W O R L D W I D E

wwPDB

P R O T E I N   D A T A   B A N K

Full wwPDB X-ray Structure Validation Report (i)

Jan 31, 2016 – 07:49 PM GMT

PDB ID	:	1HC7
Title	:	PROLYL-TRNA SYNTHETASE FROM THERMUS THERMOPHILUS
Authors	:	Yaremchuk, A.; Tukalo, M.; Cusack, S.
Deposited on	:	2001-04-26
Resolution	:	2.43 Å(reported)

The following versions of software and data (see references (i)) 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 (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.43 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.
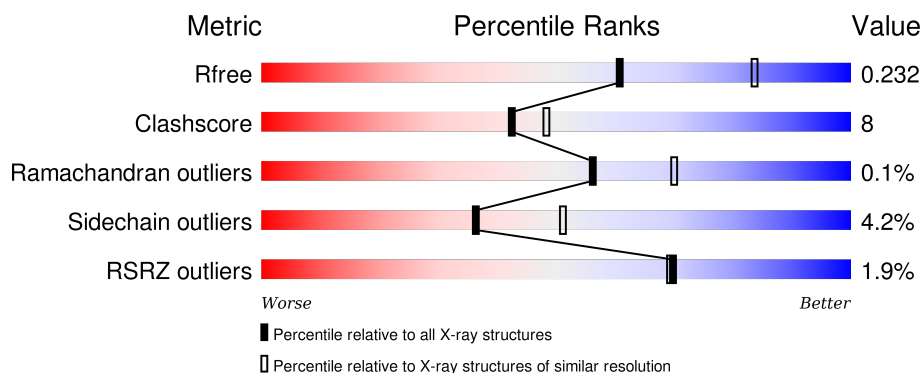
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	1003 (2.46-2.42)
Clashscore	102246	1071 (2.46-2.42)
Ramachandran outliers	100387	1065 (2.46-2.42)
Sidechain outliers	100360	1065 (2.46-2.42)
RSRZ outliers	91569	1005 (2.46-2.42)

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 <=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	477	
1	B	477	
1	C	477	
1	D	477	

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 15730 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 PROLYL-TRNA SYNTHETASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	464	Total 3747	C 2399	N 656	O 680	S 12	50	12	0
1	B	464	Total 3747	C 2399	N 656	O 680	S 12	32	7	0
1	C	464	Total 3747	C 2399	N 656	O 680	S 12	30	6	0
1	D	464	Total 3747	C 2399	N 656	O 680	S 12	36	7	0

- 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 water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	167	Total 167	O 167	0	0
3	B	160	Total 160	O 160	0	0
3	C	223	Total 223	O 223	0	0
3	D	188	Total 188	O 188	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: PROLYL-TRNA SYNTHETASE
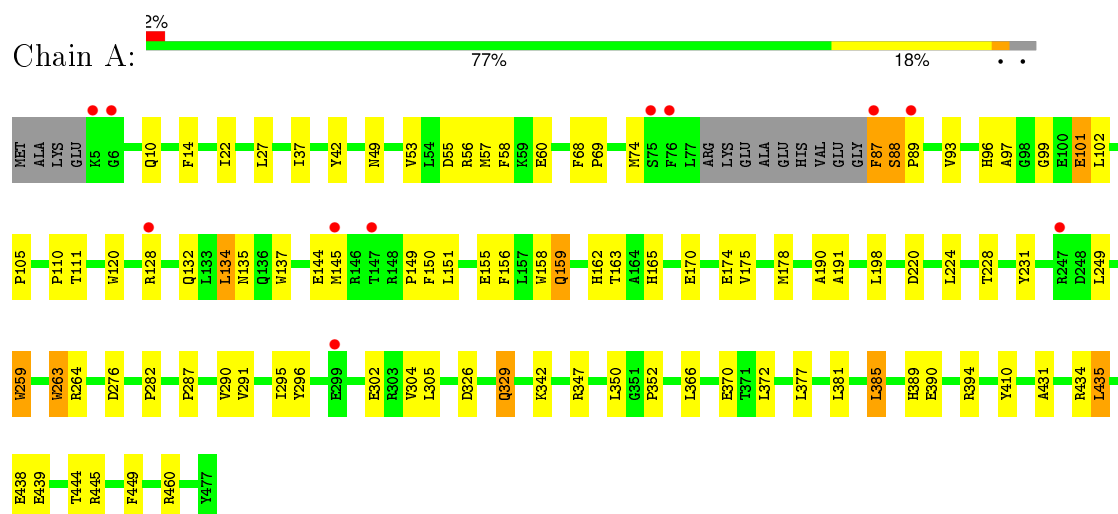
- Molecule 1: PROLYL-TRNA SYNTHETASE

