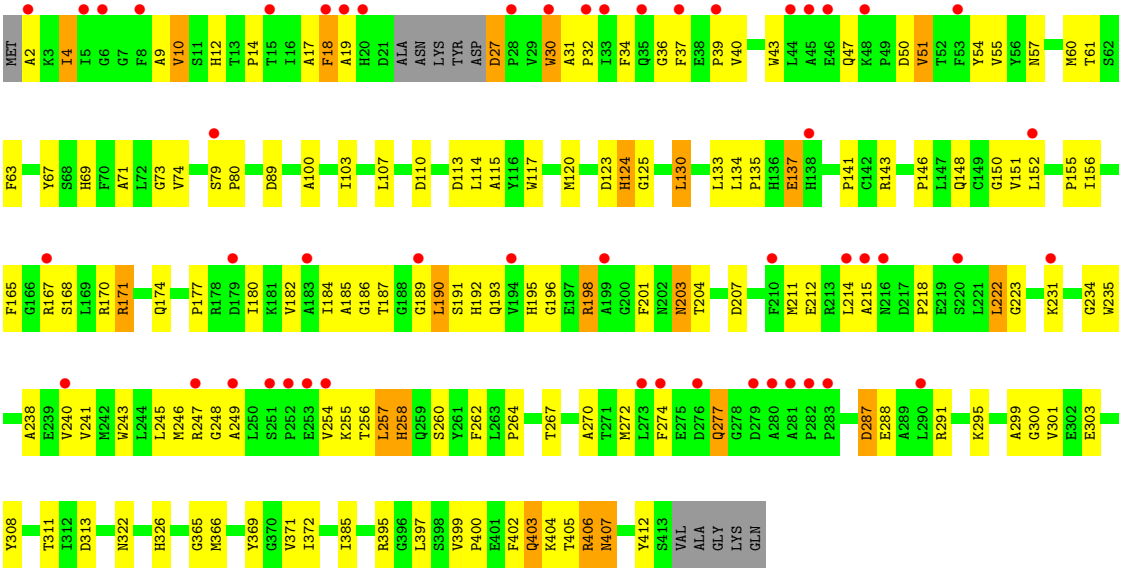
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	B	2	2	2	0	0

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 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.

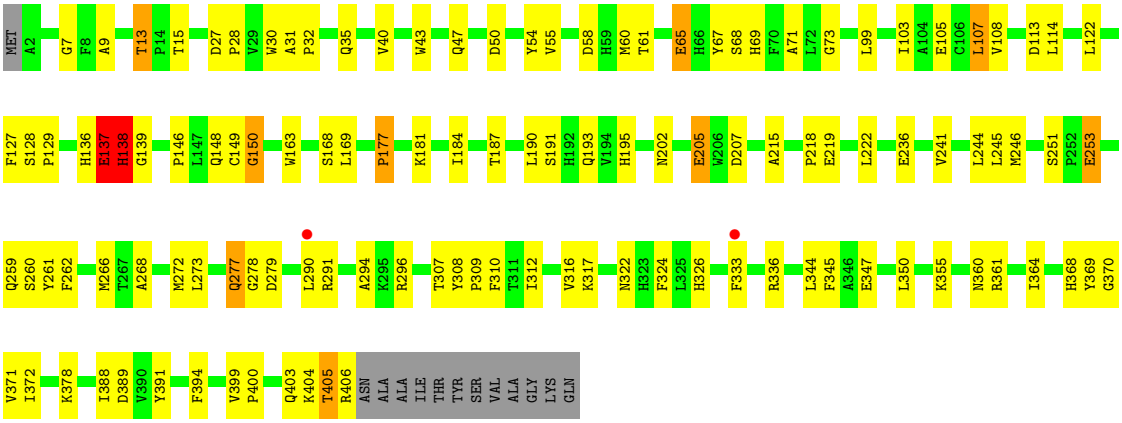
- Molecule 1: Gallate dioxygenase

Chain A:



- Molecule 1: Gallate dioxygenase

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	57.44Å 60.77Å 117.99Å 90.00° 98.58° 90.00°	Depositor
Resolution (Å)	20.00 – 2.70 56.79 – 2.70	Depositor EDS
% Data completeness (in resolution range)	100.0 (20.00-2.70) 98.2 (56.79-2.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	4.80 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.233 , 0.314 0.234 , 0.310	Depositor DCC
R_{free} test set	1100 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	56.9	Xtriage
Anisotropy	0.248	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 52.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	6466	wwPDB-VP
Average B, all atoms (Å^2)	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.57% 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: FE, GDE

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	0.51	0/3323	0.63	0/4507
1	B	0.59	0/3315	0.67	0/4496
All	All	0.55	0/6638	0.65	0/9003

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	B	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	137	GLU	Peptide

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	3229	0	3116	115	0
1	B	3220	0	3106	88	0
2	A	1	0	0	0	0
2	B	2	0	0	0	0
3	A	12	0	2	2	0
4	B	2	0	0	0	0
All	All	6466	0	6224	181	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 14.

