



Full wwPDB X-ray Structure Validation Report ⓘ

Dec 22, 2020 – 12:04 AM EST

PDB ID : 7L3O
Title : Crystal Structure of the RNA binding domain of Threonyl-tRNA synthetase from *Cryptosporidium parvum* Iowa II
Authors : Seattle Structural Genomics Center for Infectious Disease (SSGCID)
Deposited on : 2020-12-18
Resolution : 2.10 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
Xtriage (Phenix)	:	1.13
EDS	:	2.16
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)	:	2.16

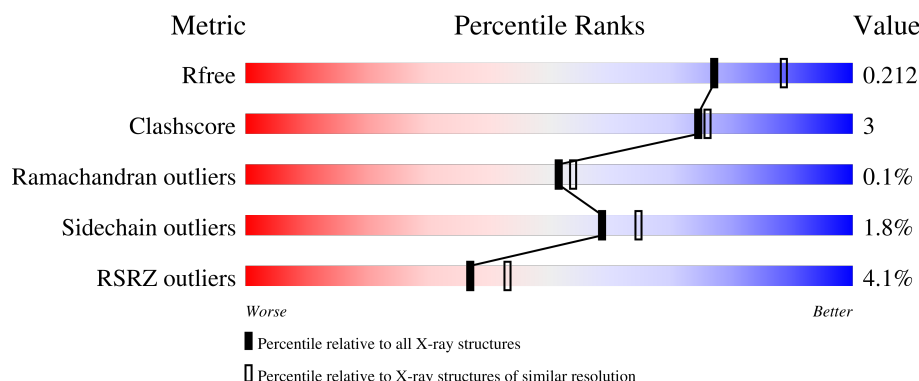
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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	442	<div> <div>4%</div> <div> <div></div> <div>83%</div> <div>8%</div> <div>10%</div> </div> </div>
1	B	442	<div> <div>4%</div> <div> <div></div> <div>82%</div> <div>8%</div> <div>9%</div> </div> </div>
1	C	442	<div> <div>4%</div> <div> <div></div> <div>79%</div> <div>11%</div> <div>9%</div> </div> </div>
1	D	442	<div> <div>3%</div> <div> <div></div> <div>83%</div> <div>7%</div> <div>10%</div> </div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 13845 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 Threonyl-tRNA synthetase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	400	Total	C	N	O	S	0	3	0
			3238	2082	555	582	19			
1	B	401	Total	C	N	O	S	0	5	0
			3255	2096	560	580	19			
1	C	401	Total	C	N	O	S	0	3	0
			3208	2064	552	572	20			
1	D	400	Total	C	N	O	S	0	3	0
			3183	2048	546	569	20			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	322	MET	-	initiating methionine	UNP Q5CYN0
A	323	ALA	-	expression tag	UNP Q5CYN0
A	324	HIS	-	expression tag	UNP Q5CYN0
A	325	HIS	-	expression tag	UNP Q5CYN0
A	326	HIS	-	expression tag	UNP Q5CYN0
A	327	HIS	-	expression tag	UNP Q5CYN0
A	328	HIS	-	expression tag	UNP Q5CYN0
A	329	HIS	-	expression tag	UNP Q5CYN0
B	322	MET	-	initiating methionine	UNP Q5CYN0
B	323	ALA	-	expression tag	UNP Q5CYN0
B	324	HIS	-	expression tag	UNP Q5CYN0
B	325	HIS	-	expression tag	UNP Q5CYN0
B	326	HIS	-	expression tag	UNP Q5CYN0
B	327	HIS	-	expression tag	UNP Q5CYN0
B	328	HIS	-	expression tag	UNP Q5CYN0
B	329	HIS	-	expression tag	UNP Q5CYN0
C	322	MET	-	initiating methionine	UNP Q5CYN0
C	323	ALA	-	expression tag	UNP Q5CYN0
C	324	HIS	-	expression tag	UNP Q5CYN0
C	325	HIS	-	expression tag	UNP Q5CYN0
C	326	HIS	-	expression tag	UNP Q5CYN0

