



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 06:56 PM GMT

PDB ID : 4N7R
Title : Crystal structure of Arabidopsis glutamyl-tRNA reductase in complex with its binding protein
Authors : Zhao, A.; Fang, Y.; Lin, Y.; Gong, W.; Liu, L.
Deposited on : 2013-10-16
Resolution : 2.80 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
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

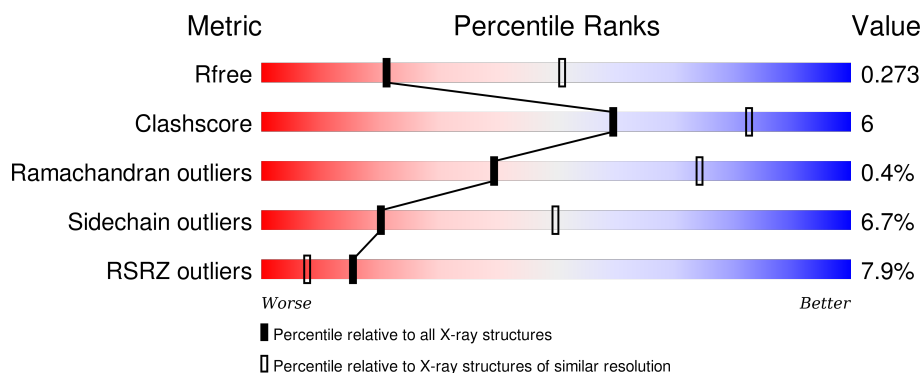
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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}	91344	2393 (2.80-2.80)
Clashscore	102246	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)
RSRZ outliers	91569	2404 (2.80-2.80)

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. 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	472	<div> <div>6%</div> <div> <div></div> <div>72%</div> <div>12%</div> <div>•</div> <div>14%</div> </div> </div>
1	B	472	<div> <div>13%</div> <div> <div></div> <div>68%</div> <div>13%</div> <div>•</div> <div>18%</div> </div> </div>
2	C	310	<div> <div>%</div> <div> <div></div> <div>62%</div> <div>18%</div> <div>•</div> <div>19%</div> </div> </div>
2	D	310	<div> <div>3%</div> <div> <div></div> <div>65%</div> <div>14%</div> <div>•</div> <div>19%</div> </div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 9918 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 Glutamyl-tRNA reductase 1, chloroplastic.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	405	Total	C	N	O	S	5	2	0
			3097	1939	558	576	24			
1	B	385	Total	C	N	O	S	1	0	0
			2844	1779	504	542	19			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	72	SER	-	EXPRESSION TAG	UNP P42804
B	72	SER	-	EXPRESSION TAG	UNP P42804

- Molecule 2 is a protein called Genomic DNA, chromosome 3, P1 clone: MXL8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	252	Total	C	N	O	S	0	0	0
			1957	1238	332	374	13			
2	D	251	Total	C	N	O	S	0	0	0
			1975	1249	336	377	13			

There are 68 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	8	MET	-	EXPRESSION TAG	UNP Q9LU39
C	9	GLY	-	EXPRESSION TAG	UNP Q9LU39
C	10	SER	-	EXPRESSION TAG	UNP Q9LU39
C	11	SER	-	EXPRESSION TAG	UNP Q9LU39
C	12	HIS	-	EXPRESSION TAG	UNP Q9LU39
C	13	HIS	-	EXPRESSION TAG	UNP Q9LU39
C	14	HIS	-	EXPRESSION TAG	UNP Q9LU39
C	15	HIS	-	EXPRESSION TAG	UNP Q9LU39
C	16	HIS	-	EXPRESSION TAG	UNP Q9LU39
C	17	HIS	-	EXPRESSION TAG	UNP Q9LU39

