



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 02:41 AM GMT

PDB ID : 2I7X  
Title : Structure of Yeast CPSF-100 (Ydh1p)  
Authors : Mandel, C.R.; Zhang, H.; Gebauer, D.; Tong, L.  
Deposited on : 2006-08-31  
Resolution : 2.50 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](mailto: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

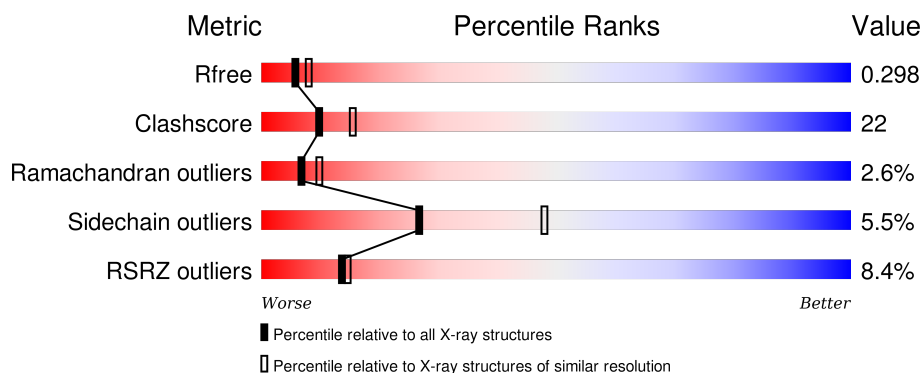
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

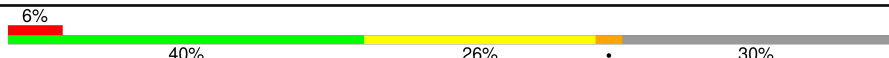
The reported resolution of this entry is 2.50 Å.

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))
$R_{free}$	91344	3553 (2.50-2.50)
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (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  $\geq 3$ , 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	717	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4084 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 Protein CFT2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	499	Total	C	N	O	S	0	0	0
			3936	2523	644	754	15			

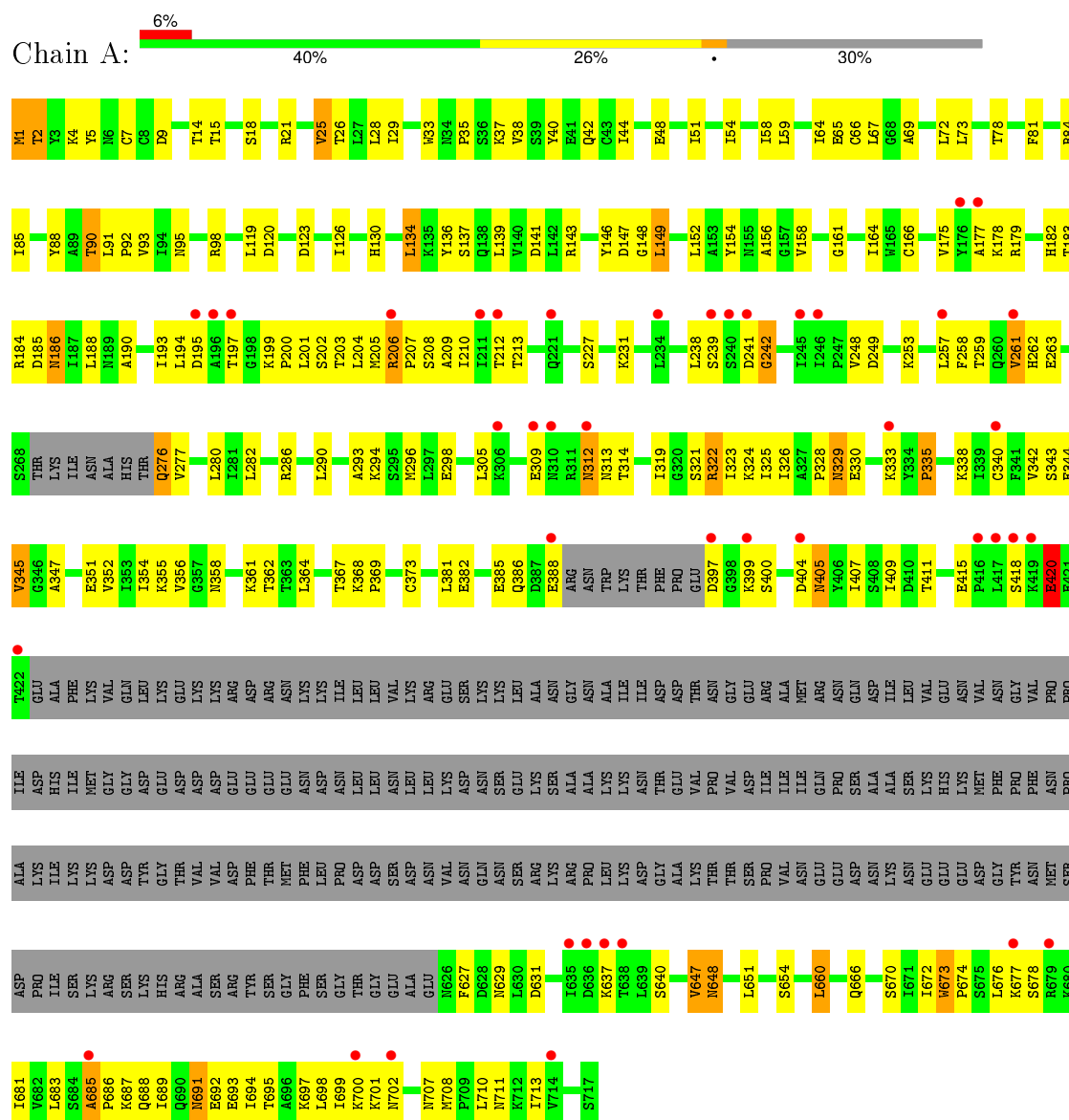
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	148	Total	O	0	0
			148	148		

