Full wwPDB X-ray Structure Validation Report (i)

Jan 31, 2016 – 10:28 PM GMT

PDB ID	:	1TRE
Title	:	THE STRUCTURE OF TRIOSEPHOSPHATE ISOMERASE FROM ESCHERICHIA COLI DETERMINED AT 2.6 ANGSTROM RESOLUTION
Authors	:	Noble, M.E.M.; Wierenga, R.K.
Deposited on	:	1992-10-12
Resolution	:	2.60 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

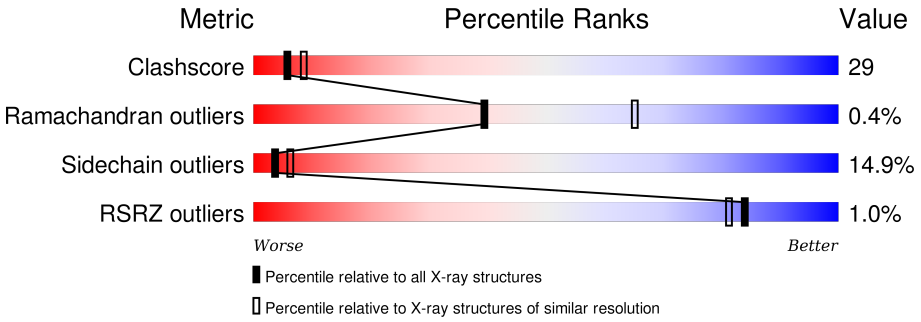
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	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 2.60 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))
Clashscore	102246	2679 (2.60-2.60)
Ramachandran outliers	100387	2635 (2.60-2.60)
Sidechain outliers	100360	2635 (2.60-2.60)
RSRZ outliers	91569	2334 (2.60-2.60)

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	255	2% 47% 38% 14%
1	B	255	44% 38% 15%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 3943 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 TRIOSEPHOSPHATE ISOMERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	255	Total	C	N	O	S	0	0	0
			1893	1187	334	362	10			
1	B	253	Total	C	N	O	S	0	0	0
			1878	1179	331	358	10			

- Molecule 2 is water.

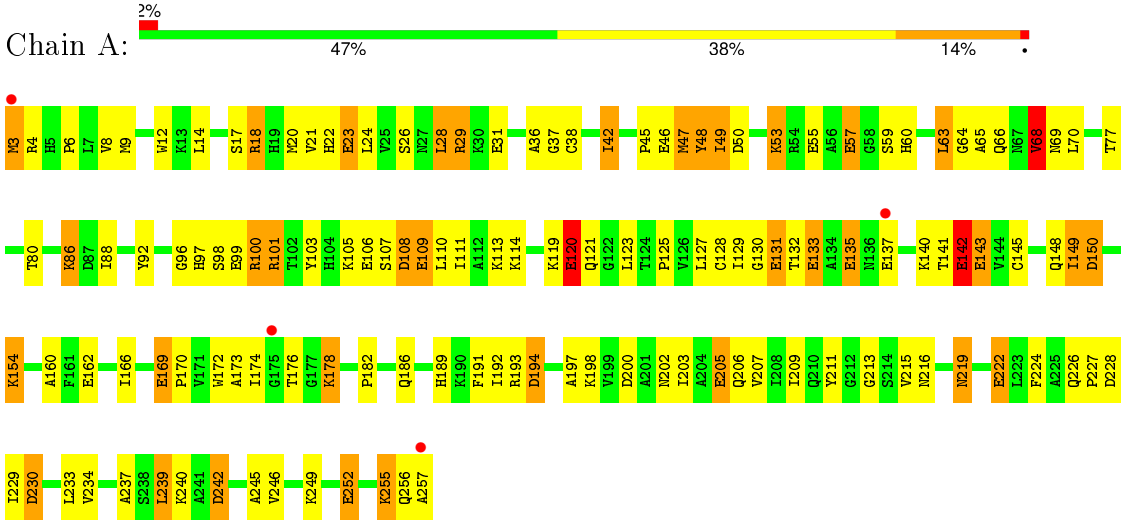
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	78	Total	O	0	0
			78	78		
2	B	94	Total	O	0	0
			94	94		

3 Residue-property plots (i)

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.

