



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 05:42 PM UTC

PDB ID : 2GFY / pdb_00002gfy
Title : Structure of E. coli FabF(K335A) mutant with covalently linked dodecanoic acid
Authors : Soisson, S.M.; Parthasarathy, G.
Deposited on : 2006-03-23
Resolution : 2.85 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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

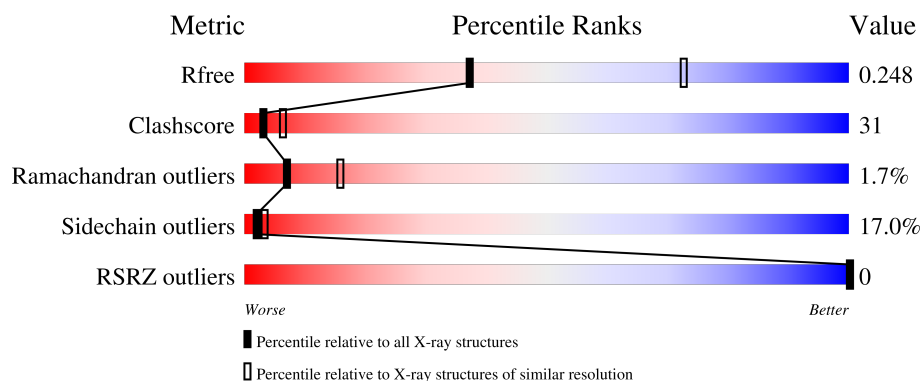
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.85 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}	180053	1407 (2.88-2.84)
Clashscore	190562	1446 (2.88-2.84)
Ramachandran outliers	187476	1406 (2.88-2.84)
Sidechain outliers	187428	1407 (2.88-2.84)
RSRZ outliers	180081	1408 (2.88-2.84)

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 $\leq 5\%$. 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	427	

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	DAO	A	1001	-	-	X	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3090 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.

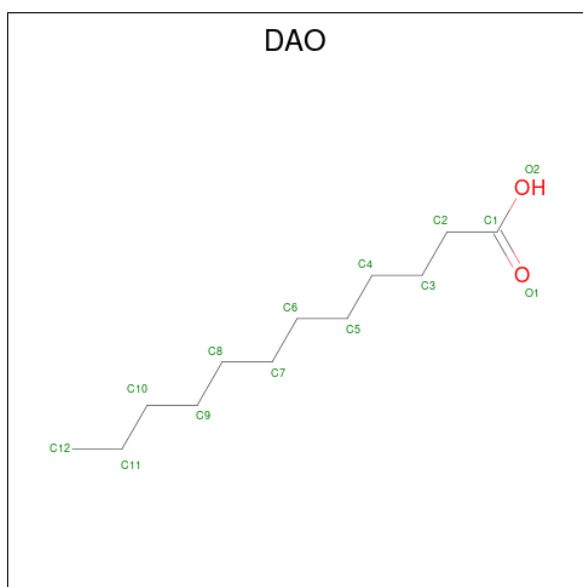
- Molecule 1 is a protein called 3-oxoacyl-[acyl-carrier-protein] synthase 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	411	Total	C	N	O	S	0	0	0
			3001	1872	526	586	17			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-14	MET	-	expression tag	UNP P0AAI5
A	-13	ARG	-	expression tag	UNP P0AAI5
A	-12	GLY	-	expression tag	UNP P0AAI5
A	-11	SER	-	expression tag	UNP P0AAI5
A	-10	HIS	-	expression tag	UNP P0AAI5
A	-9	HIS	-	expression tag	UNP P0AAI5
A	-8	HIS	-	expression tag	UNP P0AAI5
A	-7	HIS	-	expression tag	UNP P0AAI5
A	-6	HIS	-	expression tag	UNP P0AAI5
A	-5	HIS	-	expression tag	UNP P0AAI5
A	-4	GLY	-	expression tag	UNP P0AAI5
A	-3	SER	-	expression tag	UNP P0AAI5
A	-2	ALA	-	expression tag	UNP P0AAI5
A	-1	CYS	-	expression tag	UNP P0AAI5
A	0	VAL	-	expression tag	UNP P0AAI5
A	335	ALA	LYS	engineered mutation	UNP P0AAI5

