



Full wwPDB X-ray Structure Validation Report

Mar 1, 2014 – 03:17 AM GMT

PDB ID : 1G0D
Title : CRYSTAL STRUCTURE OF RED SEA BREAM TRANSGLUTAMINASE
Authors : Noguchi, K.; Ishikawa, K.; Yokoyama, K.; Ohtsuka, T.; Nio, N.; Suzuki, E.
Deposited on : 2000-10-06
Resolution : 2.50 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

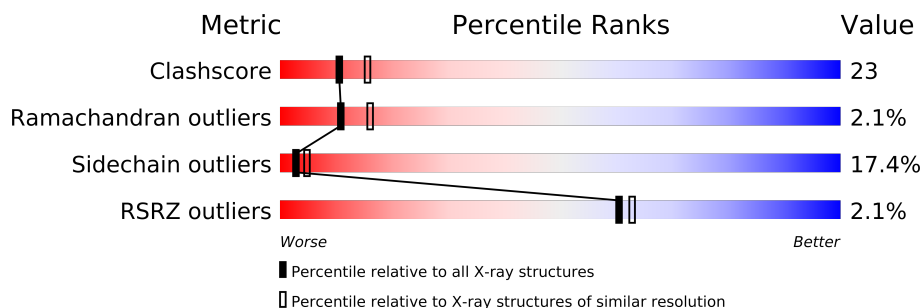
The following versions of software and data (see [references](#)) were used in the production of this report:

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

1 Overall quality at a glance

The reported resolution of this entry is 2.50 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	79885	3562 (2.50-2.50)
Ramachandran outliers	78287	3480 (2.50-2.50)
Sidechain outliers	78261	3482 (2.50-2.50)
RSRZ outliers	66119	2785 (2.50-2.50)

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

Mol	Chain	Length	Quality of chain
1	A	695	

2 Entry composition

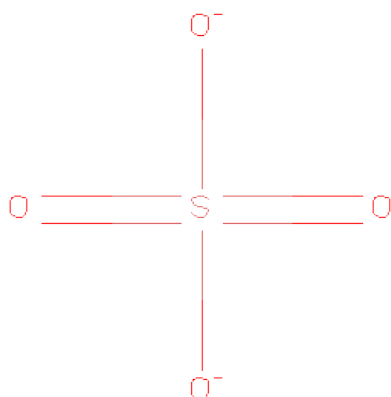
There are 3 unique types of molecules in this entry. The entry contains 5671 atoms, of which 0 are hydrogen and 0 are deuterium.

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

- Molecule 1 is a protein called PROTEIN-GLUTAMINE GAMMA-GLUTAMYLTRANSFERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	666	5283	3341	941	975	26	0	0	0

- Molecule 2 is SULFATE ION (three-letter code: SO₄) (formula: O₄S).



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

- Molecule 3 is water.