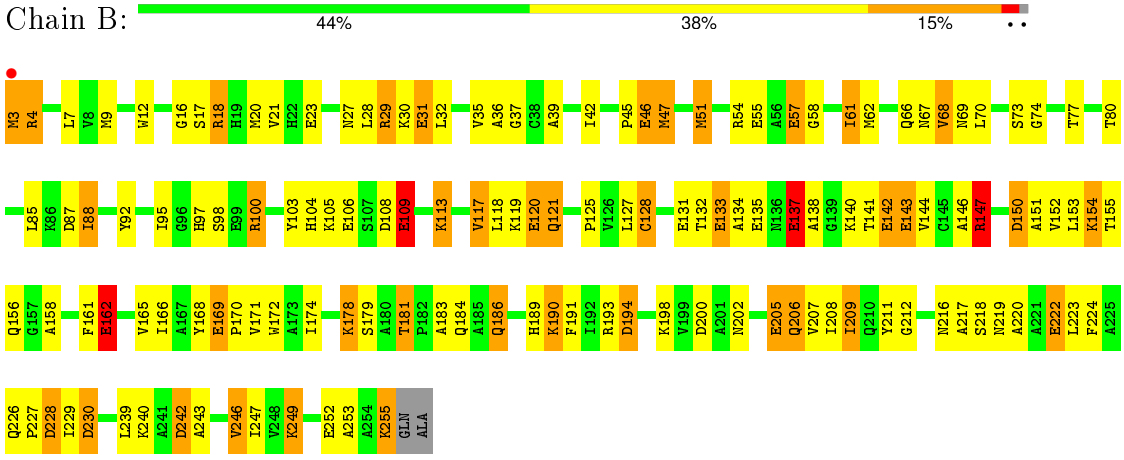
- Molecule 1: TRIOSEPHOSPHATE ISOMERASE

Chain A:



- Molecule 1: TRIOSEPHOSPHATE ISOMERASE

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	67.69Å 46.78Å 151.31Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	(Not available) – 2.60 24.09 – 2.60	Depositor EDS
% Data completeness (in resolution range)	(Not available) ((Not available)-2.60) 89.9 (24.09-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.67 (at 2.60Å)	Xtriage
Refinement program	TNT, X-PLOR	Depositor
R, R_{free}	0.119 , (Not available) 0.124 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å^2)	24.4	Xtriage
Anisotropy	0.307	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.23 , 113.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Outliers	0 of 13812 reflections	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	3943	wwPDB-VP
Average B, all atoms (Å^2)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.61% of the height of the origin peak. No significant pseudotranslation is detected.*

[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

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	1.17	17/1922 (0.9%)	1.49	23/2597 (0.9%)
1	B	1.20	19/1907 (1.0%)	1.45	25/2578 (1.0%)
All	All	1.18	36/3829 (0.9%)	1.47	48/5175 (0.9%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	6
All	All	0	7

All (36) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	46	GLU	CD-OE2	7.84	1.34	1.25
1	B	135	GLU	CD-OE1	7.61	1.34	1.25
1	B	205	GLU	CD-OE1	7.47	1.33	1.25
1	B	109	GLU	CD-OE1	7.46	1.33	1.25
1	B	120	GLU	CD-OE1	7.37	1.33	1.25
1	A	109	GLU	CD-OE1	7.35	1.33	1.25
1	A	131	GLU	CD-OE1	7.08	1.33	1.25
1	A	120	GLU	CD-OE1	6.88	1.33	1.25
1	B	31	GLU	CD-OE1	6.67	1.32	1.25
1	B	106	GLU	CD-OE2	6.63	1.32	1.25
1	A	169	GLU	CD-OE2	6.62	1.32	1.25
1	A	222	GLU	CD-OE1	6.56	1.32	1.25
1	B	142	GLU	CD-OE2	6.55	1.32	1.25
1	B	137	GLU	CD-OE2	6.54	1.32	1.25
1	A	205	GLU	CD-OE1	6.50	1.32	1.25
1	B	23	GLU	CD-OE1	6.45	1.32	1.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	23	GLU	CD-OE1	6.38	1.32	1.25
1	A	57	GLU	CD-OE1	6.34	1.32	1.25
1	B	222	GLU	CD-OE2	6.26	1.32	1.25
1	B	55	GLU	CD-OE2	6.08	1.32	1.25
1	B	162	GLU	CD-OE1	6.03	1.32	1.25
1	A	137	GLU	CD-OE2	6.00	1.32	1.25
1	A	31	GLU	CD-OE2	5.99	1.32	1.25
1	A	133	GLU	CD-OE1	5.71	1.31	1.25
1	A	143	GLU	CD-OE1	5.69	1.31	1.25
1	A	142	GLU	CD-OE2	5.68	1.31	1.25
1	B	57	GLU	CD-OE1	5.64	1.31	1.25
1	A	162	GLU	CD-OE2	5.52	1.31	1.25
1	B	133	GLU	CD-OE1	5.52	1.31	1.25
1	B	143	GLU	CD-OE1	5.51	1.31	1.25
1	B	169	GLU	CD-OE1	5.29	1.31	1.25
1	A	99	GLU	CD-OE1	-5.21	1.20	1.25
1	A	135	GLU	CD-OE1	5.20	1.31	1.25
1	B	131	GLU	CD-OE2	-5.16	1.20	1.25
1	A	252	GLU	CD-OE2	5.15	1.31	1.25
1	B	128	CYS	N-CA	-5.13	1.36	1.46