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Chain	Residue	Modelled	Actual	Comment	Reference
C	327	HIS	-	expression tag	UNP Q5CYN0
C	328	HIS	-	expression tag	UNP Q5CYN0
C	329	HIS	-	expression tag	UNP Q5CYN0
D	322	MET	-	initiating methionine	UNP Q5CYN0
D	323	ALA	-	expression tag	UNP Q5CYN0
D	324	HIS	-	expression tag	UNP Q5CYN0
D	325	HIS	-	expression tag	UNP Q5CYN0
D	326	HIS	-	expression tag	UNP Q5CYN0
D	327	HIS	-	expression tag	UNP Q5CYN0
D	328	HIS	-	expression tag	UNP Q5CYN0
D	329	HIS	-	expression tag	UNP Q5CYN0

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total 1	Zn 1	0	0
2	A	1	Total 1	Zn 1	0	0
2	D	1	Total 1	Zn 1	0	0
2	C	1	Total 1	Zn 1	0	0

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total 1	Ca 1	0	0
3	A	1	Total 1	Ca 1	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	244	Total 246	O 246	0	2
4	B	273	Total 282	O 282	0	9
4	C	224	Total 227	O 227	0	3

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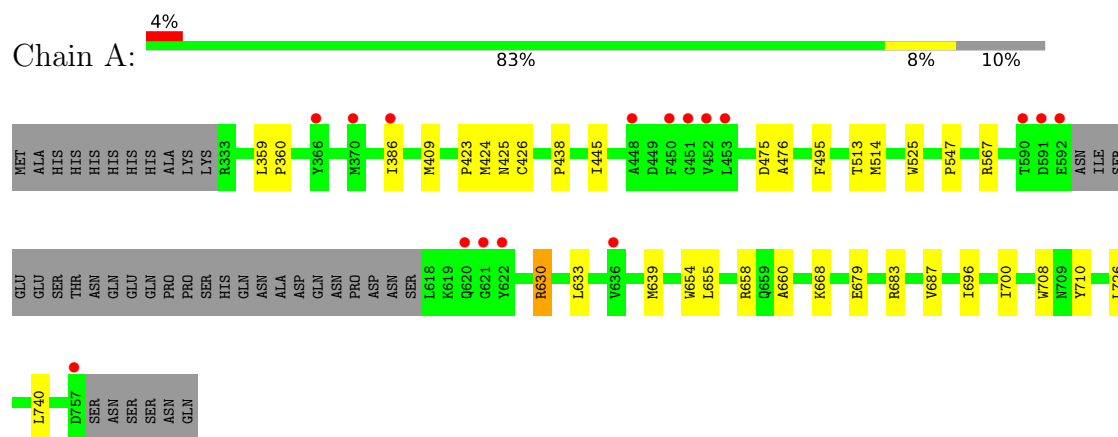
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	D	198	Total 200	O 200	0	3

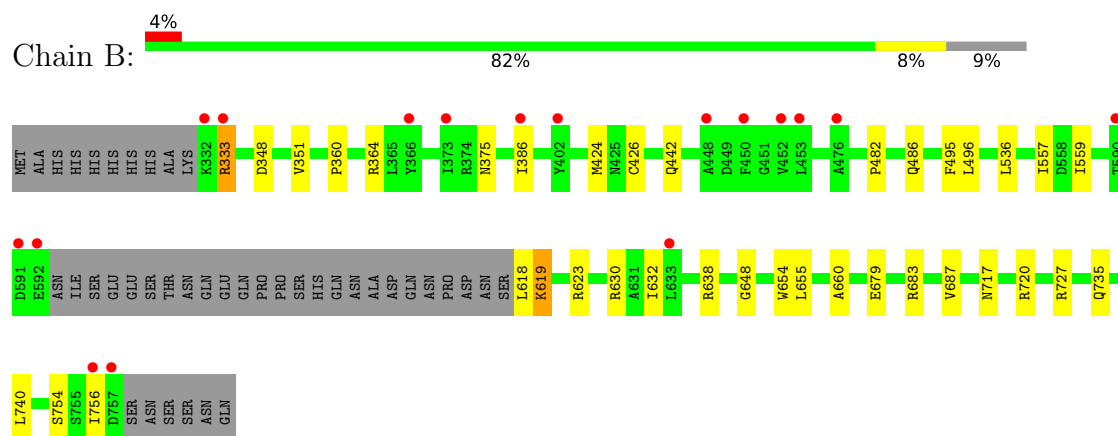
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

