

Full wwPDB X-ray Structure Validation Report (i)

Jan 23, 2021 - 03:37 PM EST

PDB ID	:	1TYH
Title	:	Crystal Structure of Transcriptional Activator tenA from Bacillus subtilis
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Deposited on	:	2004-07-07
Resolution	:	2.54 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 (i) symbol.

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

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
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 (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY \, DIFFRACTION$

The reported resolution of this entry is 2.54 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.



Motria	Whole archive	Similar resolution		
wietric	$(\# { m Entries})$	$(\# { m Entries}, { m resolution} { m range}({ m \AA}))$		
Clashscore	141614	$1332 \ (2.56-2.52)$		
Ramachandran outliers	138981	1315 (2.56-2.52)		
Sidechain outliers	138945	1315(2.56-2.52)		

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 <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain				
1	А	248	63%		24%	•	11%
1	В	248	62%		24%	•	11%
1	D	248	35%	48%	6	5%	11%
1	Е	248	40%	44%		6%	11%



$1\mathrm{TYH}$

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 7252 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.

Mol	Chain	Residues		Atoms					ZeroOcc	AltConf	Trace
1	Λ	221	Total	С	Ν	0	S	Se	0	0	0
1	Л	221	1783	1154	287	334	3	5	0	0	0
1	В	221	Total	С	Ν	0	S	Se	0	0	0
1	D	221	1783	1154	287	334	3	5	0	0	U
1	Л	221	Total	С	Ν	0	S	Se	0	0	0
	D	221	1791	1158	287	338	3	5	0	0	0
1	F	221	Total	С	Ν	0	S	Se	0	0	0
		221	1783	1154	287	334	3	5		U	U

• Molecule 1 is a protein called Transcriptional activator tenA.

There are 72 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual Comment		Reference
А	-1	MSE	-	cloning artifact	UNP P25052
А	0	SER	-	cloning artifact	UNP P25052
А	1	LEU	-	cloning artifact	UNP P25052
А	71	MSE	MET	modified residue	UNP P25052
А	83	MSE	MET	modified residue	UNP P25052
А	116	MSE	MET	modified residue	UNP P25052
А	194	MSE	MET	modified residue	UNP P25052
А	211	MSE	MET	modified residue	UNP P25052
А	237	GLU	-	expression tag	UNP P25052
А	238	GLY	-	expression tag	UNP P25052
А	239	GLY	-	expression tag	UNP P25052
А	240	SER	-	expression tag	UNP P25052
А	241	HIS	-	expression tag	UNP P25052
А	242	HIS	-	expression tag	UNP P25052
А	243	HIS	-	expression tag	UNP P25052
А	244	HIS	-	expression tag	UNP P25052
А	245	HIS	-	expression tag	UNP P25052
А	246	HIS	-	expression tag	UNP P25052
В	-1	MSE	-	cloning artifact	UNP P25052
В	0	SER	-	cloning artifact	UNP P25052
В	1	LEU	-	cloning artifact	UNP P25052



Chain	Residue	Modelled	Actual	Comment	Reference
В	71	MSE	MET	modified residue	UNP P25052
В	83	MSE	MET	modified residue	UNP P25052
В	116	MSE	MET	modified residue	UNP P25052
В	194	MSE	MET	modified residue	UNP P25052
В	211	MSE	MET	modified residue	UNP P25052
В	237	GLU	-	expression tag	UNP P25052
В	238	GLY	-	expression tag	UNP P25052
В	239	GLY	-	expression tag	UNP P25052
В	240	SER	-	expression tag	UNP P25052
В	241	HIS	_	expression tag	UNP P25052
В	242	HIS	-	expression tag	UNP P25052
В	243	HIS	_	expression tag	UNP P25052
В	244	HIS	-	expression tag	UNP P25052
В	245	HIS	-	expression tag	UNP P25052
В	246	HIS	-	expression tag	UNP P25052
D	-1	MSE	-	cloning artifact	UNP P25052
D	0	SER	-	cloning artifact	UNP P25052
D	1	LEU	-	cloning artifact	UNP P25052
D	71	MSE	MET	modified residue	UNP P25052
D	83	MSE	MET	modified residue	UNP P25052
D	116	MSE	MET	modified residue	UNP P25052
D	194	MSE	MET	modified residue	UNP P25052
D	211	MSE	MET	modified residue	UNP P25052
D	237	GLU	_	expression tag	UNP P25052
D	238	GLY	-	expression tag	UNP P25052
D	239	GLY	-	expression tag	UNP P25052
D	240	SER	-	expression tag	UNP P25052
D	241	HIS	-	expression tag	UNP P25052
D	242	HIS	-	expression tag	UNP P25052
D	243	HIS	-	expression tag	UNP P25052
D	244	HIS	-	expression tag	UNP P25052
D	245	HIS	-	expression tag	UNP P25052
D	246	HIS	_	expression tag	UNP P25052
Е	-1	MSE	_	cloning artifact	UNP P25052
Е	0	SER	-	cloning artifact	UNP P25052
Е	1	LEU	_	cloning artifact	UNP P25052
Е	71	MSE	MET	modified residue	UNP P25052
Е	83	MSE	MET	modified residue	UNP P25052
Е	116	MSE	MET	modified residue	UNP P25052
Е	194	MSE	MET	modified residue	UNP P25052
Е	211	MSE	MET	modified residue	UNP P25052
Е	237	GLU	-	expression tag	UNP P25052