- Molecule 1: PROLYL-TRNA SYNTHETASE

• Molecule 1: PROLYL-TRNA SYNTHETASE

Chain D:
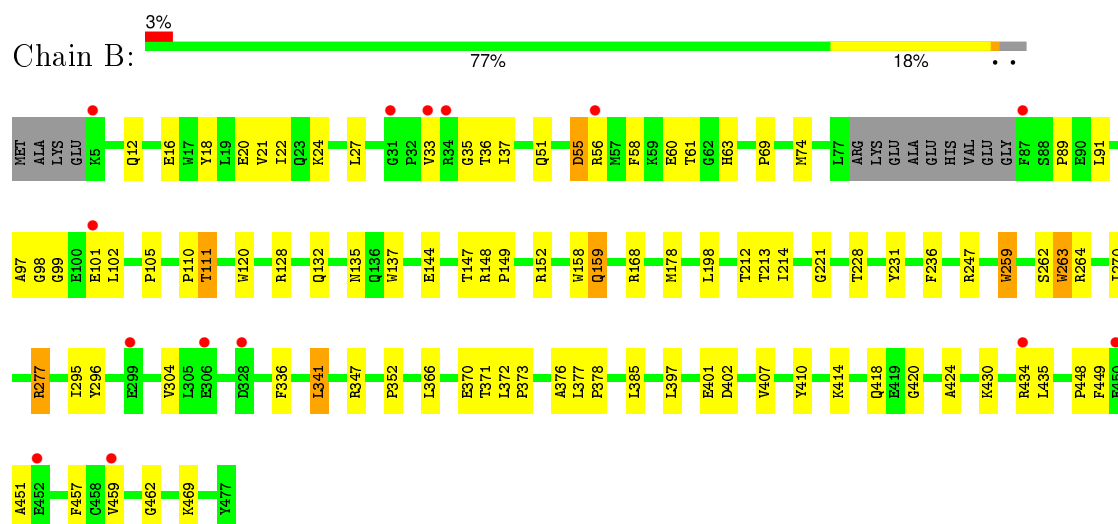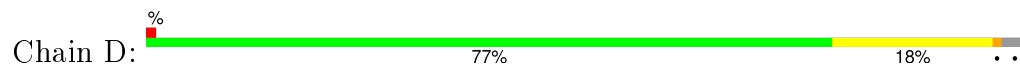
4 Data and refinement statistics (i)

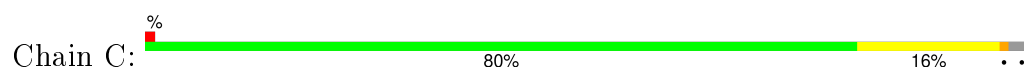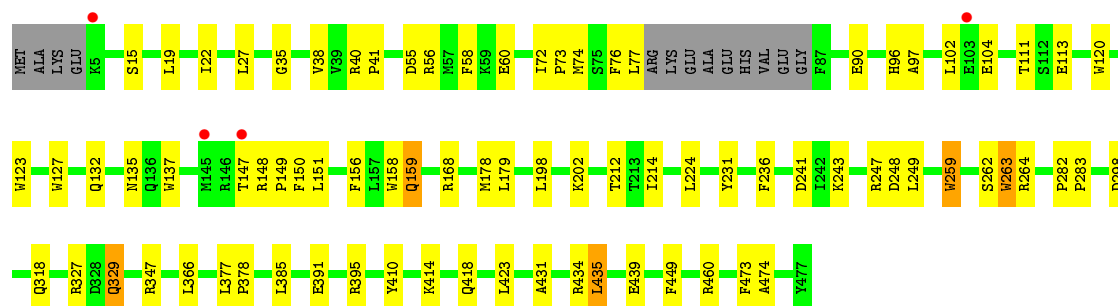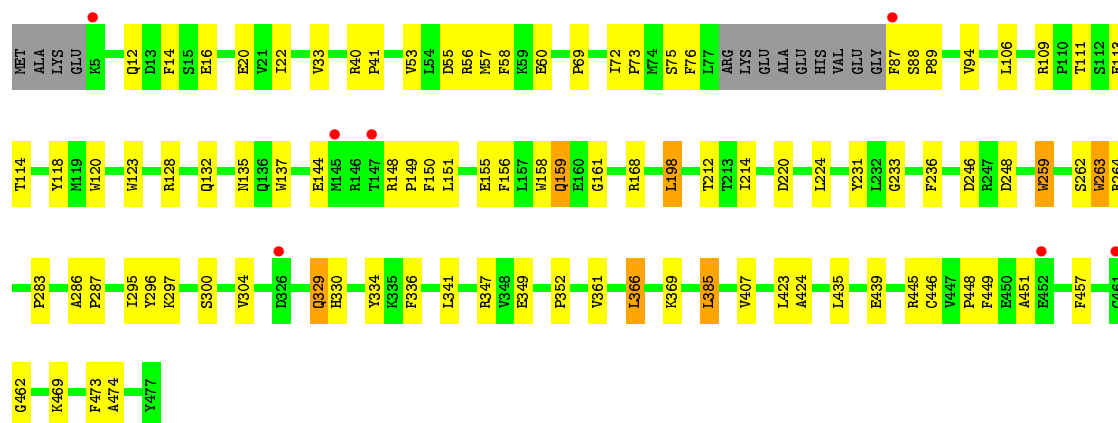| Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α, β, γ	132.30Å 191.10Å 125.10Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.43 14.96 – 2.43	Depositor EDS
% Data completeness (in resolution range)	98.6 (20.00-2.43) 98.8 (14.96-2.43)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	4.03 (at 2.42Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.206 , 0.234 0.205 , 0.232	Depositor DCC
R_{free} test set	5907 reflections (5.01%)	DCC
Wilson B-factor (Å^2)	33.8	Xtriage
Anisotropy	0.350	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 52.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< |L| > = 0.49, < L^2 > = 0.33$	Xtriage
Outliers	0 of 117865 reflections	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	15730	wwPDB-VP
Average B, all atoms (Å^2)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.03% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.
[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5　Model quality ⓘ