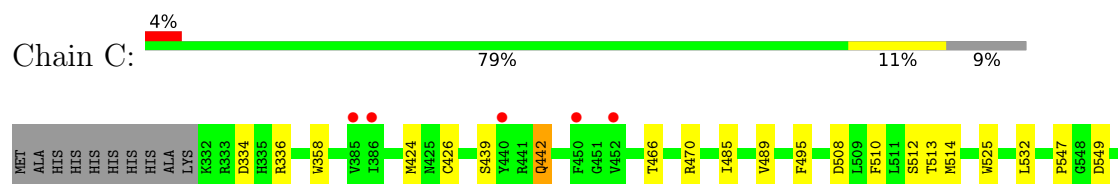
- Molecule 1: Threonyl-tRNA synthetase

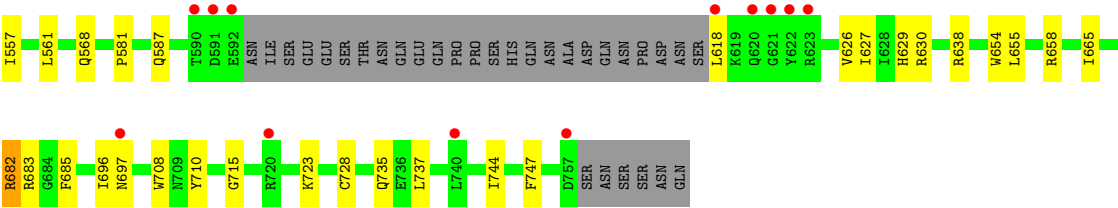


- Molecule 1: Threonyl-tRNA synthetase

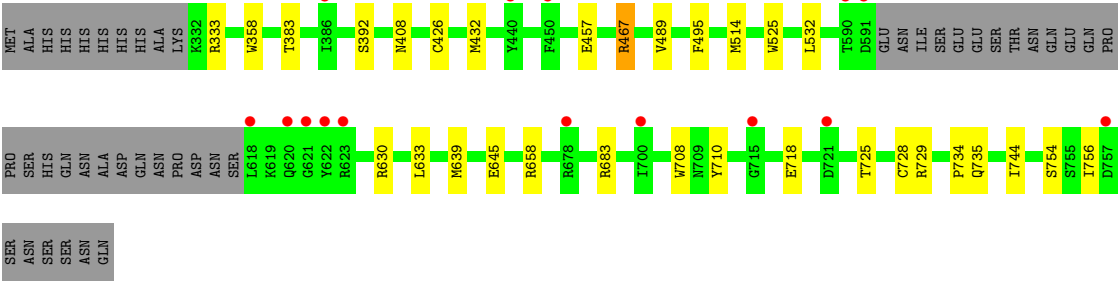
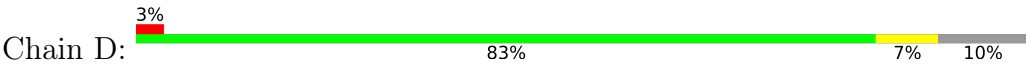


- Molecule 1: Threonyl-tRNA synthetase





● Molecule 1: Threonyl-tRNA synthetase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	65.73Å 67.45Å 143.18Å 91.58° 97.53° 120.78°	Depositor
Resolution (Å)	47.26 – 2.10 47.80 – 2.10	Depositor EDS
% Data completeness (in resolution range)	95.8 (47.26-2.10) 95.8 (47.80-2.10)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.75 (at 2.10Å)	Xtriage
Refinement program	PHENIX 1.19rc4-4035	Depositor
R, R_{free}	0.178 , 0.213 0.179 , 0.212	Depositor DCC
R_{free} test set	1978 reflections (1.70%)	wwPDB-VP
Wilson B-factor (Å ²)	33.3	Xtriage
Anisotropy	0.210	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 45.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.088 for -h-k,k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	13845	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.08% 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](#)

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

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	0.37	0/3328	0.59	0/4499
1	B	0.39	0/3351	0.59	0/4530
1	C	0.37	0/3298	0.59	0/4467
1	D	0.35	0/3272	0.57	0/4434
All	All	0.37	0/13249	0.59	0/17930

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	3238	0	3152	24	0
1	B	3255	0	3187	21	0
1	C	3208	0	3091	24	0
1	D	3183	0	3059	16	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	1	0	0	0	0
4	A	246	0	0	2	0
4	B	282	0	0	3	0
4	C	227	0	0	1	0
4	D	200	0	0	2	0
All	All	13845	0	12489	80	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 3.