All (48) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	101	ARG	NE-CZ-NH1	15.31	127.95	120.30
1	A	101	ARG	NE-CZ-NH2	-11.71	114.45	120.30
1	A	230	ASP	CB-CG-OD2	-9.24	109.99	118.30
1	B	230	ASP	CB-CG-OD1	-8.47	110.68	118.30
1	B	108	ASP	CB-CG-OD1	8.16	125.64	118.30
1	B	147	ARG	NE-CZ-NH1	8.10	124.35	120.30
1	B	242	ASP	CB-CG-OD1	-8.08	111.03	118.30
1	B	194	ASP	CB-CG-OD2	-7.86	111.22	118.30
1	A	150	ASP	CB-CG-OD2	-7.74	111.33	118.30
1	B	242	ASP	CB-CG-OD2	7.63	125.17	118.30
1	B	230	ASP	CB-CG-OD2	7.59	125.13	118.30
1	B	127	LEU	O-C-N	7.58	134.84	122.70
1	A	200	ASP	CB-CG-OD1	7.35	124.92	118.30
1	A	18	ARG	NE-CZ-NH1	7.34	123.97	120.30
1	B	4	ARG	NE-CZ-NH1	-7.11	116.75	120.30
1	B	200	ASP	CB-CG-OD2	-7.07	111.94	118.30
1	B	150	ASP	CB-CG-OD2	-6.79	112.19	118.30
1	A	194	ASP	CB-CG-OD1	-6.73	112.25	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	228	ASP	CB-CG-OD1	-6.45	112.49	118.30
1	B	194	ASP	CB-CG-OD1	6.42	124.08	118.30
1	B	151	ALA	CB-CA-C	6.39	119.69	110.10
1	B	200	ASP	CB-CG-OD1	6.35	124.02	118.30
1	A	101	ARG	CD-NE-CZ	6.32	132.44	123.60
1	A	230	ASP	CB-CG-OD1	6.22	123.90	118.30
1	A	68	VAL	CB-CA-C	-6.17	99.67	111.40
1	A	48	TYR	CB-CG-CD1	-6.17	117.30	121.00
1	A	194	ASP	CB-CG-OD2	6.16	123.84	118.30
1	B	127	LEU	CA-C-N	-6.07	103.84	117.20
1	B	228	ASP	CB-CG-OD1	-6.03	112.88	118.30
1	A	150	ASP	CB-CG-OD1	5.94	123.65	118.30
1	A	242	ASP	CB-CG-OD2	-5.81	113.07	118.30
1	A	103	TYR	N-CA-CB	5.75	120.96	110.60
1	B	146	ALA	N-CA-CB	-5.71	102.11	110.10
1	B	108	ASP	CB-CG-OD2	-5.69	113.18	118.30
1	B	228	ASP	CB-CG-OD2	5.62	123.36	118.30
1	A	50	ASP	CB-CG-OD2	5.59	123.33	118.30
1	A	29	ARG	N-CA-CB	5.49	120.47	110.60
1	B	183	ALA	CB-CA-C	-5.40	102.00	110.10
1	A	65	ALA	N-CA-CB	5.39	117.64	110.10
1	A	100	ARG	NE-CZ-NH2	-5.27	117.66	120.30
1	A	193	ARG	NE-CZ-NH2	-5.27	117.66	120.30
1	B	23	GLU	CG-CD-OE1	-5.20	107.90	118.30
1	B	150	ASP	CB-CG-OD1	5.20	122.98	118.30
1	B	87	ASP	CB-CG-OD2	-5.14	113.68	118.30
1	B	121	GLN	CB-CA-C	-5.10	100.20	110.40
1	B	4	ARG	CD-NE-CZ	-5.05	116.53	123.60
1	A	228	ASP	CB-CG-OD2	5.05	122.84	118.30
1	A	108	ASP	CB-CG-OD1	5.02	122.82	118.30