All (181) 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:A:406:ARG:O	1:A:407:ASN:HB2	1.59	0.97
1:B:58:ASP:H	1:B:148:GLN:NE2	1.67	0.91
1:A:308:TYR:H	1:B:195:HIS:HE1	1.17	0.90
1:A:103:ILE:O	1:A:107:LEU:HD23	1.71	0.89
1:B:195:HIS:HD2	1:B:236:GLU:OE2	1.54	0.89
1:B:58:ASP:N	1:B:148:GLN:HE21	1.72	0.86
1:A:204:THR:HA	1:A:207:ASP:HB2	1.59	0.85
1:B:58:ASP:H	1:B:148:GLN:HE21	0.87	0.84
1:B:195:HIS:CD2	1:B:236:GLU:OE2	2.33	0.81
1:A:255:LYS:HG2	1:A:277:GLN:HE22	1.47	0.80
1:A:171:ARG:NH2	1:A:287:ASP:OD1	2.15	0.79
1:A:117:TRP:HA	1:B:65:GLU:O	1.83	0.79
1:B:205:GLU:H	1:B:205:GLU:CD	1.85	0.79
1:A:196:GLY:O	1:B:394:PHE:HB3	1.84	0.77
1:A:258:HIS:NE2	1:A:260:SER:HB3	2.02	0.75
1:A:4:ILE:HD11	1:A:174:GLN:HE21	1.52	0.74
1:A:177:PRO:HG3	1:A:291:ARG:HD2	1.69	0.74
1:B:399:VAL:HB	1:B:400:PRO:HD3	1.70	0.74
1:A:195:HIS:HE1	1:B:308:TYR:H	1.37	0.72
1:A:155:PRO:HB2	1:B:108:VAL:HG21	1.72	0.72
1:B:307:THR:O	1:B:309:PRO:HD3	1.89	0.71
1:B:388:ILE:HA	1:B:391:TYR:HD2	1.53	0.71
1:A:51:VAL:HG23	1:A:182:VAL:HG13	1.71	0.71
1:A:300:GLY:O	1:A:303:GLU:HG2	1.92	0.69
1:A:198:ARG:HH22	1:A:231:LYS:HA	1.58	0.68
1:A:113:ASP:HB2	1:B:113:ASP:HB2	1.76	0.67
1:A:211:MET:HE2	1:A:272:MET:CG	2.26	0.65
1:A:406:ARG:O	1:A:407:ASN:CB	2.38	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:107:LEU:HD11	1:B:169:LEU:HD12	1.79	0.64
1:B:317:LYS:NZ	1:B:369:TYR:O	2.25	0.64
1:B:388:ILE:HA	1:B:391:TYR:CD2	2.32	0.64
1:B:322:ASN:HD21	1:B:371:VAL:HA	1.61	0.64
1:A:308:TYR:H	1:B:195:HIS:CE1	2.08	0.63
1:A:171:ARG:HA	1:A:171:ARG:HE	1.63	0.63
1:B:73:GLY:HA3	1:B:146:PRO:HG2	1.78	0.63
1:A:195:HIS:HE1	1:B:308:TYR:N	1.95	0.63
1:A:34:PHE:HA	1:A:37:PHE:HD2	1.64	0.62
1:A:254:VAL:HB	1:A:274:PHE:HB3	1.81	0.62
1:A:54:TYR:CE1	1:A:130:LEU:HG	2.35	0.61
1:A:215:ALA:HA	1:A:247:ARG:HE	1.65	0.61
1:A:214:LEU:HD22	1:A:243:TRP:HE3	1.67	0.60
1:A:326:HIS:HE1	1:B:61:THR:O	1.84	0.60
1:B:277:GLN:HE21	1:B:277:GLN:HA	1.67	0.59
1:B:128:SER:HB3	1:B:129:PRO:CD	2.32	0.59
1:B:277:GLN:HA	1:B:277:GLN:NE2	2.18	0.59
1:A:135:PRO:HG2	1:A:141:PRO:HG3	1.84	0.58
1:A:403:GLN:HE21	1:A:403:GLN:HA	1.67	0.58
1:B:43:TRP:CD2	1:B:273:LEU:HD11	2.39	0.58
1:A:211:MET:HE2	1:A:272:MET:HG3	1.85	0.57
1:A:287:ASP:O	1:A:291:ARG:HG3	2.04	0.57
1:A:114:LEU:H	1:B:69:HIS:HD2	1.53	0.57
1:A:322:ASN:HD21	1:A:371:VAL:HA	1.70	0.57
1:A:372:ILE:HG21	1:B:60:MET:HG3	1.87	0.55
1:B:251:SER:OG	1:B:253:GLU:O	2.22	0.55
1:B:333:PHE:CE1	1:B:344:LEU:HD11	2.42	0.55
1:A:39:PRO:HG2	1:A:258:HIS:ND1	2.21	0.55
1:A:40:VAL:HG11	1:A:133:LEU:HD13	1.87	0.55
1:A:399:VAL:HB	1:A:400:PRO:HD3	1.87	0.55
1:A:405:THR:C	1:A:406:ARG:HD2	2.28	0.55
1:A:366:MET:HB3	1:A:371:VAL:HG21	1.87	0.54
1:B:69:HIS:O	1:B:149:CYS:HA	2.08	0.54