All (80) 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:B:638[A]:ARG:NH2	4:B:903:HOH:O	2.24	0.70
1:B:727:ARG:HH11	1:B:735:GLN:HE21	1.44	0.66
1:C:508:ASP:OD2	4:C:901:HOH:O	2.16	0.63
1:D:633:LEU:HD22	1:D:639:MET:HG2	1.81	0.61
1:B:375:ASN:ND2	4:B:905:HOH:O	2.30	0.58
1:B:679:GLU:HG2	1:B:740:LEU:HD21	1.85	0.58
1:B:496[B]:LEU:HD21	1:B:559:ILE:HG21	1.86	0.56
1:B:496[A]:LEU:HD23	1:B:632:ILE:HG23	1.88	0.56
1:D:333:ARG:O	1:D:645:GLU:HG2	2.05	0.56
1:C:654:TRP:CZ3	1:C:655:LEU:HG	2.42	0.55
1:D:710:TYR:HE1	1:D:728[B]:CYS:HG	1.56	0.54
1:D:457:GLU:OE2	1:D:467:ARG:NH1	2.42	0.53
1:A:633:LEU:HD22	1:A:639:MET:HG2	1.90	0.53
1:B:717:ASN:OD1	1:B:720:ARG:NH2	2.42	0.52
1:D:734:PRO:O	4:D:901:HOH:O	2.18	0.52
1:B:482:PRO:HG2	1:B:623:ARG:NH2	2.24	0.52
1:B:754:SER:OG	1:B:756:ILE:HG12	2.10	0.51
1:B:727:ARG:NH1	1:B:735:GLN:HE21	2.08	0.51
1:A:668:LYS:NZ	4:A:912:HOH:O	2.45	0.50
1:C:587:GLN:NE2	1:C:618:LEU:HA	2.27	0.50
1:A:423:PRO:HG2	1:A:424:MET:HE3	1.93	0.50
1:A:409:MET:HG2	1:A:423:PRO:HG3	1.92	0.50
1:A:654:TRP:CZ3	1:A:655:LEU:HG	2.48	0.49
1:C:439:SER:H	1:C:442:GLN:NE2	2.10	0.48
1:C:485:ILE:HD11	1:C:626:VAL:HG21	1.94	0.48
1:C:581:PRO:HG3	1:C:627:ILE:HG13	1.94	0.48
1:A:386:ILE:HB	1:D:358:TRP:HB2	1.94	0.48
1:C:658:ARG:HB3	1:C:708:TRP:CE3	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:696:ILE:HG23	1:C:697:ASN:HD22	1.78	0.48
1:B:333:ARG:HG2	1:B:648:GLY:HA2	1.95	0.47
1:B:486[A]:GLN:HG3	4:B:1081:HOH:O	2.14	0.47
1:D:754:SER:OG	1:D:756:ILE:HG12	2.15	0.47
1:D:718:GLU:OE2	1:D:725:THR:OG1	2.21	0.46
1:C:723:LYS:HD3	1:C:737:LEU:HG	1.97	0.46
1:C:514:MET:HA	1:C:525:TRP:CZ3	2.51	0.46
1:A:567:ARG:HE	1:A:567:ARG:HB2	1.61	0.46
1:C:510:PHE:O	1:C:557:ILE:HA	2.15	0.46
1:D:683:ARG:HG3	1:D:744:ILE:HD13	1.97	0.46
1:D:408:ASN:ND2	4:D:912:HOH:O	2.49	0.45
1:A:476:ALA:HB3	1:A:630:ARG:CD	2.46	0.45
1:C:710:TYR:HE1	1:C:728[B]:CYS:HG	1.64	0.45
1:D:514:MET:HA	1:D:525:TRP:CZ3	2.52	0.45