- Molecule 2 is LAURIC ACID (CCD ID: DAO) (formula: C₁₂H₂₄O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			13	12	1		

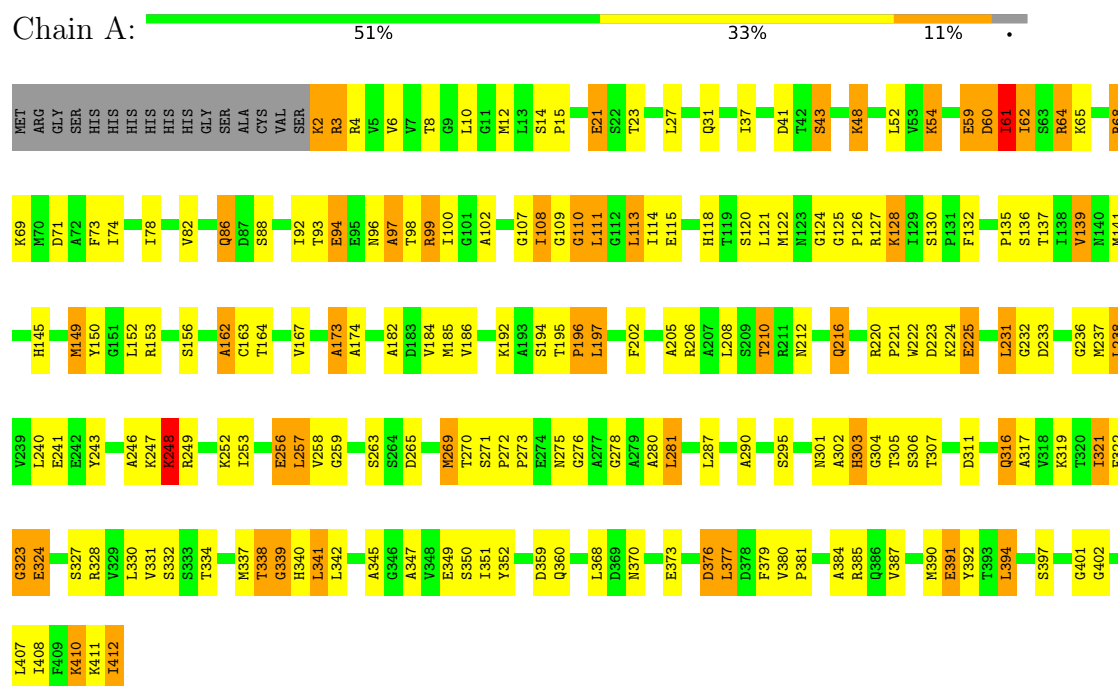
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	76	Total	O	0	0
			76	76		

3 Residue-property plots

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: 3-oxoacyl-[acyl-carrier-protein] synthase 2



4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	74.73Å 74.73Å 148.07Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	64.55 – 2.85 64.55 – 2.85	Depositor EDS
% Data completeness (in resolution range)	98.2 (64.55-2.85) 98.5 (64.55-2.85)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.75 (at 2.85Å)	Xtriage
Refinement program	BUSTER-TNT 1.3.1	Depositor
R, R_{free}	0.166 , 0.243 0.171 , 0.248	Depositor DCC
R_{free} test set	553 reflections (4.73%)	wwPDB-VP
Wilson B-factor (Å ²)	61.2	Xtriage
Anisotropy	0.553	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 49.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.033 for -h,-k,l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	3090	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.29% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 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: DAO

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	0.87	1/3053 (0.0%)	1.19	19/4129 (0.5%)

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	1	0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	269	MET	SD-CE	5.49	1.93	1.79