There are no chirality outliers.

All (7) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	18	ARG	Mainchain
1	B	121	GLN	Mainchain
1	B	162	GLU	Mainchain
1	B	181	THR	Mainchain
1	B	186	GLN	Mainchain
1	B	220	ALA	Mainchain
1	B	97	HIS	Mainchain

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	1893	0	1899	120	0
1	B	1878	0	1886	114	0
2	A	78	0	0	6	0
2	B	94	0	0	7	0
All	All	3943	0	3785	218	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 29.

All (218) 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:171:VAL:HA	1:B:174:ILE:HD12	1.27	1.09
1:A:150:ASP:HB3	1:A:154:LYS:HG2	1.40	1.03
1:B:69:ASN:HD22	1:B:80:THR:H	0.99	0.92
1:A:129:ILE:HB	1:A:148:GLN:NE2	1.89	0.88
1:B:42:ILE:HG12	1:B:61:ILE:CD1	2.04	0.88
1:B:42:ILE:HG12	1:B:61:ILE:HD11	1.59	0.83
1:A:129:ILE:HB	1:A:148:GLN:HE21	1.41	0.83
1:B:166:ILE:HD12	1:B:207:VAL:HG11	1.59	0.83
1:A:189:HIS:CE1	1:A:209:ILE:HG22	2.14	0.83
1:B:147:ARG:HG3	1:B:147:ARG:HH11	1.44	0.82
1:A:130:GLY:H	1:A:148:GLN:HE22	1.23	0.82
1:B:171:VAL:CA	1:B:174:ILE:HD12	2.09	0.81
1:A:66:GLN:HG2	1:B:77:THR:HG23	1.61	0.81
1:A:53:LYS:NZ	1:B:18:ARG:HH22	1.79	0.80
1:A:53:LYS:NZ	1:B:18:ARG:NH2	2.29	0.80
1:A:60:HIS:HA	2:A:499:HOH:O	1.82	0.80
1:B:132:THR:HG22	1:B:134:ALA:H	1.45	0.79
1:B:69:ASN:ND2	1:B:80:THR:H	1.79	0.79
1:A:53:LYS:CE	1:B:18:ARG:HH22	1.97	0.77
1:A:239:LEU:C	1:A:240:LYS:HD2	2.05	0.77
1:A:178:LYS:HD2	1:A:178:LYS:N	2.01	0.76
1:A:186:GLN:CD	1:A:227:PRO:HD2	2.08	0.74
1:A:96:GLY:O	1:A:101:ARG:HD2	1.87	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:182:PRO:HB2	1:A:226:GLN:HE21	1.51	0.74
1:B:243:ALA:O	1:B:247:ILE:HD13	1.88	0.73
1:B:109:GLU:O	1:B:113:LYS:HD3	1.90	0.71
1:B:17:SER:O	1:B:21:VAL:HG23	1.91	0.71
1:B:138:ALA:HB3	1:B:140:LYS:HG3	1.71	0.71
1:B:37:GLY:HA3	1:B:252:GLU:HG3	1.73	0.69
1:A:178:LYS:HD2	1:A:178:LYS:H	1.55	0.69
1:A:182:PRO:CB	1:A:226:GLN:HE21	2.05	0.69
1:A:9:MET:HG2	1:A:233:LEU:CD1	2.23	0.69
1:A:182:PRO:HB2	1:A:226:GLN:NE2	2.08	0.68
1:A:132:THR:HG23	1:A:135:GLU:OE1	1.94	0.68
1:B:69:ASN:HD22	1:B:80:THR:N	1.84	0.68
1:A:53:LYS:HE3	1:A:88:ILE:O	1.95	0.66