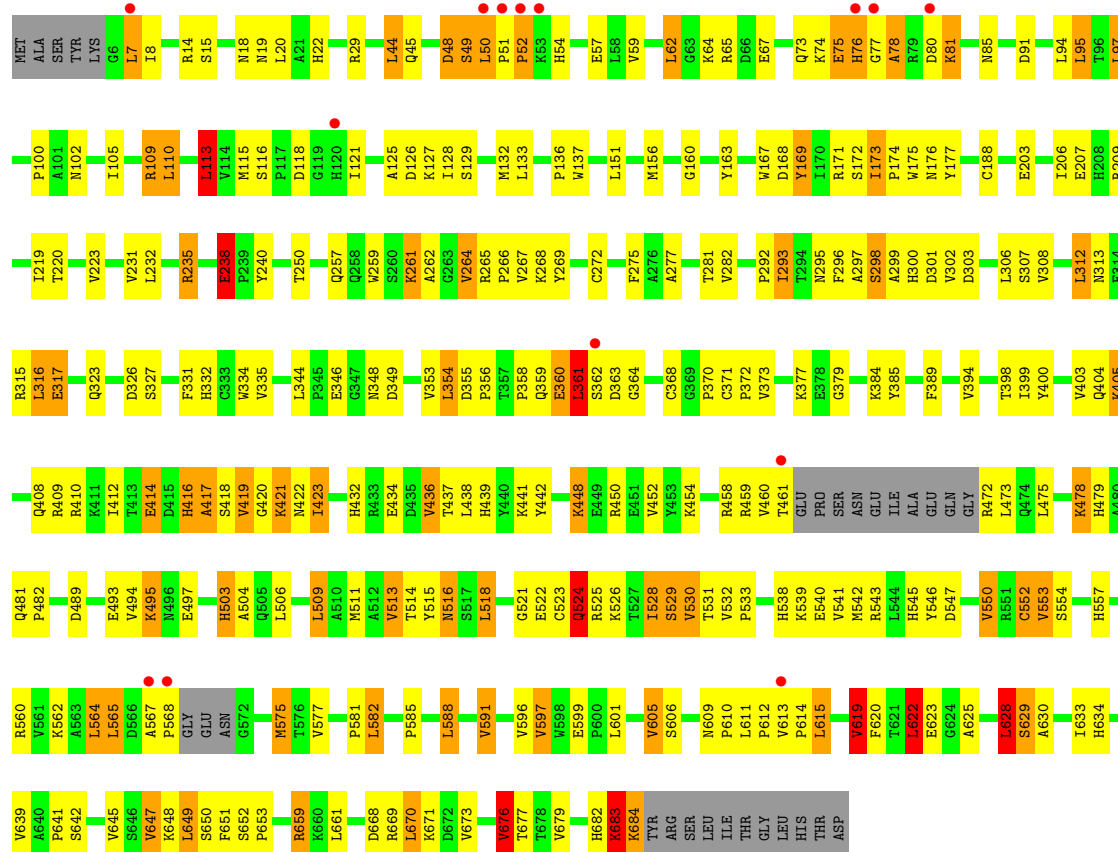
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	383	383	383	0	0

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: PROTEIN-GLUTAMINE GAMMA-GLUTAMYLTRANSFERASE

Chain A: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, α , β , γ	97.80Å 97.80Å 455.50Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	8.00 – 2.50 39.09 – 2.30	Depositor EDS
% Data completeness (in resolution range)	86.0 (8.00-2.50) 79.1 (39.09-2.30)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.45 (at 2.29Å)	Xtriage
Refinement program	X-PLOR 98.1	Depositor
R, R_{free}	0.200 , 0.249 0.196 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	27.7	Xtriage
Anisotropy	0.135	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 66.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 46507 reflections	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	5671	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.62% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SO4

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.72	0/5411	0.93	12/7351 (0.2%)

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

There are no bond length outliers.

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	509	LEU	CA-CB-CG	6.76	130.84	115.30
1	A	361	LEU	N-CA-C	6.63	128.89	111.00
1	A	619	VAL	CB-CA-C	-6.61	98.85	111.40
1	A	628	LEU	CA-CB-CG	6.49	130.22	115.30
1	A	238	GLU	N-CA-C	6.24	127.84	111.00
1	A	362	SER	N-CA-C	-6.15	94.40	111.00
1	A	622	LEU	CA-CB-CG	6.09	129.32	115.30
1	A	676	VAL	CB-CA-C	-6.01	99.98	111.40
1	A	113	LEU	CA-CB-CG	5.70	128.41	115.30
1	A	97	LEU	CA-CB-CG	5.44	127.80	115.30
1	A	95	LEU	CA-CB-CG	5.30	127.49	115.30
1	A	44	LEU	CA-CB-CG	5.26	127.39	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	163	TYR	Sidechain

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5283	0	5212	243	0
2	A	5	0	0	0	0
3	A	383	0	0	7	0
All	All	5671	0	5212	243	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 23.