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	373	GLU	N-CA-C	15.04	127.72	111.03
1	A	303	HIS	N-CA-C	-11.88	96.90	111.40
1	A	3	ARG	N-CA-C	7.43	120.51	109.59
1	A	276	GLY	N-CA-C	-7.33	105.10	115.43
1	A	139	VAL	N-CA-C	6.91	120.71	111.17
1	A	350	SER	N-CA-C	-6.85	103.90	111.36
1	A	307	THR	N-CA-C	-6.53	101.90	110.39
1	A	173	ALA	N-CA-C	-6.52	103.86	110.97
1	A	401	GLY	N-CA-C	-5.90	107.11	115.30
1	A	162	ALA	CB-CA-C	-5.83	109.86	116.63
1	A	339	GLY	N-CA-C	-5.78	103.00	112.83
1	A	21	GLU	N-CA-C	5.66	118.17	111.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	225	GLU	N-CA-C	5.59	119.19	112.93
1	A	377	LEU	N-CA-C	5.58	118.74	110.48
1	A	86	GLN	N-CA-C	-5.53	104.94	110.97
1	A	61	ILE	N-CA-C	5.32	117.22	111.58
1	A	12	MET	N-CA-C	5.23	117.03	108.76
1	A	321	ILE	N-CA-C	5.21	115.98	110.72
1	A	376	ASP	N-CA-C	-5.19	106.97	113.72

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	373	GLU	CA

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	3001	0	2961	187	0
2	A	13	0	23	8	0
3	A	76	0	0	12	0
All	All	3090	0	2984	188	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 31.