5.1　Standard geometry ⓘ

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

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	0.34	0/3844	0.60	0/5207
1	B	0.34	0/3844	0.60	0/5207
1	C	0.37	0/3844	0.62	0/5207
1	D	0.35	0/3844	0.62	0/5207
All	All	0.35	0/15376	0.61	0/20828

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 ⓘ

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	3747	0	3661	62	0
1	B	3747	0	3666	68	0
1	C	3747	0	3668	59	0
1	D	3747	0	3666	72	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	167	0	0	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	160	0	0	5	0
3	C	223	0	0	4	0
3	D	188	0	0	1	0
All	All	15730	0	14661	242	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 8.

All (242) 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:C:120:TRP:NE1	1:C:132:GLN:HG2	1.79	0.97
1:B:451:ALA:HB3	1:B:469:LYS:HD3	1.59	0.83
1:A:445:ARG:HD2	3:A:2150:HOH:O	1.76	0.83
1:C:120:TRP:HE1	1:C:132:GLN:HG2	1.44	0.82
1:D:94:VAL:HG12	1:D:106:LEU:O	1.81	0.81
1:B:120:TRP:NE1	1:B:132:GLN:HG2	1.97	0.79
1:C:150:PHE:O	1:C:264:ARG:HA	1.84	0.77
1:D:329:GLN:H	1:D:329:GLN:NE2	1.83	0.76
1:D:120:TRP:NE1	1:D:132:GLN:HG2	2.01	0.76
1:A:120:TRP:NE1	1:A:132:GLN:HG2	2.00	0.76
1:A:224:LEU:HD11	1:A:264:ARG:HD3	1.68	0.73
1:D:94:VAL:CG1	1:D:106:LEU:HB2	2.17	0.73
1:B:347:ARG:HD3	3:B:2126:HOH:O	1.88	0.73
3:A:2029:HOH:O	1:B:33:VAL:HG22	1.86	0.73
1:C:168:ARG:HG3	1:C:231:TYR:OH	1.90	0.70
1:A:69:PRO:HG3	1:B:37:ILE:O	1.92	0.70
1:A:89:PRO:O	1:B:98:GLY:HA2	1.91	0.70
1:A:150:PHE:O	1:A:264:ARG:HA	1.92	0.69
1:D:56:ARG:O	1:D:60:GLU:HG3	1.91	0.69
1:A:326:ASP:HB3	3:A:2114:HOH:O	1.93	0.69
1:B:263:TRP:HZ2	3:B:2068:HOH:O	1.76	0.69
1:C:224:LEU:HD11	1:C:264:ARG:HD3	1.74	0.68
1:B:168:ARG:HG3	1:B:231:TYR:OH	1.93	0.68
1:B:198:LEU:HD22	1:B:449:PHE:CE2	2.29	0.67
1:A:302:GLU:HB2	3:A:2108:HOH:O	1.94	0.67
1:C:15:SER:HB3	1:C:148:ARG:HH22	1.59	0.67
1:D:297:LYS:H	1:D:300:SER:HB2	1.60	0.66
1:B:448:PRO:HG2	1:B:451:ALA:HB2	1.78	0.66
1:A:56:ARG:O	1:A:60:GLU:HG3	1.95	0.66
1:D:58:PHE:HE2	1:D:159:GLN:HG3	1.62	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:58:PHE:HE2	1:A:159:GLN:HG3	1.62	0.65
1:B:377:LEU:HB3	1:B:378:PRO:HD3	1.78	0.64
1:C:198:LEU:HD22	1:C:449:PHE:CE2	2.34	0.63
1:C:148:ARG:HG2	1:C:151:LEU:HB2	1.81	0.63
1:B:56:ARG:O	1:B:60:GLU:HG3	1.99	0.63