Chain	Residue	Modelled	Actual	Comment	Reference
Е	238	GLY	-	expression tag	UNP P25052
Е	239	GLY	-	expression tag	UNP P25052
E	240	SER	-	expression tag	UNP P25052
E	241	HIS	-	expression tag	UNP P25052
E	242	HIS	-	expression tag	UNP P25052
Е	243	HIS	-	expression tag	UNP P25052
Е	244	HIS	-	expression tag	UNP P25052
E	245	HIS	-	expression tag	UNP P25052
Е	246	HIS	-	expression tag	UNP P25052

• Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	А	36	Total O 36 36	0	0
2	В	34	$\begin{array}{cc} \text{Total} & \text{O} \\ 34 & 34 \end{array}$	0	0
2	D	17	Total O 17 17	0	0
2	Ε	25	$\begin{array}{cc} \text{Total} & \text{O} \\ 25 & 25 \end{array}$	0	0



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. 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. 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.

Note EDS was not executed.



• Molecule 1: Transcriptional activator tenA

• Molecule 1: Transcriptional activator tenA



• Molecule 1: Transcriptional activator tenA



V213 V214 F2216 F2216 F2216 V2217 V2

• Molecule 1: Transcriptional activator tenA





4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source	
Space group	P 41	Depositor	
Cell constants	58.43Å 58.43Å 297.54Å	Depositor	
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor	
Resolution (Å)	50.00 - 2.54	Depositor	
% Data completeness	96.9 (50.00-2.54)	Depositor	
(in resolution range)		Depositor	
R_{merge}	0.07	Depositor	
R_{sym}	(Not available)	Depositor	
Refinement program	CNS 1.0	Depositor	
R, R_{free}	0.244 , 0.304	Depositor	
Estimated twinning fraction	No twinning to report.	Xtriage	
Total number of atoms	7252	wwPDB-VP	
Average B, all atoms $(Å^2)$	49.0	wwPDB-VP	



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).

Mal	Chain	Bond	lengths	Bond angles		
	Unam	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	0.44	0/1836	0.60	1/2483~(0.0%)	
1	В	0.44	0/1836	0.60	1/2483~(0.0%)	
1	D	0.46	0/1844	0.62	0/2493	
1	Е	0.45	0/1836	0.62	0/2483	
All	All	0.45	0/7352	0.61	2/9942~(0.0%)	

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	В	214	ARG	N-CA-C	-5.92	95.01	111.00
1	А	214	ARG	N-CA-C	-5.90	95.06	111.00

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	А	1783	0	1625	50	0
1	В	1783	0	1625	56	0
1	D	1791	0	1633	144	0
1	Е	1783	0	1625	136	0
2	А	36	0	0	8	0
2	В	34	0	0	7	0
2	D	17	0	0	5	0



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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	Е	25	0	0	7	0
All	All	7252	0	6508	374	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 27.

All (374) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom 1	Atom 2	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:A:99:GLU:HG3	2:A:268:HOH:O	1.46	1.11
1:A:220:ASP:HB2	2:A:272:HOH:O	1.71	0.90
1:E:151:PRO:HG2	1:E:157:GLN:OE1	1.70	0.90
1:D:155:ILE:HG23	1:D:156:TYR:CD1	2.09	0.88
1:A:86:HIS:CB	2:A:271:HOH:O	2.22	0.87
1:D:138:LEU:O	1:D:138:LEU:HD23	1.76	0.86
1:E:31:THR:HB	2:E:263:HOH:O	1.76	0.85
1:D:93:LEU:HD13	1:D:155:ILE:HD11	1.58	0.85
1:A:85:LEU:O	1:A:89:PHE:HB2	1.77	0.84
1:D:86:HIS:O	1:D:90:ALA:HB2	1.78	0.82
1:D:42:LEU:HD21	1:D:95:ILE:HD13	1.62	0.81
1:D:88:GLU:HG3	1:D:89:PHE:CD1	2.14	0.81
1:B:189:GLU:H	1:B:189:GLU:CD	1.84	0.81
1:D:70:ARG:HD2	1:D:174:GLU:OE2	1.82	0.80
1:E:155:ILE:HG23	1:E:156:TYR:HD1	1.48	0.79
1:D:166:ASP:O	1:D:170:GLN:HG3	1.82	0.78
1:E:2:LYS:HB2	1:E:180:ASP:OD1	1.82	0.78
1:E:88:GLU:HG3	1:E:89:PHE:CD1	2.19	0.77
1:E:166:ASP:O	1:E:170:GLN:HG3	1.83	0.77
1:E:86:HIS:O	1:E:90:ALA:HB2	1.84	0.77
1:D:195:LYS:O	1:D:199:VAL:HG23	1.83	0.77
1:E:71:MSE:HE3	1:E:71:MSE:HA	1.66	0.76
1:E:133:LEU:HB3	1:E:134:PRO:HD3	1.67	0.76
1:A:140:TYR:OH	1:A:169:ARG:HD2	1.86	0.76
1:D:179:PHE:CE1	1:D:194:MSE:HE2	2.21	0.75
1:E:189:GLU:H	1:E:189:GLU:CD	1.88	0.75
1:E:95:ILE:HG22	1:E:96:SER:N	2.02	0.74
1:D:155:ILE:HG23	1:D:156:TYR:HD1	1.49	0.74
1:B:85:LEU:O	1:B:89:PHE:HB2	1.89	0.73
1:D:168:PHE:HB2	2:D:252:HOH:O	1.89	0.73
1:E:154:PRO:HA	1:E:157:GLN:HG3	1.70	0.73
1:E:93:LEU:HD13	1:E:155:ILE:HD11	1.69	0.73



