



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 13, 2020 – 10:04 AM BST

PDB ID : 1YGB
Title : Crystal Structure of the catalytic fragment of alanyl-tRNA synthetase in complex with L-serine
Authors : Swairjo, M.A.; Schimmel, P.R.
Deposited on : 2005-01-04
Resolution : 2.48 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 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) : 1.13
EDS : 2.14.4.dev1
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) : 2.14.4.dev1

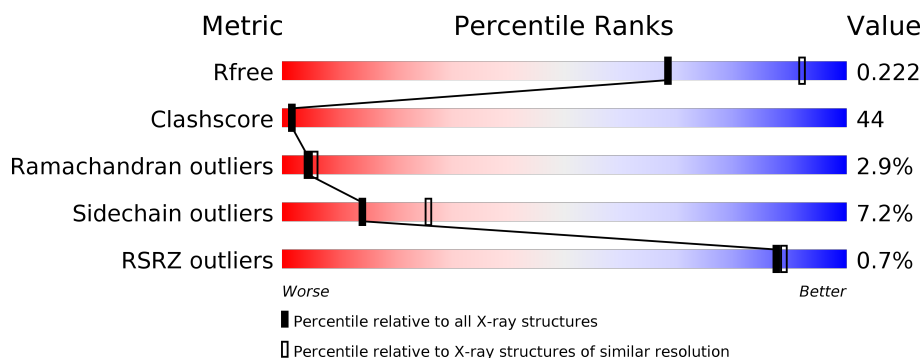
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.48 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	5857 (2.50-2.46)
Clashscore	141614	6594 (2.50-2.46)
Ramachandran outliers	138981	6469 (2.50-2.46)
Sidechain outliers	138945	6471 (2.50-2.46)
RSRZ outliers	127900	5738 (2.50-2.46)

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 ≥ 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	465	<div> <div> <div></div> <div>35%</div> <div>55%</div> <div>6%</div> <div></div> </div> <div> <div></div> <div></div> <div></div> <div></div> <div></div> </div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3794 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.

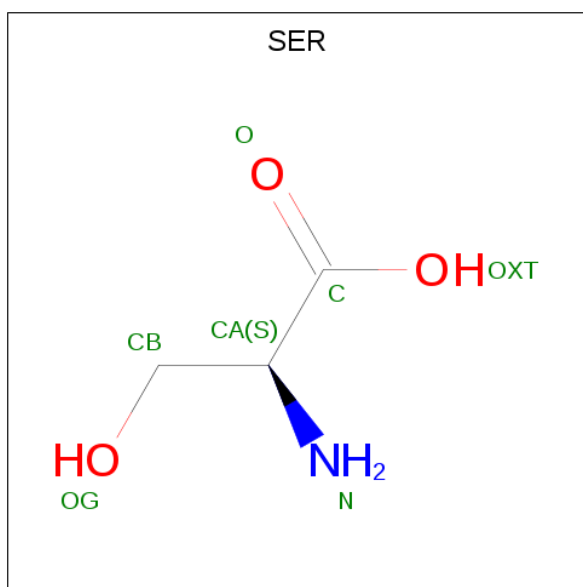
- Molecule 1 is a protein called Alanyl-tRNA synthetase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	448	Total	C	N	O	S	0	0	0
			3641	2339	615	675	12			

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	454	ALA	-	CLONING ARTIFACT	UNP O67323
A	455	ALA	-	CLONING ARTIFACT	UNP O67323
A	456	ALA	-	CLONING ARTIFACT	UNP O67323
A	457	LEU	-	CLONING ARTIFACT	UNP O67323
A	458	GLU	-	CLONING ARTIFACT	UNP O67323
A	459	HIS	-	EXPRESSION TAG	UNP O67323
A	460	HIS	-	EXPRESSION TAG	UNP O67323
A	461	HIS	-	EXPRESSION TAG	UNP O67323
A	462	HIS	-	EXPRESSION TAG	UNP O67323
A	463	HIS	-	EXPRESSION TAG	UNP O67323
A	464	HIS	-	EXPRESSION TAG	UNP O67323

- Molecule 2 is SERINE (three-letter code: SER) (formula: C₃H₇NO₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			7	3	1	3		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	146	Total	O	0	0
			146	146		

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.