All (188) 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:64:ARG:HD2	1:A:64:ARG:H	1.17	1.04
1:A:243:TYR:CZ	1:A:247:LYS:HE3	1.98	0.98
1:A:392:TYR:CE1	1:A:410:LYS:HG3	2.07	0.89
1:A:122:MET:HG2	3:A:1067:HOH:O	1.72	0.89
1:A:162:ALA:HB1	2:A:1001:DAO:H41	1.58	0.85
1:A:338:THR:HG22	1:A:339:GLY:O	1.78	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:231:LEU:HD11	1:A:342:LEU:HD11	1.58	0.84
1:A:237:MET:C	1:A:238:LEU:HD23	2.04	0.83
1:A:345:ALA:O	1:A:349:GLU:HG3	1.79	0.83
1:A:387:VAL:HG21	1:A:390:MET:HE2	1.63	0.80
1:A:280:ALA:HB1	1:A:321:ILE:HD11	1.64	0.80
1:A:243:TYR:CE2	1:A:247:LYS:HE3	2.18	0.79
1:A:231:LEU:HD11	1:A:342:LEU:CD1	2.14	0.78
1:A:115:GLU:OE2	1:A:197:LEU:HB2	1.84	0.77
1:A:210:THR:HB	3:A:1070:HOH:O	1.83	0.76
1:A:287:LEU:HD23	1:A:408:ILE:HD11	1.67	0.76
1:A:256:GLU:HG3	1:A:258:VAL:HG13	1.66	0.76
1:A:118:HIS:NE2	1:A:122:MET:HE2	2.02	0.75
1:A:68:ARG:HD3	3:A:1053:HOH:O	1.86	0.74
1:A:60:ASP:N	1:A:60:ASP:OD1	2.20	0.73
1:A:202:PHE:HZ	2:A:1001:DAO:H31	1.53	0.72
1:A:64:ARG:H	1:A:64:ARG:CD	1.96	0.72
1:A:257:LEU:HD21	1:A:407:LEU:HD22	1.70	0.71
1:A:86:GLN:HG2	3:A:1073:HOH:O	1.90	0.71
1:A:331:VAL:O	1:A:379:PHE:HA	1.90	0.70
1:A:52:LEU:O	1:A:54:LYS:HE2	1.91	0.70
1:A:64:ARG:HD2	1:A:64:ARG:N	2.00	0.69
1:A:145:HIS:O	1:A:149:MET:HG3	1.91	0.69
1:A:174:ALA:HB2	1:A:257:LEU:HD13	1.75	0.68
1:A:71:ASP:CG	1:A:110:GLY:HA2	2.18	0.68
1:A:269:MET:CG	1:A:270:THR:HG23	2.24	0.67
1:A:69:LYS:HE2	1:A:132:PHE:CZ	2.29	0.67
1:A:241:GLU:OE2	1:A:249:ARG:NH1	2.27	0.67
1:A:248:LYS:HG3	1:A:248:LYS:O	1.95	0.67
1:A:73:PHE:CE1	1:A:74:ILE:HG13	2.31	0.66
1:A:124:GLY:HA3	1:A:128:LYS:HG2	1.75	0.66
1:A:108:ILE:HD13	2:A:1001:DAO:H122	1.76	0.65
1:A:411:LYS:HG2	1:A:412:ILE:HD12	1.77	0.64
1:A:99:ARG:NE	3:A:1009:HOH:O	2.31	0.64
1:A:118:HIS:CD2	1:A:122:MET:HE2	2.33	0.64
1:A:61:ILE:HD13	1:A:61:ILE:N	2.13	0.64
1:A:202:PHE:CZ	2:A:1001:DAO:H31	2.32	0.64
1:A:287:LEU:HD23	1:A:408:ILE:CD1	2.27	0.63
1:A:108:ILE:HD13	2:A:1001:DAO:C12	2.28	0.63
1:A:127:ARG:HB2	3:A:1049:HOH:O	1.98	0.62
1:A:360:GLN:O	1:A:387:VAL:HG22	1.99	0.62
1:A:231:LEU:CD1	1:A:342:LEU:HD11	2.28	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:269:MET:HG3	1:A:270:THR:HG23	1.83	0.61
1:A:340:HIS:HD2	3:A:1076:HOH:O	1.84	0.60
1:A:135:PRO:O	1:A:141:MET:HG3	2.02	0.60
1:A:92:ILE:HD12	1:A:100:ILE:HD13	1.83	0.60
1:A:232:GLY:C	1:A:341:LEU:HD22	2.27	0.60
1:A:97:ALA:HB1	1:A:153:ARG:HG3	1.84	0.60
1:A:376:ASP:HB3	3:A:1077:HOH:O	2.02	0.59
1:A:8:THR:O	1:A:88:SER:HA	2.03	0.59
1:A:269:MET:HG2	1:A:270:THR:HG23	1.85	0.59
1:A:216:GLN:HG3	3:A:1008:HOH:O	2.03	0.59
1:A:330:LEU:HD22	1:A:380:VAL:HG22	1.85	0.59
1:A:303:HIS:CD2	1:A:305:THR:HG23	2.37	0.58
1:A:222:TRP:CD1	1:A:311:ASP:HB3	2.38	0.57
1:A:281:LEU:HD22	1:A:281:LEU:O	2.05	0.57