	lo ao pagom	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:B:70:ARG:O	1:B:73:SER:HB3	1.89	0.72
1:E:155:ILE:HG23	1:E:156:TYR:CD1	2.24	0.72
1:E:70:ARG:HD2	1:E:174:GLU:OE2	1.89	0.72
1:E:27:ILE:HA	1:E:156:TYR:CE2	2.25	0.72
1:D:189:GLU:H	1:D:189:GLU:CD	1.94	0.71
1:B:8:ARG:NH1	2:B:273:HOH:O	2.23	0.70
1:E:187:THR:O	1:E:191:ARG:HG3	1.91	0.70
1:B:114:SER:HB3	1:E:114:SER:HB3	1.72	0.69
1:E:15:TRP:CD2	1:E:138:LEU:HD12	2.26	0.69
1:D:178:ARG:HG2	1:D:182:LEU:HD11	1.75	0.69
1:A:208:PHE:HA	1:A:211:MSE:HG2	1.74	0.69
1:E:172:VAL:O	1:E:176:ILE:HG13	1.92	0.68
1:D:190:VAL:O	1:D:194:MSE:HG3	1.94	0.68
1:E:195:LYS:O	1:E:199:VAL:HG23	1.93	0.68
1:D:71:MSE:HA	1:D:71:MSE:HE3	1.76	0.68
1:D:214:ARG:HG2	1:D:214:ABG:O	1.94	0.68
1:E:64:ASP:OD2	1:E:66:TYB:HB3	1.93	0.68
1:D:154:PRO:HA	1:D:157:GLN:HG3	1.75	0.67
1:B:135:CYS:HA	1:B:205:GLU:OE2	1.95	0.67
1:D:153:HIS:HB3	1:D:155:ILE:HG22	1.76	0.67
1:E:32:LEU:HB3	1:E:156:TYR:OH	1.95	0.67
1:E:153:HIS:HB3	1:E:155:ILE:HG22	1.77	0.66
1:D:151:PRO:HG2	1:D:157:GLN:OE1	1.95	0.66
1:E:168:PHE:HB2	2:E:251:HOH:O	1.96	0.66
1:D:38:LYS:HA	1:D:93:LEU:HD21	1.78	0.66
1:D:89:PHE:O	1:D:93:LEU:HB2	1.96	0.65
1:E:146:LEU:HB3	1:E:160:ILE:HD13	1.77	0.65
1:E:13:GLU:HB2	2:E:252:HOH:O	1.97	0.65
1:E:146:LEU:HB3	1:E:160:ILE:CD1	2.26	0.65
1:B:177:ASN:O	1:B:181:GLU:HG3	1.97	0.64
1:D:2:LYS:HB2	1:D:180:ASP:OD1	1.97	0.64
1:D:2:LYS:HG3	1:D:5:GLU:CG	2.28	0.64
1:E:51:PHE:O	1:E:55:GLN:HG3	1.97	0.64
1:D:154:PRO:HA	1:D:157:GLN:CG	2.27	0.64
1:B:96:SER:O	1:B:99:GLU:HB2	1.98	0.64
1:D:34:ILE:HG23	1:D:35:ASP:N	2.13	0.64
1:B:63:LYS:HA	1:B:63:LYS:HE2	1.80	0.64
1:B:8:ARG:HG2	1:B:8:ARG:HH11	1.63	0.64
1:D:146:LEU:HB3	1:D:160:ILE:HD13	1.80	0.63
1:E:38:LYS:HA	1:E:93:LEU:HD21	1.81	0.63
1:D:170:GLN:HB2	1:D:171:GLN:NE2	2.13	0.63