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Chain	Residue	Modelled	Actual	Comment	Reference
C	18	SER	-	EXPRESSION TAG	UNP Q9LU39
C	19	SER	-	EXPRESSION TAG	UNP Q9LU39
C	20	GLY	-	EXPRESSION TAG	UNP Q9LU39
C	21	LEU	-	EXPRESSION TAG	UNP Q9LU39
C	22	VAL	-	EXPRESSION TAG	UNP Q9LU39
C	23	PRO	-	EXPRESSION TAG	UNP Q9LU39
C	24	ARG	-	EXPRESSION TAG	UNP Q9LU39
C	25	GLY	-	EXPRESSION TAG	UNP Q9LU39
C	26	SER	-	EXPRESSION TAG	UNP Q9LU39
C	27	HIS	-	EXPRESSION TAG	UNP Q9LU39
C	28	MET	-	EXPRESSION TAG	UNP Q9LU39
C	29	ALA	-	EXPRESSION TAG	UNP Q9LU39
C	30	SER	-	EXPRESSION TAG	UNP Q9LU39
C	31	MET	-	EXPRESSION TAG	UNP Q9LU39
C	32	THR	-	EXPRESSION TAG	UNP Q9LU39
C	33	GLY	-	EXPRESSION TAG	UNP Q9LU39
C	34	GLY	-	EXPRESSION TAG	UNP Q9LU39
C	35	GLN	-	EXPRESSION TAG	UNP Q9LU39
C	36	GLN	-	EXPRESSION TAG	UNP Q9LU39
C	37	MET	-	EXPRESSION TAG	UNP Q9LU39
C	38	GLY	-	EXPRESSION TAG	UNP Q9LU39
C	39	ARG	-	EXPRESSION TAG	UNP Q9LU39
C	40	GLY	-	EXPRESSION TAG	UNP Q9LU39
C	41	SER	-	EXPRESSION TAG	UNP Q9LU39
D	8	MET	-	EXPRESSION TAG	UNP Q9LU39
D	9	GLY	-	EXPRESSION TAG	UNP Q9LU39
D	10	SER	-	EXPRESSION TAG	UNP Q9LU39
D	11	SER	-	EXPRESSION TAG	UNP Q9LU39
D	12	HIS	-	EXPRESSION TAG	UNP Q9LU39
D	13	HIS	-	EXPRESSION TAG	UNP Q9LU39
D	14	HIS	-	EXPRESSION TAG	UNP Q9LU39
D	15	HIS	-	EXPRESSION TAG	UNP Q9LU39
D	16	HIS	-	EXPRESSION TAG	UNP Q9LU39
D	17	HIS	-	EXPRESSION TAG	UNP Q9LU39
D	18	SER	-	EXPRESSION TAG	UNP Q9LU39
D	19	SER	-	EXPRESSION TAG	UNP Q9LU39
D	20	GLY	-	EXPRESSION TAG	UNP Q9LU39
D	21	LEU	-	EXPRESSION TAG	UNP Q9LU39
D	22	VAL	-	EXPRESSION TAG	UNP Q9LU39
D	23	PRO	-	EXPRESSION TAG	UNP Q9LU39
D	24	ARG	-	EXPRESSION TAG	UNP Q9LU39
D	25	GLY	-	EXPRESSION TAG	UNP Q9LU39

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Chain	Residue	Modelled	Actual	Comment	Reference
D	26	SER	-	EXPRESSION TAG	UNP Q9LU39
D	27	HIS	-	EXPRESSION TAG	UNP Q9LU39
D	28	MET	-	EXPRESSION TAG	UNP Q9LU39
D	29	ALA	-	EXPRESSION TAG	UNP Q9LU39
D	30	SER	-	EXPRESSION TAG	UNP Q9LU39
D	31	MET	-	EXPRESSION TAG	UNP Q9LU39
D	32	THR	-	EXPRESSION TAG	UNP Q9LU39
D	33	GLY	-	EXPRESSION TAG	UNP Q9LU39
D	34	GLY	-	EXPRESSION TAG	UNP Q9LU39
D	35	GLN	-	EXPRESSION TAG	UNP Q9LU39
D	36	GLN	-	EXPRESSION TAG	UNP Q9LU39
D	37	MET	-	EXPRESSION TAG	UNP Q9LU39
D	38	GLY	-	EXPRESSION TAG	UNP Q9LU39
D	39	ARG	-	EXPRESSION TAG	UNP Q9LU39
D	40	GLY	-	EXPRESSION TAG	UNP Q9LU39
D	41	SER	-	EXPRESSION TAG	UNP Q9LU39