All (243) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:684:LYS:HD2	1:A:684:LYS:H	1.21	1.03
1:A:316:LEU:HD21	1:A:564:LEU:HG	1.45	0.98
1:A:450:ARG:HG2	1:A:454:LYS:HE3	1.49	0.95
1:A:596:VAL:HG13	1:A:683:LYS:HG3	1.50	0.91
1:A:516:ASN:H	1:A:516:ASN:HD22	1.17	0.90
1:A:403:VAL:HG22	1:A:409:ARG:HG2	1.52	0.90
1:A:475:LEU:HD22	1:A:565:LEU:HB2	1.54	0.88
1:A:521:GLY:HA3	1:A:552:CYS:HB3	1.57	0.86
1:A:523:CYS:O	1:A:524:GLN:HB3	1.76	0.85
1:A:7:LEU:HD12	1:A:8:ILE:N	1.94	0.82
1:A:479:HIS:HD2	1:A:481:GLN:H	1.25	0.81
1:A:682:HIS:O	1:A:683:LYS:HB2	1.81	0.80
1:A:546:TYR:O	1:A:550:VAL:HG22	1.82	0.79
1:A:203:GLU:O	1:A:207:GLU:HG3	1.84	0.78
1:A:609:ASN:O	1:A:642:SER:HA	1.83	0.78
1:A:613:VAL:HG12	1:A:614:PRO:HD2	1.66	0.78
1:A:7:LEU:HD12	1:A:8:ILE:H	1.46	0.77
1:A:8:ILE:HD12	1:A:125:ALA:HB2	1.69	0.74
1:A:303:ASP:HB2	1:A:361:LEU:HD22	1.70	0.74
1:A:605:VAL:HG13	1:A:647:VAL:HG23	1.70	0.73

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:436:VAL:HG22	1:A:439:HIS:CD2	2.23	0.73
1:A:293:ILE:HD11	1:A:334:TRP:CZ2	2.24	0.72
1:A:137:TRP:HH2	1:A:156:MET:HE2	1.55	0.71
1:A:75:GLU:O	1:A:77:GLY:N	2.24	0.71
1:A:417:ALA:O	1:A:421:LYS:NZ	2.24	0.71
1:A:174:PRO:HG3	1:A:676:VAL:CG2	2.22	0.70
1:A:482:PRO:HG2	1:A:582:LEU:HD12	1.75	0.69
1:A:295:ASN:OD1	1:A:420:GLY:HA2	1.93	0.69
1:A:596:VAL:CG1	1:A:683:LYS:HG3	2.22	0.69
1:A:167:TRP:HB3	1:A:296:PHE:HB3	1.76	0.68
1:A:359:GLN:HG2	1:A:389:PHE:CD2	2.29	0.67
1:A:174:PRO:HG3	1:A:676:VAL:HG22	1.75	0.67
1:A:78:ALA:HB3	1:A:81:LYS:HB2	1.75	0.67
1:A:167:TRP:CZ3	1:A:168:ASP:HB3	2.31	0.66
1:A:312:LEU:HD22	1:A:400:TYR:HD2	1.59	0.66
1:A:538:HIS:NE2	1:A:540:GLU:HG2	2.10	0.66
1:A:670:LEU:HD13	1:A:673:VAL:HG21	1.77	0.65
1:A:15:SER:O	1:A:19:ASN:HB2	1.96	0.65
1:A:423:ILE:HG13	1:A:437:THR:HA	1.79	0.65
1:A:51:PRO:HB2	1:A:54:HIS:CD2	2.32	0.64
1:A:684:LYS:N	1:A:684:LYS:HD2	2.05	0.64
1:A:530:VAL:HG13	1:A:532:VAL:HG23	1.80	0.64
1:A:503:HIS:O	1:A:568:PRO:HG3	1.98	0.64
1:A:109:ARG:HB3	1:A:127:LYS:HE3	1.79	0.64
1:A:259:TRP:CZ2	1:A:264:VAL:HG13	2.34	0.63
1:A:302:VAL:HG22	1:A:308:VAL:HG21	1.80	0.62
1:A:659:ARG:HB3	3:A:895:HOH:O	1.98	0.62
1:A:301:ASP:HA	1:A:360:GLU:OE2	2.00	0.62
1:A:73:GLN:NE2	1:A:77:GLY:HA3	2.14	0.61
1:A:176:ASN:OD1	1:A:625:ALA:HB2	2.01	0.61
1:A:479:HIS:CD2	1:A:481:GLN:H	2.14	0.61
1:A:57:GLU:OE2	1:A:74:LYS:NZ	2.30	0.61
1:A:522:GLU:HG3	1:A:522:GLU:O	2.02	0.60
1:A:173:ILE:HG13	1:A:173:ILE:O	2.01	0.60
1:A:78:ALA:HB3	1:A:81:LYS:HG2	1.82	0.60
1:A:450:ARG:CG	1:A:454:LYS:HE3	2.30	0.59
1:A:209:ARG:HD2	3:A:716:HOH:O	2.00	0.59
1:A:115:MET:HG2	1:A:121:ILE:HA	1.84	0.59
1:A:460:VAL:O	1:A:460:VAL:HG13	2.02	0.59
1:A:75:GLU:O	1:A:76:HIS:C	2.40	0.59
1:A:299:ALA:HB2	1:A:419:VAL:HG11	1.83	0.59
1:A:51:PRO:O	1:A:54:HIS:HB2	2.01	0.59