Chain A: ■ 35% ■ 55% ■ 6% ■

Set	Item	Category
S1	S1	Gray
	S2	Gray
	S3	Gray
	S4	Gray
	S5	Gray
	S6	Gray
	S7	Gray
	S8	Gray
	S9	Gray
	S10	Gray
	S11	Gray
	S12	Gray
S13	S13	Green
	S14	Green
	S15	Green
	S16	Green
	S17	Green
	S18	Green
	S19	Green
	S20	Green
	S21	Green
	S22	Green
	S23	Green
	S24	Green
S25	S25	Orange
	S26	Orange
	S27	Orange
	S28	Orange
	S29	Orange
	S30	Orange
	S31	Orange
	S32	Orange
	S33	Orange
	S34	Orange
	S35	Orange
	S36	Orange
S37	S37	Red
	S38	Red
	S39	Red
	S40	Red
	S41	Red
	S42	Red
	S43	Red
	S44	Red
	S45	Red
	S46	Red
	S47	Red
	S48	Red
S49	S49	Green
	S50	Green
	S51	Green
	S52	Green
	S53	Green
	S54	Green
	S55	Green
	S56	Green
	S57	Green
	S58	Green
	S59	Green
	S60	Green
S61	Green	
S62	S62	Orange
	S63	Orange
	S64	Orange
	S65	Orange
	S66	Orange
	S67	Orange
	S68	Orange
	S69	Orange
	S70	Orange
	S71	Orange
	S72	Orange
	S73	Orange
S74	Orange	
S75	Orange	
S76	S76	Green
	S77	Green
	S78	Green
	S79	Green
	S80	Green
	S81	Green
	S82	Green
	S83	Green
	S84	Green
	S85	Green
	S86	Green
	S87	Green
S88	Green	
S89	Green	
S90	Green	
S91	S91	Orange
	S92	Orange
	S93	Orange
	S94	Orange
	S95	Orange
	S96	Orange
	S97	Orange
	S98	Orange
	S99	Orange
	S100	Orange
	S101	Orange
	S102	Orange
S103	Orange	
S104	Orange	
S105	S105	Green
	S106	Green
	S107	Green
	S108	Green
	S109	Green
	S110	Green
	S111	Green
	S112	Green
	S113	Green
	S114	Green
	S115	Green
	S116	Green
S117	Green	
S118	Green	
S119	Green	
S120	S120	Orange
	S121	Orange
	S122	Orange
	S123	Orange
	S124	Orange
	S125	Orange
	S126	Orange
	S127	Orange
	S128	Orange
	S129	Orange
	S130	Orange
	S131	Orange
S132	Orange	
S133	Orange	
S134	Orange	
S135	S135	Green
	S136	Green
	S137	Green
	S138	Green
	S139	Green
	S140	Green
	S141	Green
	S142	Green
	S143	Green
	S144	Green
	S145	Green
	S146	Green
S147	Green	
S148	Green	
S149	Green	
S150	Green	
S151	Green	
S152	Green	
S153	Green	
S154	Green	
S155	Green	
S156	Green	
S157	Green	
S158	Green	
S159	Green	
S160	Green	
S161	Green	
S162	Green	
S163	Green	
S164	Green	
S165	Green	
S166	Green	
S167	Green	
S168	Green	
S169	Green	
S170	Green	
S171	Green	
S172	Green	
S173	Green	
S174	Green	
S175	Green	
S176	Green	
S177	Green	
S178	Green	
S179	Green	
S180	Green	
S181	Green	
S182	Green	
S183	Green	
S184	Green	

4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	74.09 Å 74.09 Å 173.59 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.48 37.05 – 2.48	Depositor EDS
% Data completeness (in resolution range)	(Not available) (50.00-2.48) 98.8 (37.05-2.48)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.14 (at 2.48 Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.199 , 0.232 0.187 , 0.222	Depositor DCC
R_{free} test set	1761 reflections (9.96%)	wwPDB-VP
Wilson B-factor (Å ²)	31.7	Xtriage
Anisotropy	0.167	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.13 , 50.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.39$, $\langle L^2 \rangle = 0.22$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	3794	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.79% 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 [i](#)

5.1 Standard geometry [i](#)

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	0.39	1/3725 (0.0%)	0.60	0/5016

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	352	PHE	C-O	5.15	1.33	1.23

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	439	TYR	Sidechain

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	3641	0	3601	317	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	7	0	4	0	0
3	A	146	0	0	45	0
All	All	3794	0	3605	317	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 44.