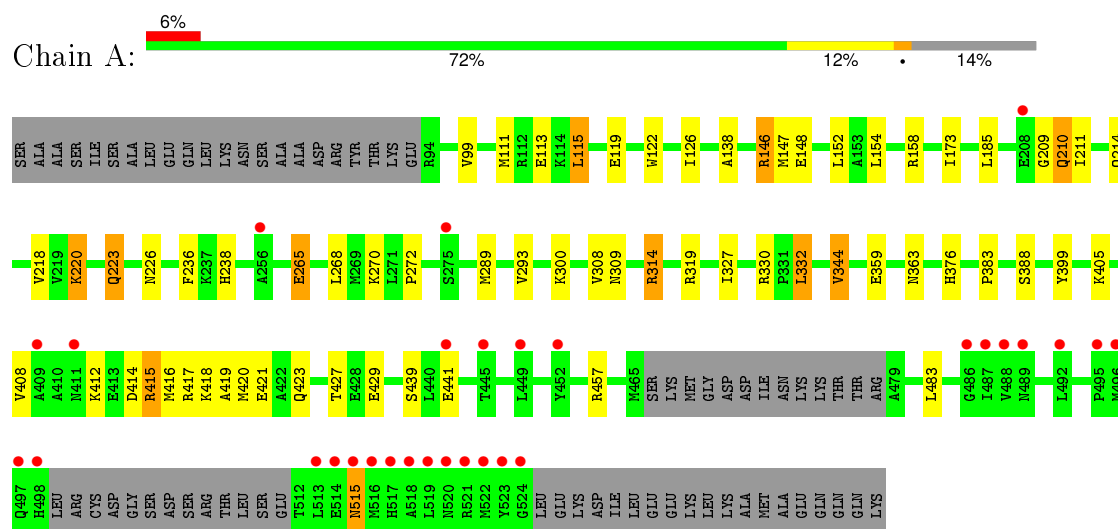
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	16	Total O 16 16	0	0
3	C	14	Total O 14 14	0	0
3	D	15	Total O 15 15	0	0

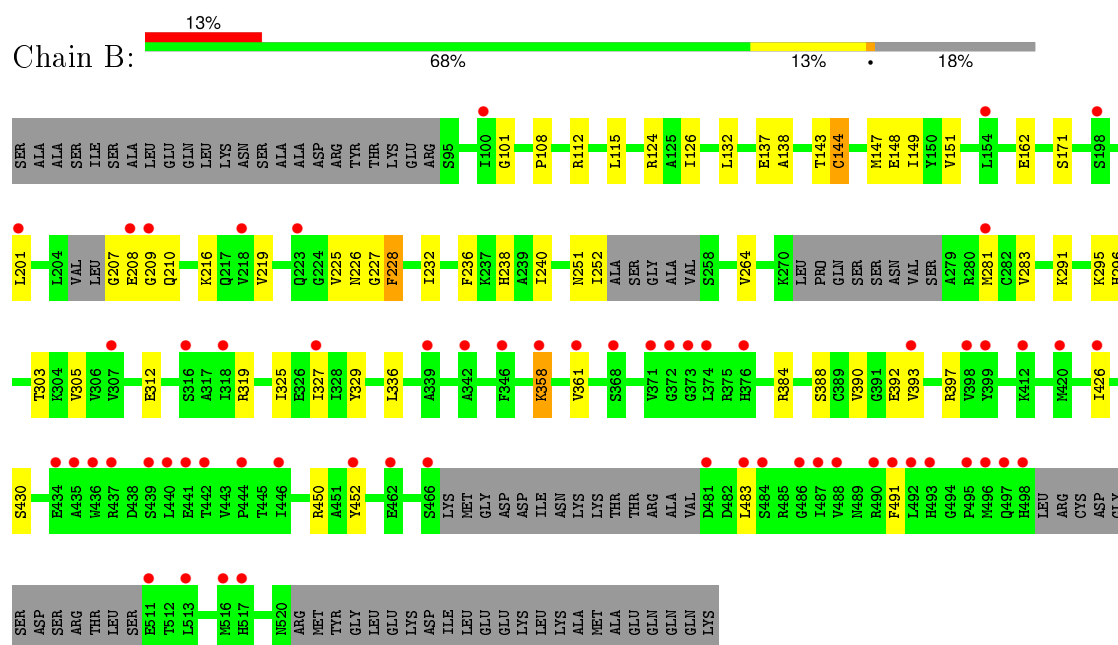
3 Residue-property plots

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.