1:A:101:ARG:NH2	1:A:108:ASP:OD1	2.29	0.66
1:A:216:ASN:H	1:A:219:ASN:HB2	1.60	0.66
1:B:193:ARG:NH2	1:B:209:ILE:HG13	2.11	0.65
1:A:198:LYS:NZ	2:A:413:HOH:O	2.29	0.65
1:A:120:GLU:HG2	1:A:121:GLN:N	2.10	0.65
1:B:3:MET:N	2:B:481:HOH:O	2.30	0.65
1:A:123:LEU:O	1:A:125:PRO:HD3	1.97	0.64
1:A:4:ARG:HD3	1:A:205:GLU:O	1.96	0.64
1:A:36:ALA:N	1:A:252:GLU:OE2	2.29	0.64
1:A:229:ILE:O	1:A:255:LYS:NZ	2.30	0.64
1:A:131:GLU:OE2	1:A:141:THR:HG23	1.98	0.64
1:A:120:GLU:HG2	1:A:121:GLN:HG2	1.79	0.64
1:B:37:GLY:CA	1:B:252:GLU:HG3	2.28	0.64
1:B:181:THR:OG1	1:B:184:GLN:HG3	1.99	0.63
1:B:132:THR:HG22	1:B:134:ALA:N	2.14	0.63
1:B:95:ILE:O	1:B:128:CYS:HB2	1.99	0.62
1:A:142:GLU:HB3	1:A:191:PHE:CZ	2.35	0.62
1:B:70:LEU:HD22	1:B:113:LYS:HB3	1.82	0.61
1:B:165:VAL:HG22	1:B:208:ILE:HB	1.82	0.61
1:B:154:LYS:NZ	1:B:155:THR:HG22	2.15	0.61
1:A:45:PRO:HB2	1:A:47:MET:HE3	1.83	0.61
1:B:222:GLU:HB2	2:B:387:HOH:O	2.00	0.60
1:B:117:VAL:HG12	1:B:118:LEU:N	2.14	0.60
1:A:53:LYS:HZ3	1:B:18:ARG:NH2	1.99	0.60
1:B:226:GLN:O	1:B:255:LYS:NZ	2.34	0.60
1:B:153:LEU:HD13	1:B:161:PHE:CE2	2.36	0.60
1:B:57:GLU:OE2	1:B:58:GLY:N	2.36	0.59
1:B:29:ARG:NH1	1:B:57:GLU:O	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:30:LYS:HG3	1:B:31:GLU:N	2.19	0.57
1:A:29:ARG:NH1	1:A:57:GLU:O	2.38	0.57
1:A:53:LYS:HE2	1:B:18:ARG:HH22	1.69	0.56
1:B:242:ASP:N	1:B:242:ASP:OD1	2.39	0.56
1:A:130:GLY:H	1:A:148:GLN:NE2	1.98	0.55
1:A:96:GLY:O	1:A:128:CYS:HB2	2.06	0.55
1:B:193:ARG:NE	1:B:228:ASP:OD2	2.36	0.55
1:A:234:VAL:HG11	1:A:237:ALA:HB3	1.88	0.55
1:A:86:LYS:HE2	1:A:121:GLN:O	2.07	0.55
1:A:186:GLN:HB2	1:A:226:GLN:HB3	1.88	0.55
1:B:70:LEU:CD2	1:B:113:LYS:HB3	2.37	0.55
1:A:194:ASP:HA	1:A:197:ALA:HB3	1.89	0.54
1:B:144:VAL:O	1:B:147:ARG:HB3	2.07	0.54
1:B:3:MET:HE2	1:B:4:ARG:HG3	1.89	0.54
1:B:3:MET:CE	1:B:4:ARG:HG3	2.38	0.54
1:A:46:GLU:OE2	1:B:46:GLU:HB3	2.07	0.54
1:A:70:LEU:HD11	1:A:110:LEU:HD12	1.89	0.54
1:A:100:ARG:HB3	1:A:106:GLU:HG3	1.90	0.53
1:A:239:LEU:O	1:A:240:LYS:HD2	2.08	0.53
1:A:242:ASP:O	1:A:246:VAL:HG23	2.09	0.53
1:A:69:ASN:OD1	1:A:80:THR:N	2.40	0.53
1:B:7:LEU:HD12	1:B:39:ALA:O	2.08	0.53