1:A:679:GLU:HG2	1:A:740:LEU:HD21	2.00	0.44
1:D:708:TRP:O	1:D:729:ARG:HB2	2.17	0.44
1:C:665:ILE:HD12	1:C:715:GLY:HA3	2.00	0.44
1:A:683:ARG:HD2	4:A:903:HOH:O	2.18	0.44
1:A:359:LEU:HD23	1:D:432:MET:HE3	2.00	0.43
1:A:476:ALA:HB3	1:A:630:ARG:HD2	2.00	0.43
1:A:658:ARG:HB3	1:A:708:TRP:CE3	2.53	0.43
1:B:679:GLU:O	1:B:683:ARG:HG2	2.18	0.43
1:B:756:ILE:HD12	1:C:682:ARG:HB3	2.00	0.43
1:B:618:LEU:O	1:B:619:LYS:HB2	2.18	0.43
1:C:466:THR:O	1:C:638:ARG:NH2	2.52	0.43
1:C:513:THR:OG1	1:C:547:PRO:HA	2.19	0.42
1:A:423:PRO:HG2	1:A:424:MET:CE	2.49	0.42
1:D:489:VAL:HG11	1:D:532:LEU:HD23	2.01	0.42
1:C:561:LEU:O	1:C:568:GLN:HA	2.20	0.42
1:B:654:TRP:CZ3	1:B:655:LEU:HG	2.55	0.41
1:A:710:TYR:CD1	1:A:726:LEU:HD11	2.54	0.41
1:C:489:VAL:HG21	1:C:532:LEU:CD2	2.50	0.41
1:A:696:ILE:O	1:A:700:ILE:HG13	2.21	0.41
1:C:512:SER:HB3	1:C:549:ASP:C	2.41	0.41
1:B:536:LEU:HD21	1:B:557:ILE:HD13	2.02	0.41
1:A:425:ASN:HB2	1:A:475:ASP:OD2	2.21	0.41
1:A:514:MET:HG3	1:A:525:TRP:CD2	2.55	0.41
1:A:679:GLU:O	1:A:683:ARG:HG2	2.21	0.41
1:A:360:PRO:HB3	1:D:383:THR:HB	2.02	0.40
1:A:438:PRO:HG3	1:A:445:ILE:HD12	2.03	0.40
1:A:660:ALA:O	1:A:687:VAL:HA	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:348:ASP:CG	1:B:351:VAL:HG22	2.41	0.40
1:B:360:PRO:O	1:B:364:ARG:HG3	2.20	0.40
1:C:334:ASP:OD2	1:C:336:ARG:HB2	2.21	0.40
1:B:386:ILE:HB	1:C:358:TRP:HB2	2.02	0.40
1:D:658:ARG:HB3	1:D:708:TRP:CE3	2.56	0.40
1:B:660:ALA:O	1:B:687:VAL:HA	2.20	0.40
1:C:685:PHE:CE1	1:C:747:PHE:HB3	2.57	0.40
1:A:424:MET:SD	1:A:424:MET:N	2.94	0.40
1:C:683:ARG:HG3	1:C:744:ILE:HD13	2.03	0.40
1:A:513:THR:OG1	1:A:547:PRO:HA	2.21	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	399/442 (90%)	394 (99%)	5 (1%)	0	100	100
1	B	402/442 (91%)	397 (99%)	4 (1%)	1 (0%)	47	49
1	C	400/442 (90%)	398 (100%)	2 (0%)	0	100	100
1	D	399/442 (90%)	395 (99%)	4 (1%)	0	100	100
All	All	1600/1768 (90%)	1584 (99%)	15 (1%)	1 (0%)	51	54