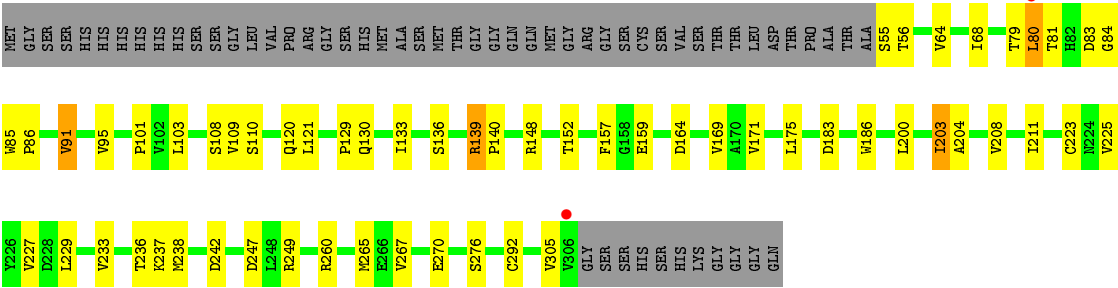
- Molecule 1: Glutamyl-tRNA reductase 1, chloroplastic



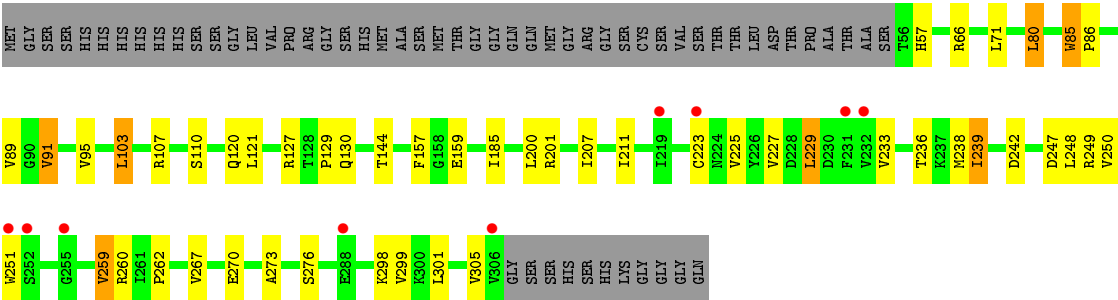
- Molecule 1: Glutamyl-tRNA reductase 1, chloroplastic



- Molecule 2: Genomic DNA, chromosome 3, P1 clone: MXL8



● Molecule 2: Genomic DNA, chromosome 3, P1 clone: MXL8



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	59.37Å 84.75Å 359.99Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.56 – 2.80 49.56 – 2.80	Depositor EDS
% Data completeness (in resolution range)	94.2 (49.56-2.80) 94.2 (49.56-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.71 (at 2.81Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.1_1168)	Depositor
R, R_{free}	0.212 , 0.270 0.213 , 0.273	Depositor DCC
R_{free} test set	2187 reflections (5.06%)	DCC
Wilson B-factor (Å ²)	67.3	Xtriage
Anisotropy	0.079	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 52.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 43253 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	9918	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 3.40% 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, 0.375 respectively for untwinned datasets, and 0.333, 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	0.30	0/3140	0.49	0/4240
1	B	0.23	0/2881	0.41	0/3900
2	C	0.34	0/2000	0.49	0/2718
2	D	0.30	0/2018	0.46	0/2738
All	All	0.29	0/10039	0.46	0/13596

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	3097	0	3133	31	0
1	B	2844	0	2763	29	0
2	C	1957	0	1886	31	0
2	D	1975	0	1930	26	0
3	A	16	0	0	1	0
3	C	14	0	0	2	0
3	D	15	0	0	0	0
All	All	9918	0	9712	112	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 6.