1:B:397:LEU:O	1:B:401:GLU:HG3	1.99	0.62
1:A:198:LEU:HD22	1:A:449:PHE:CE2	2.35	0.62
1:A:296:TYR:HB3	1:A:304:VAL:HG21	1.83	0.61
1:B:33:VAL:HB	1:B:36:THR:OG1	2.00	0.61
1:C:56:ARG:O	1:C:60:GLU:HG3	2.01	0.61
1:A:445:ARG:NH1	3:A:2150:HOH:O	2.35	0.60
1:D:198:LEU:HD22	1:D:449:PHE:CE2	2.37	0.59
1:D:148:ARG:HD3	3:D:2077:HOH:O	2.01	0.59
1:B:198:LEU:HD22	1:B:449:PHE:HE2	1.67	0.59
1:D:457:PHE:HB3	1:D:462:GLY:O	2.03	0.59
1:C:137:TRP:CZ3	1:C:159:GLN:HB2	2.37	0.59
1:C:329:GLN:HE21	1:D:128:ARG:NH1	2.01	0.59
1:C:58:PHE:HE2	1:C:159:GLN:HG3	1.68	0.58
1:B:120:TRP:CE2	1:B:132:GLN:HG2	2.38	0.58
1:B:120:TRP:HE1	1:B:132:GLN:HG2	1.68	0.58
1:C:35:GLY:HA2	1:C:147:THR:OG1	2.04	0.57
1:D:22:ILE:HD13	1:D:149:PRO:HB2	1.85	0.57
1:D:198:LEU:HD22	1:D:449:PHE:HE2	1.70	0.57
1:C:148:ARG:HD3	1:C:151:LEU:HD12	1.86	0.57
1:B:12:GLN:HG2	1:D:12:GLN:OE1	2.04	0.57
1:A:329:GLN:HB2	1:B:128:ARG:HA	1.86	0.56
1:C:40:ARG:HD3	1:D:123:TRP:CZ2	2.40	0.56
1:D:296:TYR:HB2	1:D:300:SER:HB2	1.88	0.56
1:A:87:PHE:CE2	1:A:93:VAL:HG21	2.41	0.56
1:B:137:TRP:CE3	1:B:159:GLN:HB2	2.40	0.56
1:A:137:TRP:CE3	1:A:159:GLN:HB2	2.40	0.56
1:B:24:LYS:HB3	1:B:341:LEU:HD11	1.88	0.55
1:C:137:TRP:CE3	1:C:159:GLN:HB2	2.41	0.55
1:A:10:GLN:HG3	1:A:276:ASP:OD2	2.06	0.55
1:A:96[A]:HIS:NE2	1:A:101:GLU:HG2	2.22	0.55
1:C:113:GLU:O	1:C:236:PHE:HZ	1.89	0.55
1:C:40:ARG:HD2	3:C:2018:HOH:O	2.07	0.55
1:B:58:PHE:HE2	1:B:159:GLN:HG3	1.71	0.55
1:C:97:ALA:HB3	1:C:102:LEU:HD21	1.88	0.55
1:B:430:LYS:O	1:B:434:ARG:HG2	2.07	0.55
1:C:22:ILE:HD13	1:C:149:PRO:HB2	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:110:PRO:HG2	1:B:111:THR:HG22	1.89	0.55
1:A:22:ILE:HD13	1:A:149:PRO:HB2	1.89	0.54
1:C:15:SER:CB	1:C:148:ARG:HH22	2.21	0.54
1:A:162:HIS:HD2	3:A:2056:HOH:O	1.91	0.53
1:A:156:PHE:HA	1:A:263:TRP:CZ2	2.42	0.53
1:C:329:GLN:NE2	1:D:128:ARG:HH11	2.07	0.53
1:B:137:TRP:CZ3	1:B:159:GLN:HB2	2.44	0.53
1:B:277:ARG:HG3	1:B:277:ARG:HH11	1.73	0.53
1:C:248:ASP:C	1:C:249:LEU:HD22	2.29	0.53
1:D:296:TYR:HB3	1:D:304:VAL:HG21	1.91	0.53
1:A:435:LEU:HD12	1:A:439:GLU:OE1	2.09	0.53
1:D:113:GLU:O	1:D:236:PHE:HZ	1.92	0.52
1:B:37:ILE:C	1:B:37:ILE:HD12	2.30	0.52
1:B:74:MET:HB2	1:B:105:PRO:O	2.08	0.52
1:D:120:TRP:HE1	1:D:132:GLN:HG2	1.71	0.52
1:C:329:GLN:HE21	1:D:128:ARG:HH11	1.55	0.52
1:B:402:ASP:HA	1:D:369:LYS:HE3	1.92	0.52