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:591:VAL:HG11	1:A:679:VAL:HG21	1.84	0.59
1:A:238:GLU:HA	1:A:240:TYR:CE2	2.38	0.59
1:A:268:LYS:HD3	1:A:269:TYR:CE1	2.37	0.59
1:A:257:GLN:O	1:A:261:LYS:HB2	2.03	0.59
1:A:359:GLN:HG2	1:A:389:PHE:CE2	2.37	0.58
1:A:661:LEU:HB3	1:A:677:THR:HG22	1.83	0.58
1:A:516:ASN:N	1:A:516:ASN:HD22	1.94	0.58
1:A:546:TYR:CE1	1:A:550:VAL:HG13	2.38	0.58
1:A:633:ILE:HG21	1:A:647:VAL:HG11	1.85	0.58
1:A:8:ILE:CD1	1:A:125:ALA:HB2	2.34	0.58
1:A:450:ARG:O	1:A:454:LYS:HG3	2.04	0.57
1:A:137:TRP:HH2	1:A:156:MET:CE	2.18	0.57
1:A:531:THR:O	1:A:531:THR:HG23	2.04	0.57
1:A:326:ASP:HB3	1:A:560:ARG:NH2	2.20	0.56
1:A:523:CYS:O	1:A:524:GLN:CB	2.51	0.56
1:A:633:ILE:CG2	1:A:647:VAL:HG11	2.35	0.56
1:A:73:GLN:NE2	1:A:81:LYS:HB3	2.21	0.56
1:A:504:ALA:HB2	1:A:568:PRO:HD3	1.89	0.55
1:A:48:ASP:CG	1:A:49:SER:H	2.10	0.55
1:A:408:GLN:HG2	3:A:1033:HOH:O	2.06	0.55
1:A:73:GLN:HE22	1:A:77:GLY:HA3	1.72	0.55
1:A:220:THR:OG1	1:A:354:LEU:HG	2.07	0.55
1:A:355:ASP:HB3	1:A:368:CYS:HB2	1.89	0.54
1:A:353:VAL:HG23	1:A:373:VAL:HG22	1.88	0.54
1:A:315:ARG:O	1:A:316:LEU:HB2	2.06	0.54
1:A:633:ILE:HG21	1:A:647:VAL:CG1	2.37	0.54
1:A:622:LEU:HG	1:A:649:LEU:HD12	1.90	0.54
1:A:623:GLU:HA	1:A:628:LEU:HD12	1.88	0.54
1:A:521:GLY:CA	1:A:552:CYS:HB3	2.35	0.54
1:A:597:VAL:HG23	1:A:683:LYS:HB2	1.90	0.53
1:A:360:GLU:HB3	1:A:361:LEU:HD13	1.91	0.53
1:A:78:ALA:HB3	1:A:81:LYS:CB	2.37	0.53
1:A:504:ALA:HB2	1:A:568:PRO:CD	2.38	0.53
1:A:423:ILE:HG13	1:A:437:THR:HG23	1.90	0.53
1:A:360:GLU:C	1:A:361:LEU:HD13	2.28	0.52
1:A:412:ILE:HG21	1:A:575:MET:HE2	1.91	0.52
1:A:78:ALA:HB3	1:A:81:LYS:CG	2.38	0.52
1:A:297:ALA:O	1:A:419:VAL:HG12	2.09	0.52
1:A:513:VAL:HG13	1:A:514:THR:N	2.24	0.52
1:A:521:GLY:HA3	1:A:552:CYS:CB	2.35	0.52
1:A:50:LEU:HD13	1:A:54:HIS:O	2.10	0.52
1:A:438:LEU:HG	1:A:438:LEU:O	2.09	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:293:ILE:HG12	1:A:334:TRP:NE1	2.26	0.51
1:A:546:TYR:O	1:A:550:VAL:CG2	2.57	0.51