### 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 CFT2



## 4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	75.63 Å 122.80 Å 126.86 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	28.18 – 2.50 28.18 – 2.50	Depositor EDS
% Data completeness (in resolution range)	93.7 (28.18-2.50) 99.1 (28.18-2.50)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	6.41 (at 2.51 Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.212 , 0.290 0.220 , 0.298	Depositor DCC
$R_{free}$ test set	2027 reflections (9.82%)	DCC
Wilson B-factor (Å <sup>2</sup> )	44.3	Xtriage
Anisotropy	0.592	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 49.2	EDS
Estimated twinning fraction	0.012 for -h,-l,-k	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 20806 reflections	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	4084	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.46% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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	0.37	0/4008	0.66	0/5432

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	3936	0	4031	177	0
2	A	148	0	0	8	0
All	All	4084	0	4031	177	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 22.

All (177) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:212:THR:HG22	1:A:213:THR:H	1.08	1.09
1:A:90:THR:HG23	1:A:92:PRO:HD2	1.31	1.05
1:A:685:ALA:HB1	1:A:686:PRO:HD3	1.41	0.99
1:A:685:ALA:HB1	1:A:686:PRO:CD	1.98	0.91

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:687:LYS:HG2	1:A:707:ASN:HB3	1.54	0.88
1:A:90:THR:CG2	1:A:92:PRO:HD2	2.03	0.88
1:A:7:CYS:HB3	1:A:15:THR:HG22	1.55	0.88
1:A:212:THR:HG22	1:A:213:THR:N	1.90	0.86
1:A:212:THR:CG2	1:A:213:THR:H	1.91	0.83
1:A:177:ALA:O	1:A:212:THR:HG23	1.80	0.82
1:A:95:ASN:O	1:A:98:ARG:HG2	1.79	0.81
1:A:9:ASP:OD2	1:A:710:LEU:HD13	1.84	0.76
1:A:407:ILE:HD12	1:A:409:ILE:HD11	1.68	0.76
1:A:253:LYS:HE2	1:A:253:LYS:HA	1.66	0.75
1:A:687:LYS:HE2	1:A:707:ASN:HB2	1.69	0.73
1:A:15:THR:HG23	1:A:685:ALA:HA	1.71	0.73
1:A:1:MET:SD	1:A:2:THR:HG22	2.30	0.71
1:A:91:LEU:HB3	1:A:92:PRO:HD3	1.72	0.70
1:A:152:LEU:HD13	1:A:154:TYR:OH	1.92	0.70
1:A:691:ASN:HD21	1:A:693:GLU:HB3	1.57	0.69
1:A:90:THR:HG21	1:A:161:GLY:CA	2.22	0.69
1:A:407:ILE:HD13	1:A:651:LEU:HD11	1.73	0.69
1:A:282:LEU:HD13	1:A:342:VAL:HG22	1.74	0.67
1:A:7:CYS:HB3	1:A:15:THR:CG2	2.23	0.67
1:A:356:VAL:HG22	1:A:362:THR:OG1	1.94	0.66
1:A:183:THR:HG22	1:A:184:ARG:N	2.11	0.66
1:A:687:LYS:HE2	1:A:707:ASN:CB	2.24	0.66