1:B:277:GLN:HE21	1:B:277:GLN:CA	2.21	0.54
1:A:170:ARG:HB2	1:A:249:ALA:HA	1.90	0.54
1:A:258:HIS:CE1	1:A:260:SER:HB3	2.41	0.53
1:A:195:HIS:CE1	1:B:308:TYR:H	2.23	0.53
1:A:71:ALA:HB3	1:A:148:GLN:HB3	1.90	0.53
1:B:7:GLY:HA2	1:B:184:ILE:O	2.08	0.53
1:B:54:TYR:OH	1:B:187:THR:HG21	2.09	0.53
1:A:135:PRO:O	1:A:141:PRO:HD3	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:326:HIS:CE1	1:B:61:THR:O	2.63	0.52
1:B:105:GLU:HB3	1:B:294:ALA:HB1	1.92	0.52
1:A:27:ASP:HB3	1:A:30:TRP:CD1	2.45	0.52
1:A:55:VAL:HG11	1:A:245:LEU:HD22	1.92	0.52
1:A:170:ARG:HD2	1:A:249:ALA:O	2.10	0.52
1:A:55:VAL:HB	1:A:186:GLY:HA2	1.92	0.51
1:A:9:ALA:O	1:A:10:VAL:HB	2.08	0.51
1:A:17:ALA:O	1:A:19:ALA:N	2.42	0.51
1:A:184:ILE:HG22	1:A:246:MET:HG2	1.93	0.51
3:A:502:GDE:CAG	1:B:13:THR:HG23	2.41	0.51
1:A:63:PHE:CZ	1:A:120:MET:CE	2.93	0.51
1:A:74:VAL:HG12	1:A:100:ALA:HB1	1.92	0.50
1:A:14:PRO:O	1:A:18:PHE:N	2.44	0.50
1:A:54:TYR:HA	1:A:185:ALA:HB3	1.94	0.50
1:A:54:TYR:CZ	1:A:187:THR:HG21	2.46	0.50
1:A:30:TRP:CD1	1:A:30:TRP:N	2.79	0.50
1:A:171:ARG:HH21	1:A:174:GLN:HB3	1.77	0.50
1:A:238:ALA:C	1:A:240:VAL:H	2.15	0.49
3:A:502:GDE:HAG	1:B:13:THR:HG23	1.93	0.49
1:B:43:TRP:CE2	1:B:47:GLN:HG3	2.48	0.49
1:A:190:LEU:CD2	1:A:191:SER:H	2.25	0.49
1:A:117:TRP:HB2	1:A:120:MET:HE2	1.94	0.49
1:A:214:LEU:HD22	1:A:243:TRP:CE3	2.47	0.49
1:B:324:PHE:CD1	1:B:350:LEU:HD11	2.48	0.48
1:A:63:PHE:CZ	1:A:120:MET:HE3	2.49	0.48
1:B:55:VAL:HG21	1:B:245:LEU:HD22	1.94	0.48
1:A:211:MET:CE	1:A:272:MET:HG3	2.44	0.48
1:A:4:ILE:HG22	1:A:182:VAL:O	2.13	0.48
1:A:151:VAL:HA	1:A:156:ILE:HG21	1.96	0.48
1:A:36:GLY:HA2	1:A:258:HIS:CE1	2.49	0.48
1:A:257:LEU:O	1:A:258:HIS:HB2	2.14	0.47
1:A:55:VAL:N	1:A:185:ALA:O	2.47	0.47
1:B:9:ALA:HB2	1:B:246:MET:CE	2.43	0.47
1:B:128:SER:HB3	1:B:129:PRO:HD3	1.96	0.47
1:A:201:PHE:C	1:A:201:PHE:CD2	2.88	0.47
1:A:211:MET:HE1	1:A:270:ALA:HB1	1.97	0.47
1:A:295:LYS:O	1:A:299:ALA:HB2	2.14	0.47
1:A:79:SER:HB3	1:A:80:PRO:HD2	1.97	0.47
1:B:43:TRP:CE3	1:B:273:LEU:HD11	2.50	0.47
1:A:204:THR:CA	1:A:207:ASP:HB2	2.40	0.47
1:A:36:GLY:HA2	1:A:258:HIS:NE2	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:192:HIS:CG	1:A:267:THR:HG23	2.49	0.46
1:A:67:TYR:CZ	1:A:150:GLY:HA2	2.51	0.46
1:B:31:ALA:N	1:B:32:PRO:HD2	2.31	0.46
1:B:308:TYR:CZ	1:B:368:HIS:CD2	3.04	0.45
1:B:260:SER:HB2	1:B:262:PHE:CE2	2.51	0.45
1:B:260:SER:HB2	1:B:262:PHE:HE2	1.81	0.45
1:B:122:LEU:HD12	1:B:127:PHE:CE2	2.52	0.45
1:B:259:GLN:HG2	1:B:260:SER:N	2.31	0.45
1:A:69:HIS:CD2	1:B:114:LEU:H	2.34	0.45
1:B:136:HIS:HA	1:B:139:GLY:O	2.17	0.45
1:A:167:ARG:HD2	1:A:248:GLY:O	2.17	0.45
1:B:99:LEU:HG	1:B:103:ILE:HD12	1.99	0.45
1:A:61:THR:O	1:B:326:HIS:HE1	1.99	0.45