1:A:431:ALA:HA	1:A:434:ARG:NH1	2.24	0.52
1:C:329:GLN:NE2	1:D:128:ARG:HG2	2.25	0.52
1:C:120:TRP:CE2	1:C:132:GLN:HG2	2.44	0.52
1:A:410:TYR:CZ	1:A:460:ARG:HD3	2.45	0.52
1:B:35:GLY:HA2	1:B:147:THR:OG1	2.10	0.52
1:A:74:MET:HB2	1:A:105:PRO:O	2.10	0.51
1:A:290:VAL:HG21	1:A:381:LEU:HD13	1.93	0.51
1:B:296:TYR:HB3	1:B:304:VAL:HG21	1.92	0.51
1:D:168:ARG:HG3	1:D:231:TYR:OH	2.10	0.51
1:B:135:ASN:OD1	1:B:159:GLN:HG2	2.09	0.51
1:D:137:TRP:CE3	1:D:159:GLN:HB2	2.46	0.50
1:B:457:PHE:HB3	1:B:462:GLY:O	2.11	0.50
1:D:198:LEU:HD13	1:D:212:THR:HG22	1.94	0.50
1:D:120:TRP:CE2	1:D:132:GLN:HG2	2.47	0.50
1:B:410:TYR:O	1:B:414:LYS:HG3	2.12	0.50
1:B:371:THR:O	1:B:372:LEU:HD23	2.12	0.50
1:C:73:PRO:HB2	1:C:76:PHE:CD1	2.47	0.50
1:A:178:MET:HG3	1:A:259:TRP:CE2	2.47	0.49
1:C:123:TRP:CZ2	1:D:40:ARG:HD3	2.47	0.49
1:B:144:GLU:OE1	1:B:152:ARG:HD3	2.12	0.49
1:C:241:ASP:OD1	1:C:243:LYS:NZ	2.44	0.49
1:A:370:GLU:OE1	1:A:372:LEU:HD21	2.13	0.49
1:B:18:TYR:O	1:B:21:VAL:HG12	2.13	0.49
1:B:336:PHE:CD1	1:B:347:ARG:HD2	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:137:TRP:CZ3	1:D:159:GLN:HB2	2.48	0.48
1:A:165:HIS:ND1	1:A:170:GLU:HG2	2.28	0.48
1:D:214:ILE:O	1:D:214:ILE:HG13	2.14	0.48
1:B:214:ILE:O	1:B:214:ILE:HG13	2.14	0.48
1:D:329:GLN:N	1:D:329:GLN:NE2	2.59	0.47
1:D:349:GLU:HB2	1:D:361:VAL:HB	1.97	0.47
1:A:37:ILE:O	1:B:69:PRO:HG3	2.15	0.47
1:B:295:ILE:O	1:B:352:PRO:HD3	2.13	0.47
1:A:305:LEU:HD21	1:A:326:ASP:OD1	2.14	0.47
1:B:373:PRO:HG2	1:B:376:ALA:HB3	1.96	0.47
1:D:76:PHE:HD2	1:D:114:THR:HB	1.79	0.47
1:A:249:LEU:HD22	1:A:249:LEU:N	2.30	0.47
1:A:137:TRP:CZ3	1:A:159:GLN:HB2	2.50	0.46
1:A:190:ALA:HA	1:A:282:PRO:HG3	1.97	0.46
1:D:336:PHE:CD1	1:D:347:ARG:HD2	2.51	0.46
1:D:231:TYR:CZ	1:D:233:GLY:HA2	2.50	0.46
1:D:94:VAL:O	1:D:94:VAL:HG13	2.15	0.46
1:A:89:PRO:HA	1:B:99:GLY:N	2.30	0.46
1:A:135:ASN:OD1	1:A:159:GLN:HG2	2.15	0.46
1:C:40:ARG:HB3	1:C:41:PRO:HD2	1.96	0.46
1:D:407:VAL:CG2	1:D:424:ALA:HB2	2.45	0.46
1:B:74:MET:HE1	1:B:91:LEU:HD13	1.98	0.46
1:A:68:PHE:HE1	1:A:134:LEU:HD11	1.80	0.46
1:D:135:ASN:OD1	1:D:159:GLN:HG2	2.16	0.46
1:A:87:PHE:N	1:A:87:PHE:CD2	2.82	0.46
1:D:246:ASP:HB3	1:D:248:ASP:OD2	2.15	0.46
1:D:445:ARG:O	1:D:446:CYS:HB3	2.16	0.46
1:B:97:ALA:HB3	1:B:102:LEU:HD21	1.97	0.46
1:C:178:MET:HG3	1:C:259:TRP:CE2	2.51	0.46