All (317) 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:296:ARG:HD3	1:A:300:ARG:NH2	1.20	1.49
1:A:296:ARG:HD3	1:A:300:ARG:CZ	1.80	1.10
1:A:335:GLU:HG2	1:A:338:ARG:HH12	1.14	1.09
1:A:296:ARG:CD	1:A:300:ARG:NH2	2.16	1.09
1:A:348:GLU:O	1:A:352:PHE:HB3	1.53	1.07
1:A:296:ARG:O	1:A:300:ARG:HG3	1.54	1.05
1:A:202:ARG:HH11	1:A:202:ARG:HB2	1.30	0.96
1:A:296:ARG:HD3	1:A:300:ARG:HH21	1.07	0.89
1:A:296:ARG:CD	1:A:300:ARG:HH21	1.83	0.86
1:A:442:LEU:O	1:A:443:LYS:HG3	1.73	0.86
1:A:70:VAL:HG11	1:A:298:ILE:HD11	1.61	0.83
1:A:166:VAL:HG23	1:A:166:VAL:O	1.82	0.80
1:A:211:LEU:O	1:A:214:PRO:HD3	1.81	0.78
1:A:190:LEU:HD11	1:A:224:ARG:HD3	1.66	0.78
1:A:183:TYR:O	1:A:184:GLU:CG	2.33	0.77
1:A:183:TYR:O	1:A:184:GLU:HG3	1.83	0.77
1:A:71:SER:C	1:A:75:ASN:HB2	2.06	0.76
1:A:352:PHE:O	1:A:352:PHE:CD2	2.39	0.75
1:A:202:ARG:HB2	1:A:202:ARG:NH1	2.01	0.75
1:A:92:MET:HE2	1:A:219:GLY:HA3	1.69	0.74
1:A:125:LEU:HD22	1:A:177:VAL:HG22	1.69	0.74
1:A:149:GLU:HB3	3:A:618:HOH:O	1.87	0.74
1:A:444:GLU:HA	1:A:447:LYS:HG3	1.69	0.73
1:A:302:ALA:HB1	3:A:646:HOH:O	1.89	0.73
1:A:289:GLU:HB3	1:A:438:VAL:HG23	1.70	0.73
1:A:303:MET:HE1	1:A:352:PHE:CD2	2.24	0.73
1:A:131:LYS:HA	1:A:153:ARG:HB3	1.70	0.72
1:A:367:ILE:O	1:A:371:LEU:HG	1.88	0.72
1:A:353:ILE:HG12	1:A:357:LYS:HE3	1.69	0.72
1:A:414:GLN:HE22	1:A:445:LEU:HB2	1.55	0.72
1:A:312:GLU:O	1:A:353:ILE:HD11	1.90	0.71