All (112) 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)
2:D:120:GLN:HG2	2:D:130:GLN:HG2	1.70	0.74
2:D:227:VAL:HG12	2:D:299:VAL:HB	1.69	0.72
2:C:120:GLN:HG2	2:C:130:GLN:HG2	1.74	0.70
2:C:83:ASP:O	2:C:85:TRP:N	2.24	0.70
2:C:211:ILE:HD12	2:C:238:MET:HE1	1.75	0.68
2:D:57:HIS:HB3	2:D:262:PRO:HB3	1.75	0.66
1:A:416:MET:O	1:A:420:MET:N	2.28	0.65
1:A:158:ARG:NH1	3:A:615:HOH:O	2.30	0.65
2:C:55:SER:N	2:C:56:THR:HA	2.12	0.64
2:D:242:ASP:OD1	2:D:260:ARG:NH2	2.29	0.64
1:B:207:GLY:HA2	1:B:210:GLN:HB3	1.80	0.64
2:D:236:THR:HG22	2:D:250:VAL:HA	1.80	0.64
2:C:183:ASP:O	2:D:107:ARG:NH2	2.32	0.62
1:B:137:GLU:HB2	1:B:232:ILE:HD13	1.85	0.59
1:A:210:GLN:O	1:A:214:GLN:N	2.34	0.59
1:B:303:THR:HA	1:B:325:ILE:HG13	1.85	0.58
2:C:242:ASP:OD1	2:C:260:ARG:NH2	2.34	0.57
1:B:264:VAL:HG21	1:B:296:HIS:HB3	1.86	0.57
1:B:225:VAL:HG12	1:B:227:GLY:H	1.70	0.56
2:D:248:LEU:HB2	2:D:259:VAL:HG23	1.88	0.55
1:A:265:GLU:OE1	1:A:300:LYS:NZ	2.34	0.54
1:A:483:LEU:HD23	1:B:483:LEU:HD23	1.89	0.54
2:C:139:ARG:HG3	2:C:140:PRO:HD2	1.89	0.54
2:D:71:LEU:HD11	2:D:201:ARG:HB2	1.89	0.54
1:B:251:ASN:N	1:B:252:ILE:HA	2.22	0.54
1:A:115:LEU:HB3	1:A:147:MET:HG2	1.89	0.54
2:C:101:PRO:HG2	2:C:169:VAL:HB	1.90	0.53
1:A:344:VAL:HB	1:A:376:HIS:HB2	1.91	0.53
2:C:249:ARG:NH1	2:C:305:VAL:HG11	2.23	0.53
2:C:133:ILE:HG23	2:C:171:VAL:HG13	1.92	0.52
1:B:281:MET:HB2	1:B:305:VAL:HG12	1.92	0.52
1:A:414:ASP:HA	1:A:417:ARG:HB3	1.91	0.52
2:D:223:CYS:SG	2:D:236:THR:HG21	2.50	0.51
2:C:242:ASP:CG	2:C:260:ARG:HH22	2.13	0.51
1:B:228:PHE:HE1	1:B:232:ILE:HG22	1.75	0.51
1:B:132:LEU:HD13	1:B:162:GLU:HB3	1.91	0.51
2:D:249:ARG:NH1	2:D:305:VAL:HG21	2.26	0.51
1:A:405:LYS:O	1:A:408:VAL:HG23	2.10	0.51
1:A:146[A]:ARG:HG2	1:A:148:GLU:HG3	1.92	0.51
2:C:56:THR:N	3:C:411:HOH:O	2.38	0.50
1:A:220:LYS:O	1:A:223:GLN:HB2	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:126:ILE:HG23	1:A:138:ALA:HB3	1.94	0.50
1:A:412:LYS:O	1:A:415:ARG:NH1	2.40	0.50
2:C:91:VAL:HG11	2:C:103:LEU:HD22	1.92	0.49
1:B:126:ILE:HG23	1:B:138:ALA:HB3	1.94	0.49
1:A:119:GLU:HA	1:A:122:TRP:CE2	2.48	0.48
1:B:115:LEU:HD13	1:B:171:SER:HB3	1.96	0.48
2:D:267:VAL:HG11	2:D:273:ALA:HB2	1.95	0.48
2:D:121:LEU:O	2:D:129:PRO:HD2	2.14	0.47
1:A:416:MET:HA	1:A:419:ALA:HB3	1.95	0.47
2:C:208:VAL:HA	2:C:238:MET:HE2	1.96	0.47
2:D:85:TRP:CD1	2:D:86:PRO:HD2	2.50	0.47
2:C:108:SER:O	2:C:110:SER:N	2.40	0.46
1:B:358:LYS:HE3	1:B:392:GLU:HB2	1.95	0.46
1:B:312:GLU:HG2	1:B:329:TYR:CZ	2.50	0.46
1:B:208:GLU:HA	1:B:209:GLY:HA2	1.58	0.45
2:C:86:PRO:HD3	2:D:80:LEU:HD22	1.97	0.45
1:A:119:GLU:HA	1:A:122:TRP:CD2	2.52	0.45
1:A:309:ASN:HD21	1:A:314:ARG:NH1	2.14	0.45