1:A:319:ILE:O	1:A:322:ARG:HB2	1.96	0.65
1:A:305:LEU:O	1:A:309:GLU:HG3	1.96	0.64
1:A:673:TRP:HA	1:A:673:TRP:CE3	2.32	0.64
1:A:66:CYS:SG	1:A:178:LYS:HD3	2.39	0.63
1:A:193:ILE:HB	2:A:809:HOH:O	1.98	0.63
1:A:241:ASP:HB3	1:A:361:LYS:HD2	1.79	0.63
1:A:205:MET:O	1:A:207:PRO:HD3	1.98	0.63
1:A:367:THR:HG23	1:A:660:LEU:HB2	1.81	0.62
1:A:685:ALA:CB	1:A:686:PRO:CD	2.74	0.62
1:A:691:ASN:ND2	1:A:693:GLU:HB3	2.14	0.61
1:A:418:SER:C	1:A:420:GLU:H	2.03	0.61
1:A:404:ASP:H	1:A:405:ASN:ND2	1.99	0.61
1:A:25:VAL:HG11	1:A:149:LEU:HD12	1.83	0.61
1:A:322:ARG:HG3	1:A:322:ARG:HH11	1.67	0.60
1:A:673:TRP:HE3	1:A:673:TRP:HA	1.65	0.60
1:A:205:MET:C	1:A:207:PRO:HD3	2.22	0.60
1:A:143:ARG:HG2	1:A:148:GLY:HA2	1.84	0.60
1:A:29:ILE:HG12	1:A:58:ILE:HD11	1.84	0.59

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:257:LEU:O	1:A:261:VAL:HG13	2.02	0.59
1:A:15:THR:HG21	1:A:685:ALA:H	1.67	0.58
1:A:4:LYS:HB2	1:A:21:ARG:HB2	1.84	0.58
1:A:692:GLU:H	1:A:692:GLU:CD	2.06	0.58
1:A:201:LEU:HD23	1:A:202:SER:N	2.20	0.57
1:A:1:MET:O	1:A:2:THR:HB	2.05	0.57
1:A:38:VAL:HG13	1:A:42:GLN:HB2	1.87	0.57
1:A:139:LEU:HD11	1:A:141:ASP:HB2	1.87	0.56
1:A:139:LEU:CD1	1:A:141:ASP:HB2	2.35	0.56
1:A:227:SER:O	1:A:231:LYS:HG3	2.06	0.56
1:A:183:THR:HG22	1:A:184:ARG:H	1.69	0.56
1:A:186:ASN:OD1	1:A:259:THR:HG22	2.05	0.56
1:A:400:SER:HB3	1:A:654:SER:OG	2.06	0.55
1:A:691:ASN:ND2	1:A:694:ILE:H	2.05	0.55
1:A:290:LEU:O	1:A:294:LYS:HG3	2.07	0.55
1:A:681:ILE:HD12	1:A:698:LEU:HD13	1.89	0.55
1:A:415:GLU:O	1:A:640:SER:HB2	2.07	0.55
1:A:206:ARG:NH2	1:A:677:LYS:HG3	2.21	0.55
1:A:88:TYR:HB3	1:A:134:LEU:HD21	1.89	0.55
1:A:333:LYS:O	1:A:335:PRO:HD3	2.07	0.55
1:A:9:ASP:HB3	1:A:711:ASN:ND2	2.22	0.54
1:A:258:PHE:HZ	1:A:323:ILE:HD11	1.73	0.54
1:A:120:ASP:O	1:A:123:ASP:HB2	2.08	0.54
1:A:670:SER:HB2	1:A:697:LYS:HE3	1.89	0.54
1:A:322:ARG:CG	1:A:322:ARG:HH11	2.20	0.54
1:A:84:ARG:HG3	1:A:85:ILE:N	2.23	0.54
1:A:90:THR:HG22	1:A:93:VAL:H	1.73	0.53
1:A:328:PRO:C	1:A:330:GLU:H	2.10	0.53
1:A:670:SER:HB3	1:A:694:ILE:HG23	1.91	0.53
1:A:312:ASN:C	1:A:314:THR:H	2.11	0.53
1:A:263:GLU:HG3	1:A:263:GLU:O	2.08	0.52
1:A:388:GLU:HA	2:A:840:HOH:O	2.08	0.52
1:A:15:THR:CG2	1:A:685:ALA:H	2.23	0.52
1:A:184:ARG:HG2	1:A:185:ASP:N	2.24	0.52
1:A:673:TRP:N	1:A:674:PRO:HD2	2.24	0.52
1:A:276:GLN:HA	2:A:741:HOH:O	2.09	0.51
1:A:629:ASN:ND2	1:A:631:ASP:OD2	2.40	0.51
1:A:695:THR:O	1:A:699:ILE:HG13	2.10	0.51
1:A:280:LEU:HD12	1:A:340:CYS:SG	2.50	0.51
1:A:691:ASN:HD22	1:A:694:ILE:H	1.59	0.50
1:A:282:LEU:HG	1:A:326:ILE:HD12	1.92	0.50