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:272:HIS:HE1	1:A:301:ARG:HG2	1.57	0.70
1:A:323:VAL:HG11	3:A:503:HOH:O	1.91	0.70
1:A:417:LEU:HD13	1:A:445:LEU:HB3	1.71	0.70
1:A:296:ARG:CG	1:A:300:ARG:NE	2.54	0.69
1:A:176:TYR:HB3	3:A:534:HOH:O	1.91	0.69
1:A:183:TYR:O	1:A:184:GLU:CD	2.30	0.69
1:A:421:ARG:HG3	1:A:425:ARG:NH1	2.07	0.69
1:A:303:MET:CE	1:A:352:PHE:CD2	2.77	0.68
1:A:369:LYS:NZ	1:A:375:ARG:HH22	1.91	0.68
1:A:184:GLU:HA	1:A:188:ARG:HB2	1.76	0.68
1:A:203:ASP:OD2	1:A:207:VAL:HB	1.94	0.68
1:A:421:ARG:HH22	1:A:442:LEU:HG	1.59	0.67
1:A:296:ARG:CD	1:A:300:ARG:CZ	2.65	0.67
1:A:30:PRO:HB2	1:A:33:ASP:HB3	1.77	0.66
1:A:269:ILE:HG12	3:A:646:HOH:O	1.95	0.66
1:A:325:ASP:HA	1:A:328:LYS:HE2	1.75	0.66
1:A:38:PHE:HZ	1:A:295:ILE:HD11	1.61	0.66
1:A:421:ARG:NH2	1:A:442:LEU:HG	2.11	0.66
1:A:320:VAL:HG21	1:A:345:VAL:HG21	1.77	0.65
1:A:276:ILE:O	1:A:280:ILE:HG13	1.97	0.65
1:A:111:TRP:CH2	1:A:146:ILE:HD11	2.32	0.64
1:A:166:VAL:HA	1:A:202:ARG:HG2	1.79	0.64
1:A:347:GLY:O	1:A:351:ARG:HB3	1.97	0.64
1:A:247:PHE:HZ	1:A:318:LYS:HB2	1.62	0.64
1:A:19:GLY:HA2	3:A:563:HOH:O	1.97	0.64
1:A:289:GLU:HB3	1:A:438:VAL:CG2	2.28	0.64
1:A:335:GLU:HG2	1:A:338:ARG:NH1	1.99	0.63
1:A:81:GLY:O	1:A:264:VAL:HG13	1.99	0.63
1:A:325:ASP:HA	1:A:328:LYS:CE	2.29	0.63
1:A:202:ARG:HH12	1:A:208:LEU:HD21	1.63	0.63
1:A:271:ASP:HA	3:A:572:HOH:O	1.99	0.62
1:A:206:GLY:O	1:A:208:LEU:HD12	2.00	0.62
1:A:369:LYS:HZ3	1:A:375:ARG:HH22	1.46	0.62
1:A:38:PHE:CZ	1:A:295:ILE:HD11	2.35	0.62
1:A:190:LEU:CD1	1:A:224:ARG:HD3	2.30	0.62
1:A:31:GLU:HG3	1:A:32:ASN:OD1	2.00	0.61
1:A:243:PRO:HA	1:A:246:GLN:OE1	2.00	0.61
1:A:129:VAL:HG12	1:A:173:SER:OG	1.99	0.61
1:A:7:ILE:HD11	1:A:229:LEU:HD12	1.82	0.61
1:A:37:LEU:HD22	1:A:291:ARG:NE	2.16	0.60
1:A:296:ARG:HG3	1:A:300:ARG:HE	1.66	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:438:VAL:HG11	1:A:452:VAL:HG11	1.81	0.60
1:A:320:VAL:HG12	3:A:615:HOH:O	2.01	0.60
1:A:122:LYS:HG3	1:A:123:GLU:OE2	2.02	0.60
1:A:362:TYR:O	1:A:366:VAL:HG22	2.01	0.59
1:A:374:GLY:HA2	3:A:518:HOH:O	2.03	0.59
1:A:42:GLY:N	1:A:92:MET:SD	2.67	0.59
1:A:120:LEU:HD11	1:A:229:LEU:HD21	1.84	0.59
1:A:160:PHE:HA	3:A:583:HOH:O	2.02	0.59
1:A:179:ARG:HD2	1:A:228:VAL:HG22	1.84	0.59
1:A:39:VAL:HG13	1:A:44:VAL:HB	1.85	0.59
1:A:37:LEU:HD22	1:A:291:ARG:HE	1.68	0.58
1:A:425:ARG:N	1:A:425:ARG:HD2	2.18	0.58
1:A:304:ARG:HA	1:A:356:LEU:HD21	1.85	0.58
1:A:233:ASN:HB2	3:A:565:HOH:O	2.02	0.58
1:A:189:TYR:C	3:A:534:HOH:O	2.42	0.58
1:A:70:VAL:HG12	1:A:88:THR:HG22	1.85	0.58
1:A:85:ARG:HH22	1:A:190:LEU:HD22	1.69	0.58
1:A:85:ARG:NH2	1:A:190:LEU:HD22	2.18	0.58
1:A:72:GLY:O	1:A:75:ASN:HB3	2.03	0.58
1:A:356:LEU:O	1:A:360:MET:HG2	2.03	0.57
1:A:216:ILE:HG23	3:A:517:HOH:O	2.04	0.57
1:A:21:THR:HG22	1:A:22:ARG:H	1.69	0.57
1:A:272:HIS:CE1	1:A:301:ARG:HG2	2.38	0.57
1:A:371:LEU:HB3	1:A:406:LEU:HD11	1.86	0.57
1:A:98:PHE:HA	1:A:215:ASN:OD1	2.04	0.57
1:A:211:LEU:C	1:A:213:HIS:H	2.08	0.56
1:A:316:LEU:HD21	3:A:646:HOH:O	2.04	0.56
1:A:190:LEU:N	3:A:534:HOH:O	2.37	0.56
1:A:33:ASP:C	1:A:35:THR:H	2.08	0.56
1:A:244:LEU:HB3	3:A:542:HOH:O	2.05	0.56