1:A:377:LYS:HE2	1:A:442:TYR:CD1	2.46	0.51
1:A:7:LEU:HD21	1:A:50:LEU:HD23	1.92	0.51
1:A:275:PHE:HB3	1:A:356:PRO:HB2	1.93	0.51
1:A:412:ILE:HG21	1:A:575:MET:HB2	1.92	0.51
1:A:303:ASP:CB	1:A:361:LEU:HD22	2.38	0.51
1:A:167:TRP:HD1	3:A:775:HOH:O	1.94	0.51
1:A:591:VAL:HG22	1:A:591:VAL:O	2.09	0.51
1:A:532:VAL:HG22	1:A:538:HIS:HB2	1.93	0.51
1:A:100:PRO:HB2	1:A:102:ASN:OD1	2.10	0.50
1:A:80:ASP:HB2	1:A:102:ASN:HD21	1.77	0.50
1:A:436:VAL:HG22	1:A:439:HIS:NE2	2.26	0.50
1:A:334:TRP:CD1	1:A:353:VAL:HG13	2.46	0.49
1:A:629:SER:O	1:A:630:ALA:C	2.50	0.49
1:A:349:ASP:HB2	3:A:862:HOH:O	2.12	0.49
1:A:7:LEU:HD12	1:A:8:ILE:HG13	1.94	0.49
1:A:588:LEU:O	1:A:605:VAL:HA	2.13	0.49
1:A:167:TRP:HB3	1:A:296:PHE:CB	2.42	0.49
1:A:623:GLU:HA	1:A:628:LEU:CD1	2.43	0.49
1:A:361:LEU:HD13	1:A:361:LEU:N	2.28	0.48
1:A:301:ASP:HA	1:A:360:GLU:CD	2.34	0.48
1:A:371:CYS:HB2	1:A:385:TYR:O	2.14	0.48
1:A:404:GLN:OE1	1:A:410:ARG:HD2	2.13	0.48
1:A:609:ASN:OD1	1:A:615:LEU:HD21	2.13	0.48
1:A:359:GLN:HE21	1:A:360:GLU:HB2	1.78	0.48
1:A:516:ASN:H	1:A:516:ASN:ND2	1.97	0.47
1:A:174:PRO:HG3	1:A:676:VAL:HG21	1.96	0.47
1:A:136:PRO:HB2	1:A:151:LEU:HD21	1.96	0.47
1:A:18:ASN:O	1:A:22:HIS:HD2	1.96	0.47
1:A:137:TRP:CH2	1:A:156:MET:CE	2.97	0.47
1:A:422:ASN:O	1:A:423:ILE:C	2.52	0.47
1:A:262:ALA:O	1:A:265:ARG:NH2	2.45	0.47
1:A:564:LEU:HD23	1:A:575:MET:HG3	1.97	0.47
1:A:442:TYR:CZ	1:A:448:LYS:HD3	2.49	0.47
1:A:585:PRO:HD3	1:A:610:PRO:HG3	1.97	0.47
1:A:80:ASP:HA	1:A:100:PRO:HB3	1.97	0.47
1:A:525:ARG:HG2	1:A:526:LYS:N	2.30	0.47
1:A:609:ASN:CG	1:A:615:LEU:HD21	2.35	0.46
1:A:238:GLU:O	1:A:240:TYR:N	2.49	0.46
1:A:51:PRO:HB2	1:A:54:HIS:CG	2.51	0.46
1:A:67:GLU:O	1:A:203:GLU:HG3	2.15	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:272:CYS:HG	1:A:515:TYR:HH	1.63	0.46
1:A:639:VAL:HG11	1:A:645:VAL:HG22	1.98	0.46
1:A:670:LEU:HA	1:A:670:LEU:HD23	1.84	0.46
1:A:65:ARG:HB2	1:A:65:ARG:NH2	2.31	0.46
1:A:611:LEU:C	1:A:613:VAL:H	2.20	0.45
1:A:567:ALA:HA	1:A:568:PRO:HD2	1.65	0.45
1:A:414:GLU:HG3	1:A:575:MET:HE3	1.98	0.45