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:298:GLU:HG2	2:A:839:HOH:O	2.11	0.50
1:A:178:LYS:O	1:A:179:ARG:HD3	2.12	0.50
1:A:14:THR:HB	2:A:729:HOH:O	2.11	0.50
1:A:321:SER:O	1:A:324:LYS:NZ	2.44	0.49
1:A:147:ASP:O	1:A:147:ASP:OD1	2.30	0.49
1:A:90:THR:HG21	1:A:161:GLY:HA3	1.94	0.49
1:A:197:THR:OG1	1:A:199:LYS:HG2	2.13	0.49
1:A:200:PRO:HG2	1:A:205:MET:CE	2.43	0.48
1:A:44:ILE:O	1:A:48:GLU:HG3	2.14	0.48
1:A:183:THR:CG2	1:A:184:ARG:N	2.76	0.47
1:A:206:ARG:CZ	1:A:677:LYS:HG3	2.44	0.47
1:A:64:ILE:HD11	1:A:373:CYS:SG	2.55	0.47
1:A:92:PRO:HB2	1:A:161:GLY:HA3	1.97	0.47
1:A:182:HIS:O	1:A:190:ALA:HB1	2.15	0.47
1:A:262:HIS:CD2	1:A:319:ILE:HG12	2.50	0.47
1:A:139:LEU:HD13	1:A:141:ASP:N	2.29	0.47
1:A:206:ARG:HG2	1:A:206:ARG:HH11	1.78	0.47
1:A:382:GLU:O	1:A:386:GLN:HB2	2.14	0.47
1:A:203:THR:O	1:A:204:LEU:HB2	2.14	0.47
1:A:685:ALA:HB3	1:A:689:ILE:HD11	1.96	0.47
1:A:692:GLU:N	1:A:692:GLU:CD	2.67	0.47
1:A:90:THR:HG23	1:A:92:PRO:CD	2.22	0.47
1:A:367:THR:O	1:A:367:THR:CG2	2.63	0.47
1:A:40:TYR:CE2	1:A:44:ILE:HD11	2.50	0.46
1:A:126:ILE:O	1:A:130:HIS:HD2	1.98	0.46
1:A:358:ASN:HB2	2:A:838:HOH:O	2.16	0.46
1:A:4:LYS:HB3	1:A:713:ILE:HG23	1.97	0.46
1:A:136:TYR:O	1:A:137:SER:HB2	2.16	0.46
1:A:683:LEU:O	1:A:708:MET:HB2	2.16	0.46
1:A:33:TRP:CH2	1:A:35:PRO:HG3	2.51	0.46
1:A:33:TRP:CZ3	1:A:35:PRO:HG3	2.50	0.46
1:A:691:ASN:ND2	1:A:694:ILE:HG13	2.31	0.45
1:A:195:ASP:OD2	1:A:199:LYS:HG3	2.17	0.45
1:A:329:ASN:HD22	1:A:355:LYS:HE3	1.80	0.45
1:A:156:ALA:HB2	1:A:164:ILE:HG13	1.99	0.45
1:A:40:TYR:CD1	1:A:72:LEU:HD12	2.52	0.45
1:A:286:ARG:HB3	1:A:325:ILE:HG21	1.99	0.45
1:A:672:ILE:C	1:A:674:PRO:HD2	2.37	0.45
1:A:322:ARG:CG	1:A:322:ARG:NH1	2.77	0.44
1:A:183:THR:CG2	1:A:184:ARG:H	2.29	0.44
1:A:347:ALA:O	1:A:351:GLU:HG2	2.17	0.44