2:C:204:ALA:O	2:C:208:VAL:HG23	2.17	0.45
2:D:229:LEU:HD23	2:D:233:VAL:HG21	1.98	0.44
1:A:270:LYS:HG2	1:A:399:TYR:OH	2.17	0.44
1:A:218:VAL:HG11	1:A:236:PHE:CE1	2.53	0.44
2:D:157:PHE:O	2:D:159:GLU:HG3	2.16	0.44
1:B:143:THR:HG22	1:B:144:CYS:H	1.83	0.44
1:A:308:VAL:HG12	1:A:332:LEU:HD12	1.99	0.44
2:C:247:ASP:OD1	2:C:260:ARG:HD3	2.17	0.44
2:D:91:VAL:HG11	2:D:103:LEU:HD13	1.98	0.44
2:D:211:ILE:HD12	2:D:238:MET:HE1	2.00	0.44
1:B:291:LYS:HE2	1:B:295:LYS:HE3	2.00	0.44
1:B:101:GLY:HA3	1:B:148:GLU:HG2	1.99	0.43
1:A:289:MET:O	1:A:293:VAL:HG23	2.17	0.43
1:B:236:PHE:O	1:B:240:ILE:HG13	2.18	0.43
2:C:86:PRO:HB3	2:D:80:LEU:HD13	1.99	0.43
2:C:249:ARG:HH11	2:C:305:VAL:HG11	1.83	0.43
1:B:216:LYS:HA	1:B:219:VAL:HG22	2.01	0.43
2:D:239:ILE:HG12	2:D:247:ASP:O	2.19	0.42
1:B:108:PRO:O	1:B:112:ARG:HG3	2.19	0.42
1:B:361:VAL:HG11	1:B:390:VAL:HG13	2.00	0.42
2:D:247:ASP:OD1	2:D:260:ARG:HD3	2.18	0.42
1:A:115:LEU:HA	1:A:115:LEU:HD13	1.84	0.42
1:B:426:ILE:O	1:B:430:SER:OG	2.29	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:515:ASN:N	1:A:515:ASN:OD1	2.52	0.42
1:B:319:ARG:HA	1:B:327:ILE:HD13	2.00	0.42
2:C:148:ARG:O	2:C:152:THR:HG23	2.20	0.42
1:B:384:ARG:NH1	1:B:388:SER:HB2	2.35	0.42
1:B:390:VAL:O	1:B:393:VAL:HG22	2.20	0.42
2:C:223:CYS:HB3	2:C:233:VAL:HG21	2.01	0.42
2:D:200:LEU:HD11	2:D:267:VAL:HG12	2.02	0.42
1:A:111:MET:HG3	1:A:173:ILE:HD13	2.01	0.42
2:C:175:LEU:HB2	2:C:186:TRP:CZ3	2.55	0.41
1:A:308:VAL:HA	1:A:330:ARG:O	2.20	0.41
1:A:418:LYS:HA	1:A:421:GLU:HB2	2.02	0.41
2:C:203:ILE:HD12	2:C:270:GLU:HB2	2.02	0.41
2:D:249:ARG:HH11	2:D:305:VAL:HG21	1.86	0.41
1:B:216:LYS:HG2	1:B:240:ILE:HD13	2.01	0.41
2:C:237:LYS:HE2	2:C:237:LYS:HB3	1.95	0.41
2:C:85:TRP:CD1	2:C:86:PRO:HD2	2.56	0.41
2:C:121:LEU:O	2:C:129:PRO:HD2	2.21	0.41
1:A:209:GLY:O	1:A:211:ILE:N	2.54	0.41
1:A:113:GLU:HB2	1:A:383:PRO:HA	2.03	0.41
1:A:319:ARG:HA	1:A:327:ILE:HD12	2.01	0.41
1:B:149:ILE:HG22	1:B:151:VAL:HG13	2.03	0.41
1:B:228:PHE:CE1	1:B:232:ILE:HG22	2.55	0.40
2:D:249:ARG:HD2	2:D:251:TRP:CH2	2.56	0.40
1:A:99:VAL:CG1	1:A:185:LEU:HB2	2.51	0.40
2:C:80:LEU:HD21	2:D:80:LEU:HD21	2.03	0.40
2:C:64:VAL:O	2:C:68:ILE:HG13	2.22	0.40
1:A:423:GLN:O	1:A:427:THR:HG23	2.22	0.40
2:C:139:ARG:NH2	3:C:405:HOH:O	2.54	0.40
2:D:207:ILE:HD11	2:D:270:GLU:HG3	2.03	0.40
2:C:157:PHE:O	2:C:159:GLU:HG3	2.22	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	401/472 (85%)	379 (94%)	20 (5%)	2 (0%)	34	69
1	B	373/472 (79%)	352 (94%)	21 (6%)	0	100	100
2	C	250/310 (81%)	241 (96%)	7 (3%)	2 (1%)	24	58
2	D	249/310 (80%)	239 (96%)	9 (4%)	1 (0%)	39	74
All	All	1273/1564 (81%)	1211 (95%)	57 (4%)	5 (0%)	39	74