1:A:68:VAL:HG12	1:A:69:ASN:H	1.74	0.53
1:B:21:VAL:HG11	1:B:51:MET:HG2	1.90	0.53
1:B:27:ASN:O	1:B:31:GLU:HG2	2.09	0.53
1:A:211:TYR:CZ	1:A:213:GLY:HA3	2.43	0.53
1:A:53:LYS:HZ1	1:B:18:ARG:NH2	2.04	0.52
1:A:132:THR:C	1:A:172:TRP:HB3	2.29	0.52
1:B:103:TYR:HB2	1:B:104:HIS:CD2	2.45	0.52
1:A:189:HIS:O	1:A:192:ILE:HB	2.10	0.51
1:B:4:ARG:HB2	1:B:4:ARG:NH1	2.24	0.51
1:B:42:ILE:HG12	1:B:61:ILE:HD13	1.89	0.51
1:A:186:GLN:NE2	1:A:227:PRO:HD2	2.25	0.51
1:B:147:ARG:CG	1:B:147:ARG:HH11	2.18	0.51
1:A:53:LYS:HA	1:A:63:LEU:HD13	1.91	0.51
1:B:186:GLN:HB2	1:B:226:GLN:CB	2.40	0.51
1:A:107:SER:O	1:A:111:ILE:HG13	2.11	0.51
1:B:154:LYS:HZ2	1:B:155:THR:HG22	1.75	0.51
1:B:4:ARG:NH1	1:B:230:ASP:OD1	2.44	0.51
1:A:59:SER:HB2	2:A:332:HOH:O	2.10	0.51
1:A:145:CYS:O	1:A:149:ILE:HD12	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:119:LYS:HE2	1:A:160:ALA:O	2.12	0.50
1:A:182:PRO:HG3	1:A:222:GLU:HB3	1.94	0.50
1:B:29:ARG:HH12	1:B:57:GLU:C	2.14	0.50
1:B:152:VAL:O	1:B:156:GLN:N	2.43	0.50
1:B:190:LYS:HD3	1:B:194:ASP:OD2	2.11	0.50
1:A:48:TYR:CE1	1:B:88:ILE:HD12	2.46	0.50
1:B:4:ARG:NE	1:B:205:GLU:O	2.45	0.49
1:A:166:ILE:O	1:A:209:ILE:HA	2.13	0.49
1:A:234:VAL:CG1	1:A:237:ALA:HB3	2.42	0.49
1:A:98:SER:N	1:A:169:GLU:OE2	2.41	0.49
1:A:133:GLU:HA	1:A:172:TRP:CB	2.43	0.49
1:A:133:GLU:HA	1:A:172:TRP:HB2	1.94	0.49
1:A:12:TRP:N	1:A:12:TRP:CD1	2.80	0.49
1:A:12:TRP:CH2	1:A:24:LEU:HD23	2.48	0.49
1:A:92:TYR:CD1	1:A:92:TYR:N	2.81	0.49
1:B:153:LEU:HD11	1:B:158:ALA:HA	1.95	0.48
1:A:194:ASP:O	1:A:197:ALA:HB3	2.13	0.48
1:A:114:LYS:NZ	2:A:379:HOH:O	2.30	0.48
1:A:101:ARG:O	1:A:105:LYS:HA	2.14	0.48
1:A:9:MET:HG2	1:A:233:LEU:HD11	1.94	0.48
1:A:45:PRO:HB2	1:A:47:MET:CE	2.42	0.48
1:A:14:LEU:O	1:B:73:SER:HA	2.14	0.48
1:B:68:VAL:HG13	1:B:85:LEU:CD1	2.43	0.48
1:A:66:GLN:OE1	1:B:77:THR:HA	2.13	0.48
1:A:70:LEU:HD11	1:A:110:LEU:CD1	2.44	0.48
1:B:36:ALA:N	1:B:252:GLU:OE2	2.45	0.47
1:A:143:GLU:HB2	2:A:331:HOH:O	2.14	0.47
1:B:66:GLN:O	1:B:67:ASN:HB2	2.13	0.47
1:A:17:SER:O	1:A:21:VAL:HG23	2.13	0.47
1:A:172:TRP:CZ3	1:A:173:ALA:HB2	2.49	0.47
1:A:3:MET:HG3	1:A:3:MET:O	2.09	0.47