1:B:27:ASP:O	1:B:30:TRP:N	2.48	0.45
1:A:214:LEU:O	1:A:218:PRO:HB3	2.17	0.44
1:B:312:ILE:O	1:B:316:VAL:HG23	2.17	0.44
1:A:152:LEU:O	1:B:310:PHE:HB3	2.18	0.44
1:B:324:PHE:CG	1:B:350:LEU:HD11	2.52	0.44
1:A:184:ILE:CG2	1:A:246:MET:HG2	2.48	0.43
1:A:189:GLY:HA3	1:A:190:LEU:HA	1.73	0.43
1:B:345:PHE:HB3	1:B:355:LYS:HE2	2.00	0.43
1:B:193:GLN:HE21	1:B:193:GLN:HB2	1.69	0.43
1:A:17:ALA:C	1:A:19:ALA:H	2.22	0.43
1:B:205:GLU:CD	1:B:205:GLU:N	2.64	0.43
1:B:191:SER:OG	1:B:207:ASP:OD2	2.36	0.43
1:B:215:ALA:HB2	1:B:272:MET:HE1	2.00	0.43
1:B:50:ASP:N	1:B:181:LYS:O	2.52	0.43
1:A:60:MET:HG3	1:B:372:ILE:HG21	2.01	0.42
1:A:207:ASP:O	1:A:211:MET:HG3	2.18	0.42
1:A:365:GLY:O	1:A:369:TYR:N	2.44	0.42
1:A:43:TRP:O	1:A:47:GLN:CG	2.67	0.42
1:B:277:GLN:NE2	1:B:277:GLN:CA	2.80	0.42
1:A:366:MET:HB3	1:A:371:VAL:CG2	2.50	0.42
1:B:261:TYR:CE1	1:B:268:ALA:HB1	2.54	0.42
1:A:73:GLY:HA3	1:A:146:PRO:HG2	2.01	0.42
1:A:134:LEU:HD22	1:A:141:PRO:HG2	2.02	0.42
1:A:12:HIS:CD2	1:A:125:GLY:HA2	2.55	0.42
1:B:244:LEU:HD23	1:B:244:LEU:HA	1.93	0.42
1:B:219:GLU:HA	1:B:222:LEU:HG	2.01	0.42
1:A:43:TRP:O	1:A:47:GLN:HG2	2.20	0.41
1:B:360:ASN:O	1:B:361:ARG:C	2.58	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:251:SER:CB	1:B:278:GLY:H	2.33	0.41
1:A:31:ALA:HB3	1:A:32:PRO:HD3	2.02	0.41
1:A:193:GLN:HG3	1:A:235:TRP:H	1.85	0.41
1:B:177:PRO:HG3	1:B:291:ARG:HD3	2.02	0.41
1:B:294:ALA:C	1:B:296:ARG:N	2.74	0.41
1:A:311:THR:OG1	1:A:313:ASP:OD1	2.34	0.41
1:A:165:PHE:CD2	1:A:245:LEU:HD11	2.56	0.41
1:A:203:ASN:HD22	1:A:203:ASN:HA	1.59	0.41
1:B:195:HIS:HD2	1:B:236:GLU:CD	2.22	0.41
1:A:198:ARG:NH1	1:A:234:GLY:HA2	2.36	0.41
1:A:255:LYS:O	1:A:257:LEU:N	2.54	0.41
1:B:67:TYR:CZ	1:B:150:GLY:HA2	2.56	0.41
1:B:71:ALA:HB3	1:B:148:GLN:HB3	2.01	0.41
1:B:137:GLU:O	1:B:138:HIS:HB2	2.21	0.41
1:B:163:TRP:CZ3	1:B:218:PRO:HB2	2.56	0.41
1:A:196:GLY:HA2	1:B:364:ILE:HD11	2.03	0.41
1:A:395:ARG:O	1:A:397:LEU:HG	2.21	0.41
1:B:40:VAL:HG22	1:B:273:LEU:HB2	2.03	0.41
1:A:39:PRO:O	1:A:43:TRP:HB2	2.21	0.40
1:A:406:ARG:NH2	1:B:202:ASN:HD21	2.19	0.40
1:A:412:TYR:CE1	1:B:15:THR:HG22	2.56	0.40
1:B:336:ARG:NH2	1:B:347:GLU:OE2	2.53	0.40
1:A:2:ALA:N	1:A:180:ILE:O	2.54	0.40
1:A:115:ALA:HA	1:B:68:SER:HA	2.04	0.40
1:A:51:VAL:HA	1:A:143:ARG:O	2.21	0.40
1:A:71:ALA:O	1:A:117:TRP:NE1	2.46	0.40
1:A:124:HIS:CD2	1:A:124:HIS:C	2.94	0.40
1:A:402:PHE:HZ	1:B:266:MET:SD	2.44	0.40
1:B:336:ARG:HE	1:B:336:ARG:HB3	1.61	0.40
1:A:193:GLN:HE21	1:A:235:TRP:H	1.69	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	403/418 (96%)	343 (85%)	49 (12%)	11 (3%)	5	12
1	B	403/418 (96%)	360 (89%)	33 (8%)	10 (2%)	5	14
All	All	806/836 (96%)	703 (87%)	82 (10%)	21 (3%)	5	13