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	210	GLN
2	C	84	GLY
1	A	272	PRO
2	C	109	VAL
2	D	110	SER

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	332/400 (83%)	309 (93%)	23 (7%)	19	48
1	B	291/400 (73%)	277 (95%)	14 (5%)	31	66
2	C	214/269 (80%)	196 (92%)	18 (8%)	14	37
2	D	220/269 (82%)	203 (92%)	17 (8%)	16	41
All	All	1057/1338 (79%)	985 (93%)	72 (7%)	20	49

All (72) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	115	LEU
1	A	146[A]	ARG
1	A	146[B]	ARG

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Mol	Chain	Res	Type
1	A	152	LEU
1	A	154	LEU
1	A	220	LYS
1	A	223	GLN
1	A	226	ASN
1	A	238	HIS
1	A	265	GLU
1	A	268	LEU
1	A	314	ARG
1	A	332	LEU
1	A	344	VAL
1	A	359	GLU
1	A	363	ASN
1	A	388	SER
1	A	415	ARG
1	A	429	GLU
1	A	439	SER
1	A	441	GLU
1	A	457	ARG
1	A	515	ASN
2	C	79	THR
2	C	80	LEU
2	C	81	THR
2	C	91	VAL
2	C	95	VAL
2	C	136	SER
2	C	139	ARG
2	C	164	ASP
2	C	200	LEU
2	C	203	ILE
2	C	225	VAL
2	C	227	VAL
2	C	229	LEU
2	C	236	THR
2	C	265	MET
2	C	267	VAL
2	C	276	SER
2	C	292	CYS
1	B	124	ARG
1	B	144	CYS
1	B	147	MET
1	B	201	LEU

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Mol	Chain	Res	Type
1	B	226	ASN
1	B	228	PHE
1	B	238	HIS
1	B	283	VAL
1	B	336	LEU
1	B	358	LYS
1	B	397	ARG
1	B	450	ARG
1	B	452	TYR
1	B	491	PHE
2	D	66	ARG
2	D	80	LEU
2	D	85	TRP
2	D	89	VAL
2	D	91	VAL
2	D	95	VAL
2	D	103	LEU
2	D	127	ARG
2	D	144	THR
2	D	185	ILE
2	D	225	VAL
2	D	229	LEU
2	D	239	ILE
2	D	259	VAL
2	D	276	SER
2	D	298	LYS
2	D	301	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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	405/472 (85%)	0.33	30 (7%) 17 9	15, 36, 125, 133	7 (1%)
1	B	385/472 (81%)	0.74	61 (15%) 3 1	57, 97, 139, 155	4 (1%)
2	C	252/310 (81%)	-0.03	2 (0%) 87 81	14, 31, 69, 80	0
2	D	251/310 (80%)	0.21	9 (3%) 46 34	17, 48, 99, 116	0
All	All	1293/1564 (82%)	0.36	102 (7%) 15 8	14, 55, 130, 155	11 (0%)