1:A:268:VAL:HG13	1:A:272:HIS:CE1	2.40	0.56
1:A:164:GLY:HA3	3:A:510:HOH:O	2.06	0.56
1:A:247:PHE:CZ	1:A:318:LYS:HB2	2.41	0.55
1:A:444:GLU:OE1	1:A:444:GLU:HA	2.07	0.55
1:A:156:GLU:C	1:A:158:ASP:H	2.10	0.55
1:A:277:THR:O	1:A:281:SER:HB2	2.07	0.55
1:A:319:GLY:O	1:A:322:LEU:HB3	2.06	0.55
1:A:76:ASP:HB2	3:A:536:HOH:O	2.05	0.55
1:A:69:ARG:HB2	3:A:536:HOH:O	2.07	0.54
1:A:26:ALA:H	1:A:65:GLN:HE22	1.54	0.54
1:A:107:ILE:HG23	1:A:140:TRP:CZ3	2.42	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:107:ILE:HG22	1:A:144:ILE:HD11	1.90	0.54
1:A:363:ILE:HD11	1:A:392:PHE:CE2	2.42	0.54
1:A:314:PRO:HB3	1:A:349:GLU:HB3	1.90	0.54
1:A:340:PHE:O	1:A:344:ILE:HG12	2.07	0.54
1:A:130:TYR:O	1:A:133:ASP:HB2	2.07	0.54
1:A:270:ALA:O	1:A:274:ARG:HG3	2.07	0.54
1:A:276:ILE:HG22	1:A:295:ILE:HG23	1.88	0.54
1:A:261:GLU:OE2	1:A:308:LYS:NZ	2.39	0.54
1:A:36:LEU:HD23	3:A:508:HOH:O	2.08	0.53
1:A:67:CYS:O	1:A:89:PHE:HA	2.08	0.53
1:A:95:ASN:HD21	1:A:218:THR:CG2	2.22	0.53
1:A:97:SER:HB3	1:A:216:ILE:HB	1.90	0.53
1:A:166:VAL:CG2	1:A:166:VAL:O	2.55	0.53
1:A:296:ARG:HG3	1:A:300:ARG:NE	2.20	0.53
1:A:414:GLN:NE2	1:A:445:LEU:HB2	2.23	0.53
1:A:410:LEU:H	1:A:410:LEU:HD12	1.74	0.53
1:A:338:ARG:HH11	1:A:338:ARG:CB	2.22	0.52
1:A:135:GLU:O	1:A:139:ILE:HG13	2.09	0.52
1:A:69:ARG:HD3	3:A:504:HOH:O	2.08	0.52
1:A:143:HIS:HA	3:A:596:HOH:O	2.10	0.52
1:A:444:GLU:OE1	1:A:447:LYS:HG3	2.09	0.52
1:A:221:GLY:HA3	3:A:632:HOH:O	2.09	0.52
1:A:24:LYS:HG2	3:A:639:HOH:O	2.10	0.52
1:A:321:ASP:HA	3:A:615:HOH:O	2.09	0.52
1:A:21:THR:HG22	1:A:22:ARG:N	2.25	0.51
1:A:277:THR:HB	3:A:503:HOH:O	2.09	0.51
1:A:121:PRO:O	1:A:125:LEU:HD11	2.09	0.51
1:A:393:PRO:C	1:A:395:ASP:H	2.14	0.51
1:A:192:ILE:HD12	1:A:225:ILE:HD13	1.92	0.51
1:A:38:PHE:HZ	1:A:295:ILE:CD1	2.23	0.51
1:A:295:ILE:N	1:A:295:ILE:HD12	2.25	0.51
1:A:421:ARG:HH22	1:A:442:LEU:CG	2.24	0.51
1:A:209:THR:HG22	1:A:210:PRO:O	2.11	0.51
1:A:55:LYS:O	1:A:56:ARG:HD3	2.11	0.51
1:A:200:TYR:HE1	1:A:210:PRO:HG3	1.76	0.51
1:A:181:GLU:HG3	1:A:188:ARG:NH2	2.26	0.50
1:A:224:ARG:HA	1:A:235:ASN:HD21	1.75	0.50
1:A:304:ARG:CA	1:A:356:LEU:HD21	2.41	0.50
1:A:85:ARG:HD3	3:A:635:HOH:O	2.11	0.50
1:A:383:VAL:HG21	1:A:408:ILE:HB	1.93	0.50
1:A:95:ASN:HD21	1:A:218:THR:HG21	1.77	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:33:ASP:C	1:A:35:THR:N	2.64	0.50
1:A:200:TYR:HB3	1:A:208:LEU:HB3	1.94	0.49
1:A:161:TRP:CE3	1:A:196:VAL:HG11	2.48	0.49
1:A:183:TYR:C	1:A:184:GLU:CD	2.71	0.49
1:A:304:ARG:CD	1:A:396:LEU:HD11	2.43	0.49
1:A:20:HIS:HD2	1:A:95:ASN:HB2	1.77	0.49
1:A:37:LEU:HA	1:A:291:ARG:HH21	1.77	0.49
1:A:184:GLU:CA	1:A:188:ARG:HB2	2.40	0.49
1:A:330:PRO:HG2	1:A:331:TYR:H	1.78	0.49
1:A:62:THR:O	1:A:63:SER:HB3	2.13	0.49
1:A:122:LYS:HD2	1:A:123:GLU:OE1	2.13	0.48
1:A:96:PHE:CD1	1:A:217:ASP:HA	2.47	0.48
1:A:16:GLU:C	1:A:18:LYS:H	2.16	0.48
1:A:200:TYR:HB2	1:A:208:LEU:HD23	1.93	0.48
1:A:280:ILE:HB	1:A:341:VAL:HG13	1.95	0.48
1:A:278:PHE:CE1	1:A:334:LEU:HD11	2.48	0.48
1:A:352:PHE:O	1:A:352:PHE:CG	2.67	0.48
1:A:295:ILE:H	1:A:295:ILE:HD12	1.77	0.48
1:A:140:TRP:O	1:A:144:ILE:HB	2.14	0.48
1:A:438:VAL:HG11	1:A:452:VAL:HG21	1.95	0.48