	jugen	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:E:146:LEU:O	1:E:160:ILE:HD13	1.99	0.63
1:D:2:LYS:CG	1:D:5:GLU:HG3	2.29	0.63
1:D:167:TRP:HE3	2:D:252:HOH:O	1.80	0.63
1:E:167:TRP:HE3	2:E:251:HOH:O	1.82	0.63
1:A:65:LEU:HD23	1:E:82:GLU:HG2	1.81	0.63
1:A:70:ARG:O	1:A:73:SER:HB3	1.99	0.62
1:D:170:GLN:HB2	1:D:171:GLN:HE21	1.64	0.62
1:D:2:LYS:HG3	1:D:5:GLU:HG3	1.79	0.62
1:D:153:HIS:HB3	1:D:155:ILE:CG2	2.29	0.62
1:E:27:ILE:HA	1:E:156:TYR:CD2	2.35	0.62
1:E:88:GLU:HG3	1:E:89:PHE:CE1	2.35	0.62
2:A:277:HOH:O	1:E:53:LYS:HE2	2.00	0.62
1:A:95:ILE:HG22	2:A:256:HOH:O	2.00	0.61
1:E:34:ILE:HG23	1:E:35:ASP:N	2.16	0.61
1:A:153:HIS:O	1:A:157:GLN:HG2	2.00	0.61
1:E:214:ARG:O	1:E:214:ARG:HG2	2.01	0.61
1:D:193:LYS:NZ	1:D:197:ASN:HD21	1.97	0.61
1:E:94:GLU:O	1:E:95:ILE:HB	2.00	0.61
1:E:155:ILE:HG23	1:E:156:TYR:N	2.16	0.60
1:E:93:LEU:HD13	1:E:155:ILE:CD1	2.30	0.60
1:A:43:GLN:CB	1:A:211:MSE:HE1	2.31	0.60
1:D:94:GLU:O	1:D:95:ILE:HB	2.01	0.60
1:D:26:GLY:HA2	1:D:31:THR:OG1	2.01	0.60
1:D:134:PRO:HG3	1:D:198:PHE:CD1	2.37	0.60
1:E:155:ILE:HG23	1:E:156:TYR:H	1.67	0.59
1:E:140:TYR:OH	1:E:169:ARG:HD2	2.02	0.59
1:D:116:MSE:HE2	1:D:131:ALA:O	2.02	0.59
1:B:116:MSE:HE1	2:B:258:HOH:O	2.03	0.58
1:E:4:SER:OG	1:E:137:TRP:CZ3	2.56	0.58
1:A:177:ASN:HB2	2:A:274:HOH:O	2.04	0.58
1:B:135:CYS:HB2	2:B:258:HOH:O	2.03	0.58
1:E:190:VAL:O	1:E:194:MSE:HG3	2.03	0.58
1:E:95:ILE:O	1:E:96:SER:HB3	2.04	0.58
1:A:189:GLU:CD	1:A:189:GLU:H	2.07	0.58
1:B:65:LEU:HD13	1:D:49:THR:HA	1.86	0.58
1:E:26:GLY:O	1:E:156:TYR:HE2	1.88	0.57
1:B:208:PHE:O	1:B:211:MSE:HG3	2.03	0.57
1:D:89:PHE:O	1:D:93:LEU:CB	2.51	0.57
1:A:87:ARG:O	1:A:90:ALA:HB3	2.04	0.57
1:E:156:TYR:O	1:E:159:TRP:HB3	2.04	0.57
1:A:63:LYS:HE2	1:A:63:LYS:HA	1.86	0.57



		Interatomic	Clash
Atom-1	Atom-2	distance (\AA)	overlap (Å)
1:D:4:SER:OG	1:D:137:TRP:CZ3	2.57	0.57
1:A:193:LYS:HE2	2:A:257:HOH:O	2.05	0.57
1:E:140:TYR:O	1:E:144:GLU:N	2.36	0.56
1:E:29:ASP:O	1:E:31:THR:N	2.38	0.56
1:A:114:SER:OG	1:D:118:ARG:HD2	2.05	0.56
1:D:36:ARG:HD3	1:D:213:TYR:O	2.05	0.56
1:D:29:ASP:O	1:D:31:THR:N	2.38	0.56
1:E:44:ASP:O	1:E:47:TYR:HB3	2.05	0.56
1:A:43:GLN:HB2	1:A:211:MSE:HE1	1.87	0.56
1:B:208:PHE:HA	1:B:211:MSE:HG2	1.88	0.56
1:E:208:PHE:O	1:E:211:MSE:HG3	2.05	0.56
1:D:93:LEU:CD1	1:D:155:ILE:HD11	2.34	0.55
1:D:27:ILE:C	1:D:29:ASP:H	2.09	0.55
1:A:36:ARG:HD3	1:A:213:TYR:O	2.06	0.55
1:E:95:ILE:O	1:E:96:SER:CB	2.54	0.55
1:D:107:PRO:HG2	1:D:216:GLU:CD	2.28	0.55
1:A:107:PRO:HG2	1:A:216:GLU:OE1	2.07	0.54
1:E:29:ASP:O	1:E:31:THR:HG23	2.06	0.54
1:E:107:PRO:HG2	1:E:216:GLU:CD	2.28	0.54
1:D:146:LEU:O	1:D:160:ILE:HD13	2.07	0.54
1:E:211:MSE:O	1:E:214:ARG:O	2.24	0.54
1:A:29:ASP:OD1	1:A:31:THR:HG23	2.08	0.54
1:B:140:TYR:OH	1:B:169:ARG:HD2	2.07	0.54
1:A:96:SER:O	1:A:99:GLU:HB2	2.08	0.54
1:D:187:THR:HG21	2:D:261:HOH:O	2.07	0.54
1:E:153:HIS:HB3	1:E:155:ILE:CG2	2.38	0.54
1:E:55:GLN:NE2	1:E:78:THR:OG1	2.40	0.54
1:B:188:GLU:HB2	1:B:189:GLU:OE2	2.08	0.54
1:D:134:PRO:HG3	1:D:198:PHE:CE1	2.42	0.54
1:D:27:ILE:HG22	1:D:28:GLY:N	2.22	0.54
1:B:193:LYS:HE2	2:B:261:HOH:O	2.08	0.53
1:D:18:SER:O	1:D:24:VAL:HG21	2.09	0.53
1:E:36:ARG:HD3	1:E:213:TYR:O	2.07	0.53
1:D:3:PHE:O	1:D:4:SER:C	2.47	0.53
1:E:187:THR:OG1	1:E:190:VAL:HG23	2.08	0.53
1:E:206:TYR:HA	1:E:209:TRP:CD1	2.43	0.53
1:E:134:PRO:HG3	1:E:198:PHE:CE1	2.44	0.53
1:D:178:ARG:C	1:D:182:LEU:HD12	2.29	0.53
1:D:178:ARG:HG2	1:D:182:LEU:CD1	2.39	0.53
1:E:188:GLU:HB2	1:E:189:GLU:OE2	2.09	0.53
1:E:133:LEU:O	1:E:136:TYR:HB2	2.09	0.53