1:A:258:VAL:HG23	1:A:408:ILE:HG22	1.87	0.57
1:A:111:LEU:O	1:A:115:GLU:HG3	2.05	0.57
1:A:237:MET:O	1:A:238:LEU:HD23	2.04	0.56
1:A:6:VAL:HG12	1:A:256:GLU:HB2	1.87	0.56
1:A:31:GLN:O	1:A:337:MET:HB3	2.04	0.56
1:A:394:LEU:C	1:A:394:LEU:HD23	2.30	0.56
1:A:121:LEU:O	1:A:121:LEU:HG	2.05	0.55
1:A:258:VAL:O	1:A:290:ALA:HA	2.06	0.55
1:A:265:ASP:OD1	1:A:278:GLY:HA3	2.06	0.55
1:A:317:ALA:O	1:A:321:ILE:HG12	2.07	0.55
1:A:258:VAL:CG2	1:A:408:ILE:HG22	2.38	0.54
1:A:256:GLU:CG	1:A:258:VAL:HG13	2.36	0.54
1:A:121:LEU:HD12	1:A:126:PRO:N	2.22	0.54
1:A:111:LEU:HD13	1:A:195:THR:OG1	2.08	0.54
1:A:82:VAL:HG13	1:A:150:TYR:OH	2.08	0.54
1:A:231:LEU:HD12	1:A:232:GLY:N	2.23	0.53
1:A:306:SER:HA	1:A:311:ASP:OD2	2.09	0.53
1:A:100:ILE:HG22	1:A:152:LEU:HD13	1.91	0.53
1:A:223:ASP:OD2	1:A:224:LYS:N	2.42	0.53
1:A:392:TYR:HE1	1:A:410:LYS:HG3	1.69	0.53
1:A:126:PRO:HD2	3:A:1020:HOH:O	2.09	0.52
1:A:6:VAL:HG22	1:A:241:GLU:O	2.10	0.52
1:A:222:TRP:HH2	1:A:302:ALA:CB	2.22	0.52
1:A:222:TRP:CE2	1:A:379:PHE:CE1	2.98	0.52
1:A:247:LYS:O	1:A:249:ARG:N	2.42	0.52
1:A:59:GLU:OE2	1:A:64:ARG:HG3	2.09	0.52
1:A:150:TYR:O	1:A:152:LEU:HD23	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:224:LYS:HG3	1:A:370:ASN:O	2.10	0.52
1:A:316:GLN:HB2	3:A:1060:HOH:O	2.10	0.52
1:A:2:LYS:O	1:A:2:LYS:HG3	2.08	0.51
1:A:82:VAL:O	1:A:86:GLN:HG3	2.10	0.51
1:A:392:TYR:CE1	1:A:410:LYS:NZ	2.72	0.51
1:A:238:LEU:HD23	1:A:238:LEU:N	2.25	0.51
1:A:71:ASP:HA	1:A:113:LEU:HD22	1.93	0.51
1:A:110:GLY:O	1:A:114:ILE:HG13	2.11	0.51
1:A:221:PRO:O	1:A:368:LEU:HD13	2.12	0.50
1:A:41:ASP:OD1	1:A:43:SER:OG	2.29	0.50
1:A:253:ILE:O	1:A:253:ILE:HG22	2.11	0.50
1:A:238:LEU:HD21	1:A:351:ILE:HG13	1.94	0.50
1:A:280:ALA:CB	1:A:321:ILE:HD11	2.40	0.50
1:A:222:TRP:CE3	1:A:379:PHE:CD1	3.00	0.50
1:A:132:PHE:O	1:A:136:SER:HB3	2.12	0.49
1:A:319:LYS:O	1:A:323:GLY:N	2.42	0.49
1:A:192:LYS:HE2	1:A:194:SER:OG	2.12	0.49
1:A:97:ALA:CB	1:A:153:ARG:HG3	2.43	0.49
1:A:118:HIS:CD2	1:A:122:MET:CE	2.95	0.49
1:A:392:TYR:CZ	1:A:410:LYS:NZ	2.80	0.49
1:A:60:ASP:C	1:A:61:ILE:HD13	2.38	0.49
1:A:246:ALA:O	1:A:249:ARG:HG2	2.13	0.49
1:A:21:GLU:HA	1:A:21:GLU:OE1	2.13	0.48
1:A:164:THR:HG22	1:A:164:THR:O	2.13	0.48
1:A:108:ILE:HG13	1:A:108:ILE:O	2.13	0.48
1:A:78:ILE:HD11	1:A:145:HIS:CB	2.43	0.48
1:A:93:THR:H	1:A:96:ASN:CB	2.27	0.48
1:A:93:THR:H	1:A:96:ASN:HB2	1.79	0.48
1:A:163:CYS:SG	1:A:340:HIS:HE1	2.36	0.48
1:A:192:LYS:C	1:A:192:LYS:HD3	2.39	0.47
1:A:195:THR:HB	1:A:196:PRO:HD2	1.95	0.47
1:A:163:CYS:SG	1:A:340:HIS:CE1	3.08	0.47
1:A:120:SER:HB3	1:A:128:LYS:HB3	1.96	0.47
1:A:10:LEU:HD13	1:A:351:ILE:HG23	1.96	0.47
1:A:78:ILE:O	1:A:82:VAL:HG23	2.15	0.47
1:A:306:SER:O	1:A:306:SER:OG	2.26	0.47
1:A:392:TYR:CD1	1:A:410:LYS:HG3	2.50	0.47
1:A:281:LEU:HD22	1:A:281:LEU:C	2.40	0.46