1:A:132:ASP:HB3	3:A:567:HOH:O	2.13	0.47
1:A:168:PRO:HB2	1:A:198:MET:CE	2.43	0.47
1:A:223:GLU:H	1:A:223:GLU:CD	2.16	0.47
1:A:102:PHE:CE1	1:A:214:PRO:HB2	2.49	0.47
1:A:20:HIS:N	1:A:20:HIS:ND1	2.61	0.47
1:A:223:GLU:OE1	1:A:223:GLU:N	2.42	0.47
1:A:30:PRO:HG2	3:A:508:HOH:O	2.14	0.47
1:A:367:ILE:HG21	1:A:404:LYS:HG3	1.96	0.47
1:A:394:VAL:O	1:A:394:VAL:HG12	2.14	0.47
1:A:300:ARG:HA	1:A:303:MET:CE	2.44	0.47
1:A:130:TYR:HB3	1:A:133:ASP:HB2	1.96	0.47
1:A:252:SER:OG	1:A:253:GLY:N	2.48	0.47
1:A:127:VAL:O	1:A:151:ILE:HA	2.15	0.47
1:A:440:SER:OG	1:A:441:HIS:N	2.45	0.47
1:A:325:ASP:HA	1:A:328:LYS:CD	2.45	0.47
1:A:359:GLY:O	1:A:363:ILE:HG13	2.14	0.47
1:A:360:MET:O	1:A:364:GLN:HG2	2.16	0.46
1:A:72:GLY:N	1:A:75:ASN:HB2	2.30	0.46
1:A:329:GLU:N	1:A:330:PRO:HD2	2.31	0.46
1:A:411:GLU:O	1:A:414:GLN:HB3	2.16	0.46
1:A:118:LEU:O	1:A:119:LYS:HB2	2.16	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:421:ARG:CG	1:A:425:ARG:NH1	2.78	0.46
1:A:168:PRO:HB2	1:A:198:MET:HE3	1.97	0.46
1:A:83:THR:HB	3:A:549:HOH:O	2.16	0.46
1:A:199:GLN:NE2	1:A:200:TYR:CZ	2.84	0.46
1:A:284:VAL:HG11	1:A:295:ILE:HD13	1.96	0.46
1:A:190:LEU:C	3:A:534:HOH:O	2.54	0.46
1:A:50:PHE:HB3	1:A:198:MET:HE1	1.97	0.46
1:A:303:MET:CE	1:A:352:PHE:HD2	2.27	0.46
1:A:394:VAL:HG11	3:A:509:HOH:O	2.16	0.46
1:A:338:ARG:HH11	1:A:338:ARG:HB2	1.81	0.45
1:A:229:LEU:HD13	3:A:613:HOH:O	2.16	0.45
1:A:251:VAL:HG11	1:A:315:PHE:HB2	1.98	0.45
1:A:333:GLU:N	1:A:333:GLU:OE1	2.45	0.45
1:A:421:ARG:HG3	1:A:425:ARG:CZ	2.46	0.45
1:A:264:VAL:O	1:A:268:VAL:HG23	2.16	0.45
1:A:37:LEU:HD23	1:A:291:ARG:HH21	1.81	0.45
1:A:190:LEU:O	1:A:192:ILE:HG23	2.16	0.45
1:A:371:LEU:HD12	1:A:372:GLU:N	2.32	0.45
1:A:396:LEU:HA	3:A:590:HOH:O	2.15	0.45
1:A:201:ASN:HD22	1:A:201:ASN:C	2.20	0.45
1:A:311:ILE:HG21	1:A:315:PHE:CD2	2.51	0.45
1:A:48:ASN:HB2	1:A:54:GLU:HG3	1.98	0.45
1:A:380:GLY:HA3	1:A:413:PHE:N	2.31	0.45
1:A:337:SER:O	1:A:341:VAL:HG23	2.17	0.45
1:A:204:GLU:H	1:A:204:GLU:HG3	1.49	0.45
1:A:421:ARG:HH22	1:A:442:LEU:CD1	2.30	0.45
1:A:13:SER:O	1:A:17:LYS:HG3	2.18	0.44
1:A:102:PHE:CG	1:A:103:LYS:N	2.85	0.44
1:A:192:ILE:CD1	1:A:225:ILE:HD13	2.47	0.44
1:A:442:LEU:O	1:A:442:LEU:HD22	2.17	0.44
1:A:124:LYS:HE3	3:A:622:HOH:O	2.16	0.44
1:A:148:SER:N	3:A:588:HOH:O	2.49	0.44
1:A:362:TYR:CE1	1:A:366:VAL:HG11	2.52	0.44
1:A:196:VAL:HB	1:A:217:ASP:O	2.17	0.44
1:A:161:TRP:CD2	1:A:196:VAL:HG11	2.52	0.44
1:A:242:PHE:HB3	1:A:243:PRO:HD3	2.00	0.44
1:A:260:PHE:O	1:A:263:ASP:N	2.51	0.44
1:A:290:GLY:O	1:A:294:VAL:HG23	2.18	0.44
1:A:240:ILE:O	1:A:326:ILE:HG21	2.18	0.44
1:A:394:VAL:HA	1:A:397:ILE:HD12	1.99	0.44
1:A:421:ARG:HH11	1:A:421:ARG:HB3	1.80	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:68:LEU:HD23	1:A:89:PHE:HA	1.99	0.44
1:A:107:ILE:HG23	1:A:140:TRP:CH2	2.53	0.43
1:A:174:GLU:HG2	1:A:194:ASN:HD22	1.83	0.43
1:A:38:PHE:HE2	1:A:294:VAL:HG11	1.81	0.43
1:A:329:GLU:HB2	1:A:330:PRO:HD3	2.00	0.43
1:A:421:ARG:NH1	1:A:421:ARG:HB3	2.33	0.43
1:A:156:GLU:C	1:A:158:ASP:N	2.72	0.43
1:A:224:ARG:CA	1:A:235:ASN:HD21	2.31	0.43
1:A:249:GLU:OE1	1:A:255:LYS:HA	2.17	0.43
1:A:341:VAL:O	1:A:345:VAL:HG23	2.17	0.43