All (102) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	495	PRO	8.2
1	A	496	MET	7.5
1	A	523	TYR	6.3
1	B	491	PHE	6.3
1	B	496	MET	5.7
1	B	483	LEU	5.6
1	A	489	ASN	5.2
1	B	281	MET	5.2
1	A	492	LEU	5.1
1	A	517	HIS	5.0
1	B	484	SER	4.9
1	B	201	LEU	4.9
1	A	488	VAL	4.6
1	B	435	ALA	4.5
1	A	515	ASN	4.3
1	A	524	GLY	4.2
1	A	497	GLN	4.1
1	B	498	HIS	4.1
1	B	376	HIS	4.0
1	A	449	LEU	4.0
2	D	223	CYS	3.9

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Mol	Chain	Res	Type	RSRZ
1	B	426	ILE	3.9
1	B	516	MET	3.9
1	B	318	ILE	3.8
1	B	511	GLU	3.8
1	B	513	LEU	3.7
1	B	517	HIS	3.7
1	B	487	ILE	3.7
1	B	441	GLU	3.6
1	A	522	MET	3.6
1	B	307	VAL	3.6
1	B	327	ILE	3.6
1	B	495	PRO	3.6
1	A	521	ARG	3.6
1	B	452	TYR	3.6
1	B	442	THR	3.3
2	C	306	VAL	3.3
1	B	373	GLY	3.3
1	A	498	HIS	3.2
1	B	492	LEU	3.2
1	B	374	LEU	3.1
1	B	493	HIS	3.1
1	A	519	LEU	3.0
1	B	488	VAL	3.0
1	A	275	SER	3.0
1	A	452	TYR	3.0
1	B	371	VAL	2.9
1	A	518	ALA	2.9
1	B	497	GLN	2.9
1	B	154	LEU	2.8
1	B	198	SER	2.8
1	B	439	SER	2.8
1	B	440	LEU	2.8
1	B	346	PHE	2.8
2	D	231	PHE	2.8
1	B	462	GLU	2.8
1	A	409	ALA	2.7
1	A	411	ASN	2.7
2	D	255	GLY	2.7
1	B	490	ARG	2.7
1	B	316	SER	2.6
1	A	520	ASN	2.6
1	B	100	ILE	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	516	MET	2.6
1	A	441	GLU	2.6
1	B	342	ALA	2.6
1	B	399	TYR	2.5
1	B	209	GLY	2.5
1	A	256	ALA	2.5
1	B	436	TRP	2.5
1	B	486	GLY	2.5
1	B	481	ASP	2.4
1	A	487	ILE	2.4
1	A	514	GLU	2.4
1	B	358	LYS	2.4
2	D	252	SER	2.3
1	B	420	MET	2.3
2	C	80	LEU	2.3
2	D	251	TRP	2.3
1	B	368	SER	2.3
1	B	466	SER	2.3
1	B	398	VAL	2.3
1	B	208	GLU	2.2
1	A	208	GLU	2.2
1	B	223	GLN	2.2
2	D	288	GLU	2.2
1	A	486	GLY	2.2
1	B	393	VAL	2.2
1	B	412	LYS	2.2
1	B	434	GLU	2.2
1	A	513	LEU	2.2
2	D	232	VAL	2.2
1	B	361	VAL	2.1
1	B	437	ARG	2.1
1	B	446	ILE	2.1
2	D	306	VAL	2.1
1	A	445	THR	2.1
1	B	339	ALA	2.1
1	B	372	GLY	2.1
2	D	219	ILE	2.1
1	B	218	VAL	2.0
1	B	444	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 carbohydrates in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.