1:B:51:GLN:O	1:B:55:ASP:HB2	2.16	0.46
1:A:132:GLN:O	1:A:163:THR:HA	2.15	0.45
1:B:198:LEU:CD2	1:B:449:PHE:HE2	2.29	0.45
1:B:16:GLU:O	1:B:20:GLU:HG3	2.16	0.45
1:A:191:ALA:HB2	1:A:389:HIS:CE1	2.51	0.45
1:C:423:LEU:HG	3:C:2222:HOH:O	2.15	0.45
1:A:110:PRO:HG2	1:A:111:THR:HG22	1.98	0.45
1:B:448:PRO:HG2	1:B:451:ALA:CB	2.46	0.45
1:C:73:PRO:HG3	1:D:33:VAL:CG2	2.46	0.45
1:D:40:ARG:HB3	1:D:41:PRO:HD2	1.99	0.45
1:B:221:GLY:O	1:B:420:GLY:HA2	2.16	0.45
1:B:213:THR:HB	1:B:228:THR:HG22	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:148:ARG:HD3	3:B:2061:HOH:O	2.16	0.45
1:A:291:VAL:CG1	1:A:347:ARG:HG2	2.47	0.45
1:D:295:ILE:O	1:D:352:PRO:HD3	2.16	0.45
1:C:127:TRP:CE3	1:C:247:ARG:NH1	2.85	0.45
1:C:435:LEU:HD12	1:C:439:GLU:OE1	2.17	0.44
1:B:61:THR:HG1	1:B:63:HIS:CE1	2.35	0.44
1:C:473:PHE:O	1:C:474:ALA:HB2	2.17	0.44
1:B:198:LEU:HD13	1:B:212:THR:HG22	1.98	0.44
1:D:366:LEU:HD12	1:D:366:LEU:HA	1.80	0.44
1:C:282:PRO:HA	1:C:283:PRO:HD3	1.84	0.44
1:C:391:GLU:O	1:C:395:ARG:HG3	2.17	0.44
1:B:247:ARG:NH1	3:B:2103:HOH:O	2.51	0.44
1:A:381:LEU:O	1:A:385:LEU:HD22	2.17	0.44
1:B:178:MET:HG3	1:B:259:TRP:CE2	2.53	0.44
1:C:38:VAL:HG22	1:D:69:PRO:HD3	2.00	0.44
1:B:236:PHE:HB3	3:B:2099:HOH:O	2.18	0.44
1:B:22:ILE:HD13	1:B:149:PRO:HB2	1.99	0.44
1:D:58:PHE:CE2	1:D:159:GLN:HG3	2.46	0.44
1:A:304:VAL:HG13	1:A:350:LEU:HD22	1.99	0.44
1:C:249:LEU:HD22	1:C:249:LEU:N	2.32	0.44
1:C:156:PHE:HA	1:C:263:TRP:CZ2	2.53	0.44
1:B:448:PRO:CG	1:B:451:ALA:HB2	2.47	0.43
1:C:135:ASN:OD1	1:C:159:GLN:HG2	2.18	0.43
1:B:58:PHE:CE2	1:B:159:GLN:HG3	2.52	0.43
1:D:451:ALA:HB3	1:D:469:LYS:HD3	1.99	0.43
1:C:214:ILE:O	1:C:214:ILE:HG13	2.18	0.43
1:D:156:PHE:HA	1:D:263:TRP:CZ2	2.53	0.43
1:C:347:ARG:HD3	3:C:2153:HOH:O	2.18	0.43
1:C:318:GLN:HG3	1:C:378:PRO:O	2.17	0.43
1:B:407:VAL:CG2	1:B:424:ALA:HB2	2.48	0.43
1:A:53:VAL:HG12	1:A:57:MET:CE	2.49	0.43
1:A:99:GLY:N	1:B:89:PRO:HA	2.34	0.43
1:A:295:ILE:O	1:A:352:PRO:HD3	2.18	0.43
1:C:198:LEU:HD22	1:C:449:PHE:HE2	1.79	0.43
1:D:283:PRO:HB3	1:D:385:LEU:HD12	2.01	0.43
1:A:198:LEU:HD22	1:A:449:PHE:HE2	1.81	0.43
1:C:241:ASP:CG	1:C:243:LYS:HZ2	2.21	0.43
1:D:155:GLU:HG2	1:D:156:PHE:N	2.34	0.43
1:B:262:SER:C	1:B:264:ARG:H	2.20	0.43
1:A:155:GLU:HG2	1:A:156:PHE:N	2.34	0.43
1:B:370:GLU:HG3	1:B:372:LEU:HG	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:163:THR:HG21	1:A:174:GLU:OE1	2.19	0.42