1:A:371:LEU:HD12	1:A:371:LEU:C	2.37	0.43
1:A:42:GLY:HA2	3:A:532:HOH:O	2.18	0.43
1:A:235:ASN:O	1:A:238:ILE:HG12	2.18	0.43
1:A:241:ILE:O	1:A:244:LEU:HB2	2.19	0.43
1:A:401:ALA:HB1	1:A:406:LEU:O	2.18	0.43
1:A:202:ARG:HH22	1:A:208:LEU:HD11	1.82	0.43
1:A:269:ILE:HG23	3:A:646:HOH:O	2.18	0.43
1:A:296:ARG:HD3	1:A:300:ARG:NE	2.27	0.43
1:A:365:GLU:OE1	1:A:365:GLU:HA	2.17	0.43
1:A:77:LEU:HA	1:A:80:VAL:HG23	2.01	0.43
1:A:109:TYR:HE1	3:A:597:HOH:O	2.01	0.43
1:A:190:LEU:HD21	1:A:224:ARG:CG	2.49	0.43
1:A:190:LEU:HD21	1:A:224:ARG:HG2	2.00	0.43
1:A:66:LYS:HE2	1:A:331:TYR:CE1	2.54	0.43
1:A:400:ILE:HG13	1:A:400:ILE:H	1.68	0.43
1:A:269:ILE:HA	3:A:646:HOH:O	2.18	0.43
1:A:44:VAL:N	1:A:45:PRO:HD2	2.34	0.42
1:A:64:CYS:HA	1:A:92:MET:O	2.18	0.42
1:A:137:TYR:OH	1:A:148:SER:HB2	2.18	0.42
1:A:245:ILE:O	1:A:249:GLU:HG3	2.18	0.42
1:A:76:ASP:HB2	3:A:555:HOH:O	2.19	0.42
1:A:326:ILE:HG22	1:A:326:ILE:O	2.19	0.42
1:A:102:PHE:CE1	1:A:197:PHE:HB3	2.54	0.42
1:A:202:ARG:HH12	1:A:208:LEU:CD2	2.31	0.42
1:A:354:LYS:HA	1:A:357:LYS:HD2	2.00	0.42
1:A:30:PRO:HD2	1:A:37:LEU:O	2.19	0.42
1:A:363:ILE:O	1:A:367:ILE:HG13	2.19	0.42
1:A:416:GLU:O	1:A:420:GLN:HG2	2.19	0.42
1:A:97:SER:HB2	1:A:101:TYR:CZ	2.54	0.42
1:A:118:LEU:HA	3:A:544:HOH:O	2.18	0.42
1:A:190:LEU:HD11	1:A:224:ARG:CD	2.45	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:423:ARG:HG2	1:A:427:HIS:CG	2.54	0.42
1:A:191:GLU:OE1	1:A:194:ASN:HB2	2.20	0.42
1:A:5:HIS:CD2	1:A:330:PRO:HD3	2.54	0.42
1:A:15:PHE:HB3	1:A:20:HIS:CG	2.55	0.42
1:A:200:TYR:HD1	1:A:210:PRO:HA	1.85	0.42
1:A:447:LYS:HG2	1:A:447:LYS:H	1.62	0.42
1:A:49:VAL:HG21	1:A:56:ARG:NE	2.35	0.42
1:A:70:VAL:C	1:A:71:SER:OG	2.58	0.42
1:A:161:TRP:HA	3:A:547:HOH:O	2.20	0.41
1:A:8:ARG:HH21	1:A:91:GLU:CD	2.23	0.41
1:A:18:LYS:HD2	1:A:109:TYR:CE1	2.55	0.41
1:A:303:MET:HE3	1:A:352:PHE:CD2	2.52	0.41
1:A:384:PHE:CZ	1:A:420:GLN:HG3	2.55	0.41
1:A:45:PRO:HG3	3:A:532:HOH:O	2.20	0.41
1:A:127:VAL:HG23	1:A:151:ILE:HG23	2.02	0.41
1:A:92:MET:HE2	1:A:219:GLY:CA	2.47	0.41
1:A:95:ASN:N	1:A:95:ASN:HD22	2.18	0.41
1:A:137:TYR:O	1:A:141:ASN:HB3	2.20	0.41
1:A:126:TYR:O	1:A:176:TYR:HD2	2.04	0.41
1:A:304:ARG:NH1	1:A:400:ILE:HG12	2.36	0.41
1:A:28:LEU:O	1:A:30:PRO:HD3	2.21	0.41
1:A:113:PHE:HA	1:A:117:VAL:HB	2.02	0.41
1:A:48:ASN:CB	1:A:54:GLU:HG3	2.50	0.41
1:A:211:LEU:C	1:A:213:HIS:N	2.73	0.41
1:A:241:ILE:HA	1:A:244:LEU:HD12	2.02	0.41
1:A:85:ARG:HH22	1:A:179:ARG:NH1	2.18	0.41
1:A:156:GLU:HG2	1:A:160:PHE:CB	2.50	0.41
1:A:124:LYS:HB3	1:A:178:ASP:HB3	2.03	0.41
1:A:300:ARG:NH1	1:A:391:GLY:O	2.54	0.41
1:A:300:ARG:HA	1:A:303:MET:HE3	2.03	0.41
1:A:21:THR:O	1:A:62:THR:HG22	2.21	0.41
1:A:105:GLU:HB3	1:A:109:TYR:CE2	2.56	0.40
1:A:127:VAL:CG2	1:A:151:ILE:HG12	2.51	0.40
1:A:306:GLY:HA2	1:A:309:LEU:HD12	2.03	0.40
1:A:438:VAL:HG21	1:A:452:VAL:HG11	2.03	0.40
1:A:296:ARG:CD	1:A:300:ARG:NE	2.82	0.40
1:A:8:ARG:O	1:A:9:GLU:C	2.59	0.40
1:A:30:PRO:HB2	1:A:33:ASP:CB	2.48	0.40
1:A:118:LEU:N	3:A:566:HOH:O	2.52	0.40
1:A:438:VAL:CG1	1:A:452:VAL:HG11	2.48	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	444/465 (96%)	361 (81%)	70 (16%)	13 (3%)	4 6