1:A:324:GLU:HA	1:A:324:GLU:OE2	2.15	0.46
1:A:69:LYS:HG2	1:A:132:PHE:CD2	2.50	0.46
1:A:107:GLY:HA3	2:A:1001:DAO:H62	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:27:LEU:HD22	1:A:337:MET:HE3	1.97	0.46
1:A:71:ASP:CA	1:A:113:LEU:HD22	2.46	0.46
1:A:271:SER:HA	1:A:272:PRO:HD3	1.85	0.46
1:A:392:TYR:HE1	1:A:410:LYS:HZ3	1.52	0.46
1:A:231:LEU:HD12	1:A:232:GLY:H	1.81	0.46
1:A:392:TYR:OH	1:A:410:LYS:NZ	2.49	0.46
1:A:192:LYS:HD3	1:A:192:LYS:O	2.16	0.45
1:A:202:PHE:HE2	2:A:1001:DAO:H81	1.82	0.45
2:A:1001:DAO:H82	2:A:1001:DAO:H51	1.77	0.45
1:A:197:LEU:HD12	1:A:197:LEU:HA	1.51	0.45
1:A:121:LEU:HD12	1:A:125:GLY:C	2.42	0.45
1:A:265:ASP:HB2	1:A:402:GLY:HA3	1.98	0.45
1:A:109:GLY:O	1:A:111:LEU:N	2.44	0.44
1:A:334:THR:HG21	1:A:352:TYR:CD2	2.53	0.44
1:A:132:PHE:O	1:A:136:SER:CB	2.66	0.44
1:A:303:HIS:CD2	1:A:305:THR:CG2	3.01	0.44
1:A:14:SER:OG	1:A:23:THR:HG23	2.18	0.43
1:A:110:GLY:HA3	1:A:137:THR:HA	2.00	0.43
1:A:387:VAL:HG21	1:A:390:MET:CE	2.40	0.43
1:A:248:LYS:HE2	1:A:248:LYS:HB2	1.80	0.43
1:A:48:LYS:HG3	1:A:212:ASN:CG	2.43	0.43
1:A:259:GLY:HA3	1:A:290:ALA:HB2	1.99	0.43
1:A:2:LYS:HG3	1:A:2:LYS:HZ2	1.77	0.43
1:A:61:ILE:C	1:A:62:ILE:HG13	2.43	0.43
1:A:94:GLU:C	1:A:96:ASN:H	2.26	0.43
1:A:102:ALA:O	1:A:156:SER:HA	2.17	0.43
1:A:360:GLN:C	1:A:387:VAL:HG22	2.44	0.43
1:A:359:ASP:O	1:A:360:GLN:C	2.62	0.42
1:A:99:ARG:CD	3:A:1009:HOH:O	2.67	0.42
1:A:263:SER:HB2	1:A:281:LEU:HD13	2.01	0.42
1:A:368:LEU:HD23	1:A:381:PRO:HB3	2.00	0.42
1:A:96:ASN:O	1:A:97:ALA:C	2.62	0.42
1:A:97:ALA:O	1:A:99:ARG:N	2.52	0.42
1:A:341:LEU:HD23	1:A:341:LEU:N	2.34	0.42
1:A:173:ALA:HB3	1:A:240:LEU:HD12	2.02	0.42
1:A:256:GLU:CG	1:A:258:VAL:CG1	2.97	0.42
1:A:128:LYS:HD2	1:A:128:LYS:HA	1.58	0.42
1:A:192:LYS:HE2	1:A:233:ASP:OD2	2.19	0.42
1:A:322:PHE:N	1:A:322:PHE:CD1	2.88	0.42
1:A:59:GLU:HG3	1:A:64:ARG:HE	1.84	0.42
1:A:15:PRO:O	1:A:54:LYS:HE3	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:391:GLU:O	1:A:410:LYS:HA	2.20	0.41
1:A:205:ALA:O	1:A:206:ARG:HB2	2.19	0.41
1:A:247:LYS:C	1:A:249:ARG:N	2.77	0.41
1:A:273:PRO:C	1:A:275:ASN:N	2.76	0.41
1:A:69:LYS:HG2	1:A:132:PHE:CE2	2.56	0.41
1:A:3:ARG:NH2	1:A:182:ALA:O	2.53	0.41
1:A:108:ILE:HG21	1:A:111:LEU:HG	2.03	0.41
1:A:222:TRP:CD2	1:A:379:PHE:CE1	3.08	0.41
1:A:222:TRP:CZ3	1:A:379:PHE:CD1	3.09	0.41
1:A:2:LYS:HZ3	1:A:2:LYS:C	2.29	0.41
1:A:27:LEU:HD23	1:A:27:LEU:HA	1.73	0.41
1:A:301:ASN:ND2	1:A:349:GLU:HB3	2.36	0.41
1:A:4:ARG:NH2	1:A:243:TYR:CE2	2.89	0.40
1:A:236:GLY:O	1:A:347:ALA:HB1	2.20	0.40
1:A:281:LEU:HD23	1:A:281:LEU:HA	1.83	0.40
1:A:27:LEU:HD22	1:A:337:MET:CE	2.51	0.40
1:A:330:LEU:HD23	1:A:330:LEU:HA	1.86	0.40
1:A:184:VAL:HG12	1:A:185:MET:N	2.36	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	409/427 (96%)	362 (88%)	40 (10%)	7 (2%)	7 16