1:A:128:ARG:HH11	1:A:128:ARG:HG2	1.84	0.42
1:D:72:ILE:HA	1:D:73:PRO:HD3	1.93	0.42
1:D:262:SER:C	1:D:264:ARG:H	2.21	0.42
1:A:434:ARG:O	1:A:438:GLU:HG3	2.19	0.42
1:C:435:LEU:HG	1:C:460:ARG:NH2	2.34	0.42
1:D:448:PRO:HG2	1:D:451:ALA:HB2	2.00	0.42
1:D:53:VAL:HG12	1:D:57:MET:CE	2.49	0.42
1:A:444:THR:O	3:A:2150:HOH:O	2.20	0.42
1:A:58:PHE:CE2	1:A:159:GLN:HG3	2.48	0.42
1:A:88:SER:HA	1:A:89:PRO:HD3	1.92	0.42
1:B:377:LEU:HB3	1:B:378:PRO:CD	2.50	0.42
1:C:40:ARG:HD3	1:D:123:TRP:CH2	2.54	0.42
1:D:113:GLU:O	1:D:236:PHE:CZ	2.73	0.42
1:B:424:ALA:HB1	1:B:459:VAL:HB	2.02	0.42
1:D:150:PHE:O	1:D:264:ARG:HA	2.20	0.42
1:C:202:LYS:HE3	3:C:2206:HOH:O	2.19	0.42
1:D:76:PHE:HE2	1:D:118:TYR:HB2	1.85	0.41
1:D:161:GLY:HA3	1:D:259:TRP:CZ3	2.56	0.41
1:D:109:ARG:HG3	1:D:109:ARG:O	2.18	0.41
1:D:286:ALA:HA	1:D:287:PRO:HD3	1.95	0.41
1:D:330:HIS:HB3	1:D:334:TYR:CD2	2.55	0.41
1:D:473:PHE:O	1:D:474:ALA:HB2	2.21	0.41
1:D:224:LEU:HD11	1:D:264:ARG:HD3	2.01	0.41
1:C:74:MET:HE1	1:C:77:LEU:HD12	2.02	0.41
1:D:88:SER:HA	1:D:89:PRO:HD3	1.93	0.41
1:D:435:LEU:HD12	1:D:439:GLU:OE1	2.21	0.41
1:B:27:LEU:HD23	1:B:270:ILE:HD11	2.03	0.41
1:C:96:HIS:CD2	1:D:87:PHE:HD1	2.39	0.41
1:D:329:GLN:H	1:D:329:GLN:CD	2.24	0.41
1:D:14:PHE:CG	1:D:220:ASP:HB3	2.55	0.41
1:A:42:TYR:CZ	1:A:342:LYS:HB3	2.56	0.41
1:D:16:GLU:O	1:D:20:GLU:HG3	2.21	0.41
1:C:73:PRO:HG3	1:D:33:VAL:HG22	2.03	0.41
1:A:14:PHE:CD2	1:A:220:ASP:HB3	2.55	0.41
1:A:97:ALA:HB3	1:A:102:LEU:HD21	2.02	0.41
1:A:329:GLN:CB	1:B:128:ARG:HA	2.51	0.40
1:A:175:VAL:HG21	1:A:231:TYR:HB2	2.03	0.40
1:C:262:SER:C	1:C:264:ARG:H	2.24	0.40
1:C:19:LEU:HD13	1:C:148:ARG:HH21	1.85	0.40
1:A:49:ASN:HD21	1:A:287:PRO:HA	1.85	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:159:GLN:CD	1:A:159:GLN:C	2.80	0.40
1:C:72:ILE:HA	1:C:73:PRO:HD3	1.93	0.40
1:D:73:PRO:HB2	1:D:76:PHE:CD1	2.57	0.40
1:C:431:ALA:HA	1:C:434:ARG:NH1	2.35	0.40
1:C:410:TYR:O	1:C:414:LYS:HG3	2.22	0.40
1:C:179:LEU:HD22	1:C:212:THR:HB	2.02	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	460/477 (96%)	439 (95%)	20 (4%)	1 (0%)	52	64
1	B	460/477 (96%)	442 (96%)	18 (4%)	0	100	100
1	C	460/477 (96%)	442 (96%)	17 (4%)	1 (0%)	52	64
1	D	460/477 (96%)	442 (96%)	18 (4%)	0	100	100
All	All	1840/1908 (96%)	1765 (96%)	73 (4%)	2 (0%)	56	70