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:277:VAL:O	1:A:322:ARG:NH1	2.51	0.44
1:A:418:SER:C	1:A:420:GLU:N	2.69	0.44
1:A:210:ILE:HD11	1:A:676:LEU:HD12	1.99	0.44
1:A:354:ILE:CD1	1:A:411:THR:OG1	2.66	0.44
1:A:700:LYS:C	1:A:702:ASN:H	2.20	0.44
1:A:184:ARG:HG3	1:A:188:LEU:O	2.18	0.44
1:A:15:THR:HG23	1:A:685:ALA:CA	2.46	0.43
1:A:407:ILE:CD1	1:A:651:LEU:HD11	2.45	0.43
1:A:666:GLN:HB3	1:A:694:ILE:HD11	1.98	0.43
1:A:193:ILE:HG22	1:A:194:LEU:CD1	2.48	0.43
1:A:175:VAL:HG22	1:A:204:LEU:HD22	1.99	0.43
1:A:5:TYR:CE1	1:A:18:SER:HB3	2.52	0.43
1:A:691:ASN:HD22	1:A:694:ILE:HG13	1.83	0.43
1:A:282:LEU:HG	1:A:326:ILE:CD1	2.47	0.43
1:A:293:ALA:HA	1:A:296:MET:HG2	2.00	0.43
1:A:239:SER:O	1:A:242:GLY:N	2.49	0.43
1:A:687:LYS:HE2	1:A:707:ASN:HB3	2.00	0.43
1:A:158:VAL:HG21	1:A:179:ARG:HB3	2.01	0.43
1:A:197:THR:HG1	1:A:199:LYS:HG2	1.83	0.43
1:A:352:VAL:O	1:A:356:VAL:HG12	2.18	0.43
1:A:333:LYS:NZ	2:A:825:HOH:O	2.52	0.42
1:A:166:CYS:HB2	1:A:204:LEU:HD21	2.01	0.42
1:A:248:VAL:HG22	1:A:249:ASP:N	2.34	0.42
1:A:692:GLU:HG2	1:A:693:GLU:N	2.34	0.42
1:A:21:ARG:NH2	2:A:801:HOH:O	2.52	0.42
1:A:26:THR:HG22	1:A:54:ILE:HD13	2.02	0.42
1:A:381:LEU:O	1:A:385:GLU:HG3	2.19	0.41
1:A:182:HIS:NE2	1:A:183:THR:OG1	2.53	0.41
1:A:673:TRP:N	1:A:674:PRO:CD	2.84	0.41
1:A:351:GLU:OE1	1:A:411:THR:HG23	2.20	0.41
1:A:695:THR:HG22	1:A:699:ILE:CD1	2.51	0.41
1:A:343:SER:O	1:A:345:VAL:N	2.41	0.41
1:A:25:VAL:HG13	1:A:146:TYR:CG	2.56	0.41
1:A:51:ILE:HA	1:A:51:ILE:HD13	1.90	0.41
1:A:69:ALA:O	1:A:73:LEU:HG	2.21	0.41
1:A:208:SER:O	1:A:209:ALA:HB2	2.20	0.41
1:A:203:THR:O	1:A:204:LEU:CB	2.68	0.41
1:A:368:LYS:HA	1:A:369:PRO:HD3	1.93	0.41
1:A:695:THR:HG22	1:A:699:ILE:HD11	2.03	0.41
1:A:397:ASP:N	1:A:399:LYS:HZ2	2.19	0.40
1:A:88:TYR:HB3	1:A:134:LEU:CD2	2.51	0.40