1:A:74:LYS:O	1:A:75:GLU:HG2	2.17	0.45
1:A:313:ASN:OD1	1:A:317:GLU:HG3	2.16	0.45
1:A:489:ASP:HB3	1:A:541:VAL:HG13	1.98	0.45
1:A:295:ASN:HB2	1:A:334:TRP:CH2	2.51	0.45
1:A:78:ALA:CB	1:A:81:LYS:HG2	2.46	0.45
1:A:532:VAL:HA	1:A:533:PRO:HD3	1.62	0.45
1:A:532:VAL:HG22	1:A:538:HIS:CB	2.47	0.45
1:A:67:GLU:HB3	1:A:203:GLU:HA	1.98	0.45
1:A:528:ILE:HG23	1:A:529:SER:N	2.31	0.45
1:A:109:ARG:HG3	1:A:129:SER:HB3	1.97	0.45
1:A:293:ILE:HD11	1:A:334:TRP:CE2	2.51	0.45
1:A:268:LYS:HA	1:A:269:TYR:HA	1.78	0.45
1:A:612:PRO:C	1:A:641:PRO:HB3	2.37	0.45
1:A:412:ILE:CG2	1:A:575:MET:HB2	2.46	0.45
1:A:298:SER:OG	1:A:332:HIS:HB3	2.16	0.44
1:A:169:TYR:CD2	1:A:581:PRO:HD2	2.52	0.44
1:A:562:LYS:HG2	1:A:577:VAL:HG22	1.99	0.44
1:A:652:SER:O	1:A:653:PRO:C	2.56	0.44
1:A:601:LEU:HD11	1:A:651:PHE:CZ	2.52	0.44
1:A:115:MET:HE2	1:A:115:MET:HB2	1.57	0.44
1:A:620:PHE:CD2	1:A:647:VAL:HG21	2.53	0.43
1:A:295:ASN:O	1:A:331:PHE:HA	2.18	0.43
1:A:231:VAL:HA	1:A:259:TRP:CD1	2.53	0.43
1:A:543:ARG:HG2	1:A:545:HIS:CE1	2.53	0.43
1:A:511:MET:HG2	1:A:511:MET:O	2.17	0.43
1:A:684:LYS:CD	1:A:684:LYS:H	2.03	0.43
1:A:175:TRP:NE1	1:A:277:ALA:HB1	2.34	0.43
1:A:399:ILE:HD12	1:A:459:ARG:CZ	2.48	0.43
1:A:596:VAL:HG13	1:A:683:LYS:CG	2.35	0.43
1:A:73:GLN:HE22	1:A:77:GLY:CA	2.32	0.43
1:A:358:PRO:CB	1:A:364:GLY:HA2	2.48	0.43
1:A:495:LYS:HE2	1:A:495:LYS:HB2	1.65	0.43
1:A:51:PRO:HA	1:A:52:PRO:HD2	1.74	0.43
1:A:478:LYS:HE2	1:A:493:GLU:HB3	2.01	0.43
1:A:493:GLU:OE1	1:A:539:LYS:HE2	2.18	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:105:ILE:HB	1:A:132:MET:O	2.18	0.43
1:A:220:THR:HG1	1:A:354:LEU:HG	1.83	0.42
1:A:219:ILE:O	1:A:223:VAL:HG23	2.19	0.42
1:A:423:ILE:HG12	1:A:423:ILE:H	1.27	0.42
1:A:531:THR:CG2	1:A:531:THR:O	2.67	0.42
1:A:48:ASP:CG	1:A:49:SER:N	2.71	0.42
1:A:622:LEU:O	1:A:630:ALA:HA	2.18	0.42
1:A:62:LEU:HD13	1:A:206:ILE:CG2	2.50	0.42
1:A:384:LYS:HG2	3:A:823:HOH:O	2.18	0.42
1:A:553:VAL:HG13	1:A:557:HIS:HA	2.02	0.42
1:A:614:PRO:HA	1:A:639:VAL:O	2.19	0.42