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	88	SER
1	C	327	ARG

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	385/395 (98%)	365 (95%)	20 (5%)	29	40
1	B	385/395 (98%)	372 (97%)	13 (3%)	44	60
1	C	385/395 (98%)	369 (96%)	16 (4%)	36	51
1	D	385/395 (98%)	370 (96%)	15 (4%)	39	54
All	All	1540/1580 (98%)	1476 (96%)	64 (4%)	36	51

All (64) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	27	LEU
1	A	55	ASP
1	A	87	PHE
1	A	101	GLU
1	A	134	LEU
1	A	144	GLU
1	A	145	MET
1	A	151	LEU
1	A	158	TRP
1	A	159	GLN
1	A	228	THR
1	A	259	TRP
1	A	263	TRP
1	A	329	GLN
1	A	366	LEU
1	A	377	LEU
1	A	385	LEU
1	A	390	GLU
1	A	394[A]	ARG
1	A	435	LEU
1	B	55	ASP
1	B	101	GLU
1	B	111	THR
1	B	158	TRP
1	B	159	GLN
1	B	259	TRP
1	B	263	TRP
1	B	277	ARG
1	B	341	LEU
1	B	366	LEU

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Mol	Chain	Res	Type
1	B	385	LEU
1	B	418	GLN
1	B	435	LEU
1	C	27	LEU
1	C	55	ASP
1	C	90	GLU
1	C	104	GLU
1	C	111	THR
1	C	158	TRP
1	C	159	GLN
1	C	259	TRP
1	C	263	TRP
1	C	298	ASP
1	C	329	GLN
1	C	366	LEU
1	C	377	LEU
1	C	385	LEU
1	C	418	GLN
1	C	435	LEU
1	D	55	ASP
1	D	75	SER
1	D	111	THR
1	D	144	GLU
1	D	151	LEU
1	D	158	TRP
1	D	159	GLN
1	D	198	LEU
1	D	259	TRP
1	D	263	TRP
1	D	329	GLN
1	D	341	LEU
1	D	366	LEU
1	D	385	LEU
1	D	423	LEU

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	12	GLN
1	A	132	GLN
1	A	309	GLN
1	B	96	HIS

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Mol	Chain	Res	Type
1	B	132	GLN
1	B	309	GLN
1	C	12	GLN
1	C	132	GLN
1	C	250	GLN
1	C	309	GLN
1	C	329	GLN
1	D	132	GLN
1	D	309	GLN
1	D	329	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

Of 4 ligands modelled in this entry, 4 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 (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	464/477 (97%)	-0.36	11 (2%)	62	61	18, 35, 57, 84	12 (2%)
1	B	464/477 (97%)	-0.32	14 (3%)	54	52	17, 34, 60, 76	7 (1%)
1	C	464/477 (97%)	-0.53	4 (0%)	85	87	12, 28, 55, 71	6 (1%)
1	D	464/477 (97%)	-0.39	7 (1%)	76	77	16, 31, 57, 78	7 (1%)
All	All	1856/1908 (97%)	-0.40	36 (1%)	70	69	12, 32, 58, 84	32 (1%)

All (36) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	5	LYS	5.1
1	A	87	PHE	4.1
1	D	87	PHE	3.9
1	A	75	SER	3.6
1	C	145	MET	3.4
1	C	5	LYS	3.4
1	A	247	ARG	3.2
1	B	87	PHE	3.2
1	C	103	GLU	3.2
1	C	147	THR	3.0
1	B	5	LYS	3.0
1	D	145	MET	2.9
1	D	5	LYS	2.9
1	A	128	ARG	2.8
1	A	299	GLU	2.8
1	B	31	GLY	2.7
1	A	89	PRO	2.7
1	B	299	GLU	2.6
1	A	76[A]	PHE	2.6
1	D	326	ASP	2.5
1	A	145	MET	2.5

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Mol	Chain	Res	Type	RSRZ
1	D	147	THR	2.4
1	B	450	GLU	2.3
1	B	306	GLU	2.3
1	A	6	GLY	2.3
1	D	461	CYS	2.2
1	B	434	ARG	2.2
1	B	328	ASP	2.2
1	B	33	VAL	2.2
1	A	147	THR	2.1
1	B	34[B]	ARG	2.1
1	D	452	GLU	2.1
1	B	452	GLU	2.1
1	B	56	ARG	2.0
1	B	101	GLU	2.0
1	B	459	VAL	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)

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	RSCC	RSR	LLDF	B-factors($Å^2$)	Q<0.9
2	ZN	C	490	1/1	0.99	0.03	-1.64	35,35,35,35	0
2	ZN	D	490	1/1	0.96	0.06	-2.08	42,42,42,42	0
2	ZN	A	490	1/1	0.99	0.03	-2.32	42,42,42,42	0
2	ZN	B	490	1/1	0.90	0.07	-2.63	55,55,55,55	0

6.5 Other polymers (i)

There are no such residues in this entry.