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	619	LYS

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	345/395 (87%)	342 (99%)	3 (1%)	78	84
1	B	347/395 (88%)	341 (98%)	6 (2%)	60	67
1	C	336/395 (85%)	327 (97%)	9 (3%)	44	48
1	D	332/395 (84%)	326 (98%)	6 (2%)	59	65
All	All	1360/1580 (86%)	1336 (98%)	24 (2%)	59	65

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	426	CYS
1	A	495	PHE
1	A	630	ARG
1	B	333	ARG
1	B	424	MET
1	B	426	CYS
1	B	442	GLN
1	B	495	PHE
1	B	630	ARG
1	C	424	MET
1	C	426	CYS
1	C	442	GLN
1	C	470	ARG
1	C	495	PHE
1	C	629	HIS
1	C	630	ARG
1	C	682	ARG
1	C	735	GLN
1	D	392	SER
1	D	426	CYS
1	D	467	ARG
1	D	495	PHE
1	D	630	ARG
1	D	735	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	518	HIS
1	B	735	GLN
1	C	486	GLN
1	C	697	ASN
1	D	546	ASN
1	D	570	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 ⓘ

Of 6 ligands modelled in this entry, 6 are monoatomic - leaving 0 for Mogul analysis.

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 ⓘ

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	400/442 (90%)	0.12	16 (4%) 38 44	24, 39, 58, 99	0
1	B	401/442 (90%)	0.08	17 (4%) 36 42	22, 35, 56, 94	0
1	C	401/442 (90%)	0.11	17 (4%) 36 42	21, 40, 67, 87	0
1	D	400/442 (90%)	0.14	15 (3%) 40 46	23, 43, 69, 94	0
All	All	1602/1768 (90%)	0.12	65 (4%) 37 43	21, 39, 65, 99	0

All (65) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	622	TYR	6.0
1	C	591	ASP	5.7
1	D	621	GLY	5.1
1	B	757	ASP	4.7
1	C	622	TYR	4.3
1	D	757	ASP	4.2
1	D	618	LEU	4.2
1	D	590	THR	4.1
1	B	756	ILE	4.0
1	D	620	GLN	3.9
1	C	618	LEU	3.7
1	C	620	GLN	3.5
1	B	590	THR	3.5
1	D	591	ASP	3.5
1	A	450	PHE	3.3
1	C	757	ASP	3.3
1	A	591	ASP	3.2
1	C	720	ARG	3.1
1	B	592	GLU	3.1
1	A	453	LEU	3.1
1	C	590	THR	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	590	THR	3.0
1	B	450	PHE	2.9
1	A	451	GLY	2.9
1	D	715	GLY	2.9
1	A	636	VAL	2.9
1	A	452	VAL	2.8
1	D	721	ASP	2.8
1	A	622	TYR	2.8
1	B	402	TYR	2.8
1	D	386	ILE	2.8
1	B	333	ARG	2.8
1	A	620	GLN	2.7
1	B	453	LEU	2.7
1	C	450	PHE	2.7
1	C	621	GLY	2.7
1	A	366	TYR	2.6
1	C	385	VAL	2.6
1	B	386	ILE	2.6
1	B	452	VAL	2.6
1	C	452	VAL	2.5
1	A	386	ILE	2.5
1	A	592	GLU	2.5
1	C	386	ILE	2.5
1	B	633	LEU	2.4
1	C	592	GLU	2.4
1	A	448	ALA	2.4
1	B	448	ALA	2.4
1	D	450	PHE	2.4
1	B	476	ALA	2.4
1	C	623	ARG	2.4
1	A	757	ASP	2.4
1	C	697	ASN	2.3
1	B	373	ILE	2.2
1	A	621	GLY	2.2
1	A	370	MET	2.2
1	C	440	TYR	2.1
1	B	332	LYS	2.1
1	D	440	TYR	2.1
1	B	591	ASP	2.1
1	B	366	TYR	2.1
1	C	740	LEU	2.0
1	D	623	ARG	2.0

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Mol	Chain	Res	Type	RSRZ
1	D	678	ARG	2.0
1	D	700	ILE	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	CA	B	801	1/1	0.89	0.09	68,68,68,68	0
3	CA	A	801	1/1	0.91	0.08	69,69,69,69	0
2	ZN	D	800	1/1	0.99	0.11	40,40,40,40	0
2	ZN	B	800	1/1	0.99	0.12	32,32,32,32	0
2	ZN	A	800	1/1	0.99	0.10	33,33,33,33	0
2	ZN	C	800	1/1	0.99	0.08	35,35,35,35	0

6.5 Other polymers [i](#)

There are no such residues in this entry.