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	338	ARG
1	A	443	LYS
1	A	131	LYS
1	A	2	LEU
1	A	37	LEU
1	A	132	ASP
1	A	198	MET
1	A	290	GLY
1	A	260	PHE
1	A	157	GLU
1	A	352	PHE
1	A	212	PRO
1	A	330	PRO

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	388/404 (96%)	360 (93%)	28 (7%)	14 26

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

Mol	Chain	Res	Type
1	A	20	HIS
1	A	35	THR
1	A	36	LEU
1	A	43	MET
1	A	56	ARG
1	A	74	HIS
1	A	92	MET
1	A	95	ASN
1	A	122	LYS
1	A	130	TYR
1	A	132	ASP
1	A	134	GLU
1	A	182	GLU
1	A	201	ASN
1	A	202	ARG
1	A	205	ASN
1	A	263	ASP
1	A	289	GLU
1	A	301	ARG
1	A	304	ARG
1	A	325	ASP
1	A	335	GLU
1	A	338	ARG
1	A	395	ASP
1	A	427	HIS
1	A	440	SER
1	A	441	HIS
1	A	442	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	5	HIS
1	A	65	GLN
1	A	86	HIS
1	A	95	ASN
1	A	162	GLN
1	A	201	ASN
1	A	235	ASN
1	A	272	HIS
1	A	414	GLN
1	A	420	GLN

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 ⓘ

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	SER	A	501	-	3,6,6	1.04	0	1,7,7	0.48	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	SER	A	501	-	-	0/2/6/6	-

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.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [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	448/465 (96%)	-0.76	3 (0%) 87 89	18, 22, 25, 27	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	352	PHE	2.7
1	A	300	ARG	2.6
1	A	184	GLU	2.5

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	SER	A	501	7/7	0.93	0.24	25,26,27,27	0

6.5 Other polymers

There are no such residues in this entry.