	ti a	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:E:167:TRP:HB2	2:E:260:HOH:O	2.09	0.52
1:E:133:LEU:HD11	1:E:176:ILE:HG12	1.91	0.52
1:B:94:GLU:O	1:B:95:ILE:HB	2.09	0.52
1:A:208:PHE:O	1:A:211:MSE:HG3	2.09	0.52
1:D:38:LYS:HD3	1:D:42:LEU:HD11	1.91	0.52
1:D:52:ALA:HA	1:D:55:GLN:HE21	1.75	0.52
1:A:93:LEU:HG	1:A:155:ILE:CD1	2.40	0.52
1:B:76:GLN:O	1:B:79:TYR:HB3	2.11	0.51
1:E:89:PHE:HE2	1:E:155:ILE:O	1.94	0.51
1:E:61:TYR:O	1:E:63:LYS:HE3	2.10	0.51
1:D:95:ILE:HG22	1:D:96:SER:N	2.26	0.51
1:E:29:ASP:OD1	1:E:31:THR:HG23	2.10	0.51
1:A:15:TRP:HH2	1:A:137:TRP:CG	2.29	0.51
1:E:27:ILE:HG22	1:E:28:GLY:N	2.25	0.51
1:E:3:PHE:O	1:E:4:SER:C	2.49	0.50
1:D:88:GLU:HG3	1:D:89:PHE:CE1	2.45	0.50
1:D:99:GLU:O	1:D:102:ALA:N	2.44	0.50
1:D:34:ILE:HD11	1:D:155:ILE:HD13	1.94	0.50
1:E:181:GLU:O	1:E:185:ASN:HB2	2.12	0.50
1:D:36:ARG:HG3	2:D:259:HOH:O	2.12	0.50
1:E:13:GLU:CB	2:E:252:HOH:O	2.58	0.49
1:D:133:LEU:HB3	1:D:134:PRO:HD3	1.93	0.49
1:A:172:VAL:O	1:A:176:ILE:HG13	2.11	0.49
1:E:179:PHE:CE1	1:E:194:MSE:HE2	2.47	0.49
1:D:64:ASP:OD2	1:D:66:TYR:HB3	2.12	0.49
1:A:56:SER:HB2	1:E:60:ALA:HB2	1.94	0.49
1:B:95:ILE:O	1:B:99:GLU:HG3	2.12	0.49
1:E:31:THR:CB	2:E:263:HOH:O	2.45	0.49
1:B:27:ILE:O	1:B:151:PRO:HB3	2.13	0.49
1:E:116:MSE:HE2	1:E:131:ALA:O	2.12	0.49
1:E:25:GLN:C	1:E:27:ILE:N	2.66	0.49
1:A:8:ARG:HH11	1:A:8:ARG:HG2	1.77	0.49
1:B:64:ASP:OD2	1:B:66:TYR:HB3	2.13	0.49
1:E:178:ARG:HG2	1:E:182:LEU:HD11	1.95	0.49
1:D:34:ILE:CG2	1:D:35:ASP:N	2.75	0.48
1:B:8:ARG:HG2	1:B:8:ARG:NH1	2.24	0.48
1:B:37:PHE:O	1:B:41:VAL:HG23	2.13	0.48
1:E:124:ASN:OD1	1:E:126:ALA:HB3	2.14	0.48
1:E:4:SER:HA	1:E:179:PHE:HE2	1.78	0.48
1:B:15:TRP:HH2	1:B:137:TRP:CG	2.31	0.48
1:D:25:GLN:C	1:D:27:ILE:N	2.67	0.48



	,	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:E:89:PHE:O	1:E:93:LEU:HB2	2.13	0.48
1:A:121:LEU:HD22	1:D:117:TYR:HB3	1.95	0.48
1:B:121:LEU:CD2	1:E:117:TYR:HB3	2.44	0.48
1:A:115:HIS:O	1:A:118:ARG:HB3	2.13	0.48
1:E:167:TRP:O	1:E:170:GLN:HB2	2.14	0.48
1:D:178:ARG:O	1:D:182:LEU:HD12	2.14	0.47
1:E:88:GLU:H	1:E:88:GLU:HG2	1.52	0.47
1:A:37:PHE:O	1:A:41:VAL:HG23	2.14	0.47
1:B:153:HIS:O	1:B:157:GLN:HG2	2.15	0.47
1:D:135:CYS:O	1:D:139:TYR:HB2	2.14	0.47
1:E:157:GLN:H	1:E:157:GLN:HG2	1.30	0.47
1:B:81:ALA:O	1:B:82:GLU:C	2.51	0.47
1:A:93:LEU:HG	1:A:155:ILE:HD12	1.97	0.47
1:D:146:LEU:HB3	1:D:160:ILE:CD1	2.44	0.47
1:B:56:SER:HB2	1:D:60:ALA:HB2	1.96	0.47
1:D:138:LEU:HD23	1:D:138:LEU:C	2.35	0.47
1:D:158:LYS:O	1:D:162:THR:OG1	2.31	0.47
1:E:189:GLU:CD	1:E:189:GLU:N	2.64	0.47
1:E:203:TYR:O	1:E:207:GLN:HG2	2.14	0.47
1:A:155:ILE:HG23	1:A:156:TYR:CD1	2.50	0.47
1:D:70:ARG:O	1:D:73:SER:HB3	2.15	0.47
1:E:84:ALA:O	1:E:88:GLU:HG2	2.15	0.47
1:E:98:GLU:OE1	1:E:98:GLU:HA	2.14	0.47
1:D:172:VAL:HG12	1:D:176:ILE:HG13	1.96	0.47
1:D:168:PHE:O	1:D:171:GLN:HG2	2.14	0.47
1:E:153:HIS:O	1:E:156:TYR:N	2.47	0.47
1:E:35:ASP:O	1:E:38:LYS:HB3	2.15	0.47
1:B:85:LEU:HA	1:B:89:PHE:CD1	2.50	0.46
1:A:21:HIS:ND1	1:A:22:PRO:HD2	2.30	0.46
1:D:208:PHE:O	1:D:211:MSE:HG3	2.15	0.46
2:A:277:HOH:O	1:E:53:LYS:CE	2.61	0.46
1:A:116:MSE:HE2	1:A:131:ALA:O	2.16	0.46
1:B:117:TYR:HB3	1:E:121:LEU:HD22	1.98	0.46
1:D:140:TYR:OH	1:D:169:ARG:HD2	2.14	0.46
1:D:187:THR:O	1:D:191:ARG:HG3	2.15	0.46
1:D:26:GLY:O	1:D:32:LEU:HB3	2.15	0.46
1:B:140:TYR:HB2	1:B:172:VAL:HG21	1.97	0.46
1:D:187:THR:OG1	1:D:190:VAL:HG23	2.16	0.46
1:D:35:ASP:O	1:D:38:LYS:HB3	2.15	0.46
1:D:172:VAL:HG12	1:D:176:ILE:CD1	2.46	0.46
1:E:43:GLN:CB	1:E:211:MSE:HE1	2.45	0.46