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	110	GLY
1	A	248	LYS
1	A	304	GLY

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Mol	Chain	Res	Type
1	A	323	GLY
1	A	97	ALA
1	A	98	THR
1	A	384	ALA

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	306/319 (96%)	254 (83%)	52 (17%)	2 3

All (52) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	LYS
1	A	37	ILE
1	A	43	SER
1	A	48	LYS
1	A	54	LYS
1	A	59	GLU
1	A	60	ASP
1	A	61	ILE
1	A	62	ILE
1	A	64	ARG
1	A	65	LYS
1	A	68	ARG
1	A	94	GLU
1	A	99	ARG
1	A	108	ILE
1	A	111	LEU
1	A	113	LEU
1	A	128	LYS
1	A	130	SER
1	A	139	VAL
1	A	149	MET
1	A	167	VAL

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Mol	Chain	Res	Type
1	A	186	VAL
1	A	196	PRO
1	A	197	LEU
1	A	208	LEU
1	A	210	THR
1	A	216	GLN
1	A	220	ARG
1	A	225	GLU
1	A	231	LEU
1	A	238	LEU
1	A	248	LYS
1	A	252	LYS
1	A	256	GLU
1	A	257	LEU
1	A	281	LEU
1	A	295	SER
1	A	316	GLN
1	A	324	GLU
1	A	327	SER
1	A	328	ARG
1	A	332	SER
1	A	338	THR
1	A	341	LEU
1	A	377	LEU
1	A	385	ARG
1	A	391	GLU
1	A	394	LEU
1	A	397	SER
1	A	410	LYS
1	A	412	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	123	ASN
1	A	214	ASN
1	A	275	ASN
1	A	301	ASN
1	A	340	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand is 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	DAO	A	1001	1	11,12,13	0.75	0	10,11,13	1.67	2 (20%)

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	DAO	A	1001	1	-	6/10/10/11	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	A	1001	DAO	C10-C9-C8	-4.25	92.91	114.37
2	A	1001	DAO	C5-C4-C3	-2.01	104.19	114.37

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1001	DAO	O1-C1-C2-C3
2	A	1001	DAO	C9-C10-C11-C12
2	A	1001	DAO	C11-C10-C9-C8
2	A	1001	DAO	C4-C5-C6-C7
2	A	1001	DAO	C6-C7-C8-C9
2	A	1001	DAO	C3-C4-C5-C6

There are no ring outliers.

1 monomer is involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1001	DAO	8	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	411/427 (96%)	-0.62	0 100 100	37, 51, 77, 103	0

There are no RSRZ outliers to report.

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 oligosaccharides 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	DAO	A	1001	13/14	0.95	0.14	38,39,42,43	0

6.5 Other polymers [i](#)

There are no such residues in this entry.