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:676:LEU:O	1:A:678:SER:N	2.48	0.40
1:A:238:LEU:HD23	1:A:242:GLY:O	2.20	0.40
1:A:647:VAL:HG13	1:A:648:ASN:N	2.36	0.40
1:A:90:THR:HG21	1:A:161:GLY:O	2.21	0.40
1:A:81:PHE:HA	1:A:85:ILE:HB	2.02	0.40
1:A:126:ILE:O	1:A:130:HIS:CD2	2.75	0.40
1:A:4:LYS:HB3	1:A:713:ILE:CG2	2.51	0.40
1:A:280:LEU:HD11	1:A:338:LYS:HD2	2.03	0.40
1:A:64:ILE:HG13	1:A:65:GLU:N	2.37	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	491/717 (68%)	441 (90%)	37 (8%)	13 (3%)	<b>7</b> <b>10</b>

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	2	THR
1	A	344	GLU
1	A	627	PHE
1	A	685	ALA
1	A	688	GLN
1	A	312	ASN
1	A	329	ASN
1	A	701	LYS
1	A	335	PRO
1	A	420	GLU
1	A	691	ASN
1	A	637	LYS

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	A	242	GLY

### 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	457/651 (70%)	432 (94%)	25 (6%)	27	48

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	25	VAL
1	A	28	LEU
1	A	37	LYS
1	A	59	LEU
1	A	67	LEU
1	A	78	THR
1	A	90	THR
1	A	119	LEU
1	A	134	LEU
1	A	149	LEU
1	A	186	ASN
1	A	206	ARG
1	A	261	VAL
1	A	276	GLN
1	A	313	ASN
1	A	322	ARG
1	A	345	VAL
1	A	364	LEU
1	A	405	ASN
1	A	420	GLU
1	A	647	VAL
1	A	648	ASN
1	A	660	LEU
1	A	673	TRP

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

Mol	Chain	Res	Type
1	A	42	GLN
1	A	130	HIS
1	A	138	GLN
1	A	189	ASN
1	A	313	ASN
1	A	329	ASN
1	A	358	ASN
1	A	386	GLN
1	A	405	ASN
1	A	691	ASN

### 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](#)

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	499/717 (69%)	0.45	42 (8%) 14 14	22, 47, 85, 101	0

All (42) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	197	THR	7.0
1	A	418	SER	5.0
1	A	636	ASP	5.0
1	A	196	ALA	4.9
1	A	419	LYS	4.6
1	A	417	LEU	4.5
1	A	677	LYS	3.9
1	A	310	ASN	3.7
1	A	685	ALA	3.6
1	A	637	LYS	3.3
1	A	312	ASN	3.3
1	A	397	ASP	3.3
1	A	246	ILE	3.1
1	A	257	LEU	3.0
1	A	221	GLN	3.0
1	A	679	ARG	2.8
1	A	635	ILE	2.7
1	A	211	ILE	2.7
1	A	404	ASP	2.7
1	A	714	VAL	2.7
1	A	416	PRO	2.7
1	A	245	ILE	2.6
1	A	261	VAL	2.6
1	A	234	LEU	2.6
1	A	212	THR	2.6
1	A	388	GLU	2.5
1	A	422	THR	2.4

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	A	195	ASP	2.4
1	A	702	ASN	2.4
1	A	309	GLU	2.4
1	A	176	TYR	2.3
1	A	239	SER	2.2
1	A	306	LYS	2.2
1	A	638	THR	2.2
1	A	399	LYS	2.2
1	A	340	CYS	2.1
1	A	700	LYS	2.1
1	A	206	ARG	2.1
1	A	240	SER	2.1
1	A	241	ASP	2.1
1	A	333	LYS	2.0
1	A	177	ALA	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.