	i agem	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:E:34:ILE:CG2	1:E:35:ASP:N	2.79	0.46
1:E:50:HIS:O	1:E:54:VAL:HG23	2.15	0.46
1:D:27:ILE:O	1:D:29:ASP:N	2.48	0.46
1:D:99:GLU:O	1:D:100:ARG:C	2.54	0.46
1:E:70:ARG:O	1:E:73:SER:HB3	2.15	0.46
1:D:50:HIS:O	1:D:54:VAL:HG23	2.15	0.45
1:D:36:ARG:CG	2:D:259:HOH:O	2.64	0.45
1:D:40:TYR:OH	1:D:139:TYR:OH	2.21	0.45
1:A:187:THR:HB	1:A:189:GLU:OE1	2.17	0.45
1:D:32:LEU:O	1:D:33:PRO:C	2.51	0.45
1:B:176:ILE:O	1:B:179:PHE:HB3	2.17	0.45
1:D:38:LYS:CD	1:D:42:LEU:HD11	2.47	0.45
1:D:76:GLN:O	1:D:79:TYR:HB3	2.16	0.45
1:A:81:ALA:O	1:A:82:GLU:C	2.55	0.45
1:D:187:THR:HB	1:D:189:GLU:OE1	2.17	0.45
1:D:34:ILE:HG23	1:D:35:ASP:H	1.80	0.45
1:E:26:GLY:HA2	1:E:31:THR:OG1	2.17	0.45
1:A:83:MSE:O	1:A:86:HIS:N	2.50	0.45
1:B:133:LEU:HB3	1:B:134:PRO:HD3	1.99	0.45
1:D:93:LEU:HD13	1:D:155:ILE:CD1	2.40	0.45
1:D:188:GLU:O	1:D:191:ARG:N	2.50	0.44
1:E:27:ILE:O	1:E:156:TYR:HD2	2.01	0.44
1:E:206:TYR:HA	1:E:209:TRP:HD1	1.82	0.44
1:D:140:TYR:O	1:D:141:GLU:C	2.55	0.44
1:D:16:GLU:HA	1:D:19:PHE:CD2	2.52	0.44
1:E:18:SER:O	1:E:24:VAL:HG21	2.17	0.44
1:A:8:ARG:NH1	1:A:8:ARG:HG2	2.31	0.44
1:D:156:TYR:N	1:D:156:TYR:CD1	2.85	0.44
1:B:94:GLU:O	1:B:95:ILE:CB	2.65	0.44
1:D:70:ARG:HH11	1:D:70:ARG:HA	1.82	0.44
1:D:81:ALA:O	1:D:84:ALA:HB3	2.17	0.44
1:D:156:TYR:N	1:D:156:TYR:HD1	2.15	0.44
1:E:8:ARG:HG2	1:E:8:ARG:HH11	1.82	0.44
1:B:195:LYS:HD3	2:B:272:HOH:O	2.17	0.44
1:D:140:TYR:O	1:D:143:GLY:N	2.51	0.44
1:D:133:LEU:HD11	1:D:176:ILE:HG12	2.00	0.44
1:E:140:TYR:CZ	1:E:144:GLU:OE2	2.71	0.44
1:E:188:GLU:OE1	1:E:191:ARG:HD3	2.18	0.44
1:A:53:LYS:HD3	1:A:117:TYR:OH	2.18	0.43
1:D:124:ASN:OD1	1:D:126:ALA:HB3	2.18	0.43
1:D:95:ILE:CG2	1:D:96:SER:N	2.81	0.43



		Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:E:88:GLU:C	1:E:90:ALA:H	2.20	0.43
1:B:52:ALA:HA	1:B:55:GLN:HE21	1.83	0.43
1:A:117:TYR:HB3	1:D:121:LEU:HD22	2.00	0.43
1:E:25:GLN:C	1:E:27:ILE:H	2.21	0.43
1:D:14:TRP:CG	1:D:203:TYR:HA	2.54	0.43
1:D:34:ILE:CG2	1:D:35:ASP:H	2.31	0.43
1:D:27:ILE:C	1:D:29:ASP:N	2.72	0.43
1:E:94:GLU:O	1:E:95:ILE:CB	2.63	0.43
1:D:203:TYR:O	1:D:207:GLN:HG2	2.18	0.43
1:D:36:ARG:NH1	1:D:213:TYR:CE2	2.87	0.43
1:B:93:LEU:O	1:B:94:GLU:CB	2.67	0.43
1:D:31:THR:O	1:D:32:LEU:C	2.56	0.43
1:E:31:THR:O	1:E:32:LEU:C	2.57	0.43
1:E:55:GLN:OE1	1:E:136:TYR:OH	2.34	0.43
1:D:157:GLN:HG2	1:D:157:GLN:H	1.38	0.43
1:D:188:GLU:HB2	1:D:189:GLU:OE2	2.18	0.43
1:A:16:GLU:HA	1:A:19:PHE:CD2	2.54	0.43
1:B:121:LEU:HD12	1:B:121:LEU:HA	1.74	0.43
1:A:121:LEU:CD2	1:D:117:TYR:HB3	2.48	0.43
1:D:107:PRO:HD3	1:D:218:TRP:CE2	2.54	0.42
1:B:26:GLY:HA3	1:B:32:LEU:HB2	2.01	0.42
1:D:176:ILE:O	1:D:179:PHE:HB3	2.20	0.42
1:D:189:GLU:CD	1:D:189:GLU:N	2.69	0.42
1:B:89:PHE:O	1:B:93:LEU:HB2	2.18	0.42
1:D:22:PRO:HB2	1:D:213:TYR:CE1	2.55	0.42
1:E:95:ILE:HG22	1:E:96:SER:O	2.19	0.42
1:D:141:GLU:HA	1:D:144:GLU:HB2	2.00	0.42
1:E:19:PHE:CE1	1:E:145:LYS:HE3	2.54	0.42
1:E:202:SER:O	1:E:205:GLU:HB2	2.19	0.42
1:A:52:ALA:HA	1:A:55:GLN:HE21	1.84	0.42
1:B:169:ARG:O	1:B:173:GLU:HG3	2.19	0.42
1:D:165:GLY:C	1:D:167:TRP:H	2.22	0.42
1:D:172:VAL:O	1:D:173:GLU:C	2.58	0.42
1:E:71:MSE:CE	1:E:71:MSE:HA	2.44	0.42
1:D:112:TYR:CE1	1:D:116:MSE:HE3	2.54	0.42
1:D:89:PHE:HE2	1:D:155:ILE:O	2.02	0.42
1:D:211:MSE:O	1:D:214:ARG:O	2.37	0.42
1:D:25:GLN:C	1:D:27:ILE:H	2.22	0.42
1:D:29:ASP:OD1	1:D:31:THR:HG23	2.19	0.42
1:E:188:GLU:O	1:E:191:ARG:N	2.52	0.42
1:B:183:ALA:HB2	1:B:194:MSE:HE1	2.02	0.42



		Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:B:79:TYR:HA	1:D:65:LEU:HD21	2.02	0.42
1:D:97:GLU:C	1:D:97:GLU:CD	2.77	0.42
1:E:108:THR:HG1	1:E:216:GLU:CD	2.23	0.42
1:D:72:ALA:O	1:D:75:ALA:HB3	2.20	0.42
1:E:112:TYR:CE1	1:E:116:MSE:HE3	2.54	0.42
1:A:15:TRP:CD2	1:A:138:LEU:HD12	2.55	0.42
1:A:26:GLY:HA3	1:A:32:LEU:HB2	2.02	0.42
1:B:81:ALA:O	1:B:83:MSE:N	2.53	0.42
1:D:124:ASN:O	1:D:128:ILE:HG13	2.20	0.42
1:D:202:SER:O	1:D:205:GLU:HB2	2.20	0.42
1:E:89:PHE:O	1:E:93:LEU:CB	2.68	0.42
1:E:95:ILE:HG22	1:E:96:SER:H	1.82	0.42
1:D:32:LEU:HD21	1:D:37:PHE:HB2	2.02	0.42
1:E:22:PRO:CB	1:E:213:TYR:CE1	3.03	0.42
1:E:38:LYS:O	1:E:41:VAL:HB	2.20	0.42
1:B:42:LEU:HB2	2:B:268:HOH:O	2.19	0.41
1:D:27:ILE:HA	1:D:156:TYR:CD2	2.55	0.41
1:D:36:ARG:O	1:D:39:TYR:HB3	2.20	0.41
1:E:37:PHE:CD2	1:E:155:ILE:HD11	2.55	0.41
1:A:157:GLN:HG2	1:A:157:GLN:H	1.70	0.41
1:E:32:LEU:CB	1:E:156:TYR:OH	2.67	0.41
1:E:32:LEU:O	1:E:33:PRO:C	2.56	0.41
1:B:153:HIS:HA	1:B:154:PRO:HD3	1.91	0.41
1:B:63:LYS:HE3	2:B:259:HOH:O	2.21	0.41
1:D:12:ALA:O	1:D:13:GLU:C	2.58	0.41
1:D:29:ASP:OD1	1:D:29:ASP:O	2.38	0.41
1:E:188:GLU:O	1:E:191:ARG:HB2	2.20	0.41
1:E:4:SER:HG	1:E:137:TRP:HZ3	1.63	0.41
1:D:4:SER:HG	1:D:137:TRP:HZ3	1.61	0.41
1:A:34:ILE:HG13	1:A:93:LEU:CD2	2.50	0.41
1:D:199:VAL:O	1:D:202:SER:HB2	2.19	0.41
1:D:29:ASP:C	1:D:31:THR:H	2.23	0.41
1:E:22:PRO:HB2	1:E:213:TYR:CE1	2.55	0.41
1:B:134:PRO:HG3	1:B:198:PHE:CE1	2.56	0.41
1:B:155:ILE:HG23	1:B:156:TYR:CD1	2.56	0.41
1:D:88:GLU:HG2	1:D:88:GLU:H	1.54	0.41
1:A:86:HIS:O	1:A:90:ALA:HB2	2.21	0.41
1:B:175:GLN:OE1	1:B:175:GLN:HA	2.20	0.41
1:B:189:GLU:N	1:B:189:GLU:CD	2.62	0.41
1:B:95:ILE:O	1:B:96:SER:CB	2.69	0.41
1:B:15:TRP:HZ3	1:B:141:GLU:CD	2.24	0.41