1:A:73:GLN:NE2	1:A:77:GLY:CA	2.80	0.42
1:A:110:LEU:O	1:A:127:LYS:HA	2.19	0.42
1:A:354:LEU:HD13	1:A:370:PRO:HA	2.01	0.42
1:A:312:LEU:HA	1:A:317:GLU:O	2.20	0.42
1:A:65:ARG:HB2	1:A:65:ARG:CZ	2.50	0.42
1:A:250:THR:HG22	3:A:707:HOH:O	2.20	0.42
1:A:293:ILE:O	1:A:293:ILE:HG13	2.14	0.42
1:A:232:LEU:HD23	1:A:267:VAL:HB	2.01	0.42
1:A:668:ASP:OD2	1:A:669:ARG:N	2.52	0.42
1:A:265:ARG:O	1:A:266:PRO:C	2.58	0.42
1:A:405:LYS:HA	1:A:405:LYS:HD3	1.78	0.42
1:A:377:LYS:HE2	1:A:442:TYR:CE1	2.55	0.42
1:A:188:CYS:SG	1:A:282:VAL:HG13	2.59	0.42
1:A:348:ASN:HB3	1:A:372:PRO:CG	2.50	0.42
1:A:379:GLY:HA3	1:A:452:VAL:HG13	2.02	0.41
1:A:300:HIS:O	1:A:360:GLU:HG3	2.21	0.41
1:A:235:ARG:HG2	1:A:240:TYR:CD1	2.55	0.41
1:A:177:TYR:OH	1:A:292:PRO:HG2	2.21	0.41
1:A:384:LYS:HA	1:A:385:TYR:HA	1.70	0.41
1:A:91:ASP:N	1:A:91:ASP:OD1	2.50	0.41
1:A:619:VAL:HG13	1:A:634:HIS:CD2	2.55	0.41
1:A:128:ILE:O	1:A:128:ILE:HG13	2.20	0.41
1:A:238:GLU:HA	1:A:240:TYR:CZ	2.56	0.41
1:A:177:TYR:O	1:A:281:THR:OG1	2.32	0.41
1:A:67:GLU:HB2	1:A:206:ILE:HD12	2.03	0.41
1:A:15:SER:O	1:A:19:ASN:CB	2.66	0.41
1:A:475:LEU:HD13	1:A:494:VAL:HG22	2.02	0.41
1:A:116:SER:HB3	1:A:118:ASP:OD2	2.20	0.41
1:A:7:LEU:CD1	1:A:8:ILE:CG1	2.99	0.41
1:A:81:LYS:HD3	1:A:81:LYS:HA	1.72	0.41
1:A:50:LEU:HD23	1:A:50:LEU:HA	1.76	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:301:ASP:HA	1:A:360:GLU:HG3	2.02	0.41
1:A:57:GLU:HB3	1:A:113:LEU:HB2	2.01	0.41
1:A:312:LEU:CD2	1:A:400:TYR:HD2	2.29	0.41
1:A:54:HIS:CE1	1:A:116:SER:HA	2.56	0.41
1:A:514:THR:OG1	1:A:518:LEU:HB2	2.21	0.41
1:A:7:LEU:HD23	1:A:51:PRO:HD3	2.04	0.40
1:A:7:LEU:HD12	1:A:8:ILE:CG1	2.52	0.40
1:A:416:HIS:O	1:A:417:ALA:O	2.39	0.40
1:A:219:ILE:HA	1:A:219:ILE:HD13	1.90	0.40
1:A:7:LEU:CD1	1:A:8:ILE:HG12	2.52	0.40
1:A:303:ASP:CG	1:A:361:LEU:HB2	2.42	0.40
1:A:503:HIS:O	1:A:568:PRO:CG	2.69	0.40
1:A:160:GLY:HA3	1:A:177:TYR:CE2	2.56	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	660/695 (95%)	599 (91%)	47 (7%)	14 (2%)	11	16