All (21) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	18	PHE
1	A	256	THR
1	A	407	ASN
1	A	89	ASP
1	A	258	HIS
1	A	264	PRO
1	B	138	HIS
1	A	10	VAL
1	A	257	LEU
1	B	190	LEU
1	B	378	LYS
1	B	403	GLN
1	B	405	THR
1	A	137	GLU
1	A	222	LEU
1	A	223	GLY
1	B	137	GLU
1	B	28	PRO
1	B	150	GLY
1	B	177	PRO
1	B	370	GLY

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	332/340 (98%)	304 (92%)	28 (8%)	11	25
1	B	331/340 (97%)	315 (95%)	16 (5%)	25	53
All	All	663/680 (98%)	619 (93%)	44 (7%)	16	38

All (44) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	ILE
1	A	27	ASP
1	A	30	TRP
1	A	50	ASP
1	A	51	VAL
1	A	57	ASN
1	A	110	ASP
1	A	123	ASP
1	A	124	HIS
1	A	130	LEU
1	A	137	GLU
1	A	168	SER
1	A	171	ARG
1	A	190	LEU
1	A	198	ARG
1	A	203	ASN
1	A	212	GLU
1	A	222	LEU
1	A	241	VAL
1	A	262	PHE
1	A	277	GLN
1	A	287	ASP
1	A	288	GLU
1	A	301	VAL
1	A	385	ILE
1	A	403	GLN
1	A	404	LYS
1	A	406	ARG
1	B	13	THR
1	B	35	GLN
1	B	65	GLU
1	B	107	LEU
1	B	138	HIS
1	B	168	SER
1	B	205	GLU