Atom_1	Atom_2	Interatomic	Clash
Atom-1	Atom-2	distance (\AA)	overlap (Å)
1:E:15:TRP:CE2	1:E:138:LEU:HD12	2.56	0.41
1:E:209:TRP:O	1:E:212:ALA:HB3	2.21	0.41
1:E:34:ILE:HG23	1:E:35:ASP:H	1.85	0.41
1:D:167:TRP:O	1:D:171:GLN:NE2	2.40	0.40
1:B:38:LYS:C	1:B:38:LYS:HD2	2.41	0.40
1:D:153:HIS:HA	1:D:154:PRO:HD3	1.94	0.40
1:E:146:LEU:C	1:E:148:HIS:H	2.24	0.40
1:E:41:VAL:HG12	1:E:42:LEU:N	2.36	0.40
1:A:189:GLU:CD	1:A:189:GLU:N	2.74	0.40
1:E:3:PHE:O	1:E:4:SER:O	2.39	0.40
1:E:46:TYR:CE1	1:E:105:PRO:HG3	2.56	0.40
1:D:106:SER:O	1:D:107:PRO:C	2.60	0.40
1:E:155:ILE:CG2	1:E:156:TYR:H	2.33	0.40
1:E:74:HIS:O	1:E:77:GLY:N	2.55	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	А	219/248 (88%)	208~(95%)	9~(4%)	2(1%)	17 24
1	В	219/248~(88%)	206 (94%)	8 (4%)	5(2%)	6 6
1	D	219/248~(88%)	180 (82%)	30 (14%)	9~(4%)	3 1
1	Ε	219/248~(88%)	181 (83%)	30 (14%)	8 (4%)	3 2
All	All	876/992~(88%)	775 (88%)	77~(9%)	24 (3%)	5 4

All (24) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	30	GLY
	<u> </u>	1	,



Mol	Chain	Res	Type
1	D	95	ILE
1	D	187	THR
1	Е	95	ILE
1	Е	96	SER
1	В	95	ILE
1	Е	4	SER
1	Е	30	GLY
1	Е	136	TYR
1	Е	187	THR
1	В	94	GLU
1	D	44	ASP
1	D	136	TYR
1	Ε	151	PRO
1	Ε	216	GLU
1	А	220	ASP
1	В	82	GLU
1	В	216	GLU
1	D	29	ASP
1	В	96	SER
1	D	140	TYR
1	A	216	GLU
1	D	32	LEU
1	D	28	GLY

Continued from previou	s paqe
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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	А	175/201~(87%)	170~(97%)	5(3%)	42 57
1	В	175/201~(87%)	169~(97%)	6 (3%)	37 50
1	D	177/201 (88%)	161 (91%)	16 (9%)	9 11
1	Е	175/201 (87%)	167~(95%)	8 (5%)	27 36
All	All	702/804~(87%)	667~(95%)	35~(5%)	24 33

All (35) residues with a non-rotameric side chain are listed below:



\mathbf{Mol}	Chain	Res	Type
1	А	2	LYS
1	А	63	LYS
1	А	70	ARG
1	А	112	TYR
1	А	121	LEU
1	В	2	LYS
1	В	38	LYS
1	В	63	LYS
1	В	112	TYR
1	В	121	LEU
1	В	211	MSE
1	D	2	LYS
1	D	27	ILE
1	D	38	LYS
1	D	41	VAL
1	D	55	GLN
1	D	63	LYS
1	D	97	GLU
1	D	111	SER
1	D	139	TYR
1	D	144	GLU
1	D	145	LYS
1	D	157	GLN
1	D	185	ASN
1	D	186	SER
1	D	211	MSE
1	D	214	ARG
1	E	2	LYS
1	Е	27	ILE
1	E	63	LYS
1	Е	139	TYR
1	Ε	157	GLN
1	E	185	ASN
1	Е	211	MSE
1	E	214	ARG

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

Mol	Chain	Res	Type
1	А	197	ASN
1	А	207	GLN
1	В	55	GLN
1	В	197	ASN



Mol	Chain	Res	Type
1	В	207	GLN
1	D	25	GLN
1	D	55	GLN
1	D	148	HIS
1	D	171	GLN
1	D	207	GLN
1	Е	25	GLN
1	Е	55	GLN
1	Е	148	HIS
1	Е	207	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 monosaccharides 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 (i)

6.1 Protein, DNA and RNA chains (i)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.