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	52	PRO
1	A	76	HIS
1	A	78	ALA
1	A	416	HIS
1	A	417	ALA
1	A	418	SER
1	A	524	GLN
1	A	683	LYS
1	A	360	GLU
1	A	363	ASP

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Mol	Chain	Res	Type
1	A	75	GLU
1	A	48	ASP
1	A	238	GLU
1	A	264	VAL

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution. The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	580/604 (96%)	479 (83%)	101 (17%)	3 5

All (101) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	LEU
1	A	14	ARG
1	A	20	LEU
1	A	29	ARG
1	A	44	LEU
1	A	45	GLN
1	A	49	SER
1	A	50	LEU
1	A	59	VAL
1	A	62	LEU
1	A	64	LYS
1	A	81	LYS
1	A	85	ASN
1	A	94	LEU
1	A	95	LEU
1	A	97	LEU
1	A	109	ARG
1	A	110	LEU
1	A	113	LEU
1	A	126	ASP
1	A	133	LEU
1	A	169	TYR
1	A	171	ARG
1	A	172	SER

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Mol	Chain	Res	Type
1	A	173	ILE
1	A	235	ARG
1	A	261	LYS
1	A	293	ILE
1	A	298	SER
1	A	306	LEU
1	A	307	SER
1	A	312	LEU
1	A	316	LEU
1	A	317	GLU
1	A	323	GLN
1	A	327	SER
1	A	335	VAL
1	A	344	LEU
1	A	346	GLU
1	A	354	LEU
1	A	361	LEU
1	A	394	VAL
1	A	398	THR
1	A	405	LYS
1	A	414	GLU
1	A	419	VAL
1	A	421	LYS
1	A	423	ILE
1	A	432	HIS
1	A	434	GLU
1	A	436	VAL
1	A	441	LYS
1	A	448	LYS
1	A	458	ARG
1	A	461	THR
1	A	472	ARG
1	A	473	LEU
1	A	478	LYS
1	A	495	LYS
1	A	497	GLU
1	A	503	HIS
1	A	506	LEU
1	A	509	LEU
1	A	513	VAL
1	A	516	ASN
1	A	518	LEU

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Mol	Chain	Res	Type
1	A	524	GLN
1	A	528	ILE
1	A	529	SER
1	A	530	VAL
1	A	542	MET
1	A	547	ASP
1	A	550	VAL
1	A	552	CYS
1	A	553	VAL
1	A	554	SER
1	A	564	LEU
1	A	565	LEU
1	A	575	MET
1	A	582	LEU
1	A	588	LEU
1	A	591	VAL
1	A	597	VAL
1	A	599	GLU
1	A	605	VAL
1	A	606	SER
1	A	615	LEU
1	A	619	VAL
1	A	622	LEU
1	A	628	LEU
1	A	629	SER
1	A	647	VAL
1	A	648	LYS
1	A	649	LEU
1	A	650	SER
1	A	659	ARG
1	A	670	LEU
1	A	671	LYS
1	A	676	VAL
1	A	683	LYS
1	A	684	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	55	HIS
1	A	73	GLN
1	A	86	GLN

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Mol	Chain	Res	Type
1	A	300	HIS
1	A	359	GLN
1	A	408	GLN
1	A	479	HIS
1	A	516	ASN
1	A	556	HIS
1	A	557	HIS
1	A	590	GLN
1	A	632	GLN
1	A	634	HIS
1	A	636	ASN

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

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	SO4	A	696	-	4,4,4	1.91	2 (50%)	6,6,6	0.60	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	SO4	A	696	-	-	0/0/0/0	0/0/0/0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	696	SO4	O1-S	-2.50	1.38	1.47
2	A	696	SO4	O3-S	-2.23	1.39	1.47

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	666/695 (95%)	-0.49	14 (2%) 60 63	7, 25, 57, 88	0

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	567	ALA	5.0
1	A	568	PRO	4.0
1	A	76	HIS	3.9
1	A	52	PRO	3.4
1	A	53	LYS	3.3
1	A	51	PRO	2.7
1	A	77	GLY	2.6
1	A	50	LEU	2.5
1	A	613	VAL	2.5
1	A	80	ASP	2.4
1	A	120	HIS	2.4
1	A	461	THR	2.3
1	A	7	LEU	2.2
1	A	362	SER	2.0

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 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	RSR	LLDF	B-factors(Å ²)	Q<0.9
2	SO4	A	696	5/5	0.06	-2.08	34,37,41,45	0

6.5 Other polymers

There are no such residues in this entry.