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Mol	Chain	Res	Type
1	B	241	VAL
1	B	253	GLU
1	B	277	GLN
1	B	279	ASP
1	B	290	LEU
1	B	389	ASP
1	B	404	LYS
1	B	405	THR
1	B	406	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (29) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	12	HIS
1	A	20	HIS
1	A	57	ASN
1	A	69	HIS
1	A	118	GLN
1	A	124	HIS
1	A	154	HIS
1	A	164	ASN
1	A	174	GLN
1	A	193	GLN
1	A	195	HIS
1	A	203	ASN
1	A	277	GLN
1	A	322	ASN
1	A	326	HIS
1	A	403	GLN
1	A	407	ASN
1	B	42	GLN
1	B	69	HIS
1	B	118	GLN
1	B	136	HIS
1	B	148	GLN
1	B	154	HIS
1	B	193	GLN
1	B	195	HIS
1	B	202	ASN
1	B	277	GLN
1	B	322	ASN
1	B	326	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)

Of 4 ligands modelled in this entry, 3 are monoatomic - leaving 1 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	$\#\|Z\| > 2$
3	GDE	A	502	2	12,12,12	0.92	1 (8%)	17,17,17	0.86	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	GDE	A	502	2	-	4/4/4/4	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	502	GDE	CAJ-CAL	-2.35	1.37	1.40

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	502	GDE	OAB-CAH-CAK-CAG
3	A	502	GDE	OAA-CAH-CAK-CAG
3	A	502	GDE	OAB-CAH-CAK-CAF
3	A	502	GDE	OAA-CAH-CAK-CAF

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	502	GDE	2	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	407/418 (97%)	0.62	51 (12%)	3	3	28, 75, 106, 126	4 (0%)
1	B	405/418 (96%)	-0.03	2 (0%)	91	92	25, 46, 82, 90	2 (0%)
All	All	812/836 (97%)	0.30	53 (6%)	18	17	25, 59, 99, 126	6 (0%)

All (53) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	281	ALA	6.4
1	A	253	GLU	4.5
1	A	152	LEU	4.4
1	A	276	ASP	4.4
1	A	274	PHE	4.4
1	A	48	LYS	4.3
1	A	189	GLY	4.0
1	A	167	ARG	3.9
1	A	37	PHE	3.8
1	A	32	PRO	3.7
1	A	280	ALA	3.4
1	A	30	TRP	3.4
1	A	6	GLY	3.3
1	A	273	LEU	3.3
1	A	279	ASP	3.3
1	A	254	VAL	3.3
1	B	290	LEU	3.2
1	A	19	ALA	3.1
1	A	18	PHE	2.9
1	A	282	PRO	2.9
1	A	45	ALA	2.9
1	A	8	PHE	2.8
1	B	333	PHE	2.8
1	A	251	SER	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	44	LEU	2.8
1	A	247	ARG	2.6
1	A	179	ASP	2.6
1	A	39	PRO	2.6
1	A	28	PRO	2.6
1	A	249	ALA	2.6
1	A	290	LEU	2.6
1	A	210	PHE	2.6
1	A	283	PRO	2.5
1	A	53	PHE	2.5
1	A	2	ALA	2.4
1	A	33	ILE	2.4
1	A	20	HIS	2.4
1	A	183	ALA	2.4
1	A	194	VAL	2.4
1	A	46	GLU	2.4
1	A	215	ALA	2.3
1	A	138	HIS	2.3
1	A	216	ASN	2.3
1	A	240	VAL	2.2
1	A	35	GLN	2.2
1	A	15	THR	2.2
1	A	79	SER	2.1
1	A	220	SER	2.1
1	A	231	LYS	2.1
1	A	5	ILE	2.1
1	A	199	ALA	2.1
1	A	214	LEU	2.0
1	A	252	PRO	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	FE	A	501	1/1	0.90	0.09	112,112,112,112	0
3	GDE	A	502	12/12	0.97	0.15	25,28,30,31	0
2	FE	B	501[B]	1/1	0.98	0.10	23,23,23,23	1
2	FE	B	501[A]	1/1	0.98	0.10	14,14,14,14	1

6.5 Other polymers (i)

There are no such residues in this entry.