1:A:106:GLU:CD	1:A:114:LYS:HZ2	2.16	0.47
1:B:28:LEU:O	1:B:32:LEU:HG	2.14	0.47
1:A:14:LEU:HG	1:B:73:SER:HA	1.96	0.47
1:A:77:THR:HG23	1:B:66:GLN:HB3	1.96	0.47
1:B:168:TYR:O	1:B:212:GLY:N	2.43	0.47
1:B:45:PRO:HB2	1:B:47:MET:CE	2.44	0.47
1:A:60:HIS:HD2	2:A:499:HOH:O	1.97	0.47
1:B:181:THR:HG1	1:B:184:GLN:HG3	1.81	0.46
1:A:170:PRO:HD2	1:A:213:GLY:CA	2.45	0.46
1:B:153:LEU:HD13	1:B:161:PHE:HE2	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:35:VAL:HG12	1:B:36:ALA:N	2.30	0.46
1:B:118:LEU:HD12	1:B:125:PRO:HB3	1.98	0.46
1:B:4:ARG:HG2	2:B:441:HOH:O	2.16	0.46
1:A:256:GLN:O	1:A:257:ALA:HB3	2.16	0.46
1:A:22:HIS:HD2	1:A:55:GLU:OE2	1.99	0.45
1:B:103:TYR:HB2	1:B:104:HIS:HD2	1.81	0.45
1:A:154:LYS:HD2	1:A:154:LYS:N	2.30	0.45
1:B:223:LEU:HA	1:B:223:LEU:HD12	1.74	0.45
1:B:132:THR:CG2	1:B:133:GLU:N	2.80	0.45
1:A:142:GLU:HB3	1:A:191:PHE:CE2	2.51	0.45
1:B:154:LYS:NZ	1:B:155:THR:CG2	2.79	0.45
1:A:203:ILE:O	1:A:206:GLN:HB2	2.16	0.45
1:A:46:GLU:CD	1:B:46:GLU:HB3	2.37	0.45
1:A:245:ALA:O	1:A:249:LYS:HG3	2.17	0.45
1:B:132:THR:HG22	1:B:133:GLU:N	2.32	0.45
1:B:51:MET:HA	1:B:54:ARG:CZ	2.47	0.45
1:A:224:PHE:O	1:A:255:LYS:HE3	2.17	0.44
1:B:16:GLY:HA2	1:B:20:MET:CE	2.48	0.44
1:A:37:GLY:N	1:A:252:GLU:OE2	2.48	0.44
1:A:28:LEU:HD12	1:A:28:LEU:HA	1.78	0.44
1:B:189:HIS:ND1	1:B:229:ILE:HG12	2.33	0.44
1:B:9:MET:HE3	1:B:92:TYR:HB2	2.00	0.44
1:B:170:PRO:O	1:B:174:ILE:HG13	2.18	0.44
1:A:130:GLY:HA3	1:A:169:GLU:O	2.17	0.44
1:B:224:PHE:O	1:B:255:LYS:HE3	2.18	0.43
1:A:17:SER:HA	1:A:48:TYR:OH	2.18	0.43
1:B:211:TYR:CD2	1:B:223:LEU:HD21	2.53	0.43
1:A:142:GLU:H	1:A:142:GLU:HG3	1.56	0.43
1:B:253:ALA:HB3	2:B:505:HOH:O	2.18	0.43
1:A:96:GLY:C	1:A:101:ARG:HD2	2.38	0.43
1:A:142:GLU:CB	1:A:191:PHE:CZ	3.00	0.43
1:B:186:GLN:HB2	1:B:226:GLN:HB3	1.99	0.43
1:A:174:ILE:HG22	1:A:174:ILE:O	2.19	0.43
1:B:154:LYS:HE3	1:B:154:LYS:HB3	1.60	0.43
1:B:226:GLN:HA	1:B:227:PRO:HD3	1.89	0.43
1:A:14:LEU:HB3	1:B:74:GLY:O	2.17	0.43
1:B:98:SER:HB3	1:B:169:GLU:OE2	2.19	0.43
1:A:97:HIS:O	1:A:101:ARG:HG3	2.18	0.42
1:A:186:GLN:OE1	1:A:227:PRO:HD2	2.19	0.42
1:A:150:ASP:CB	1:A:154:LYS:HG2	2.28	0.42
1:B:137:GLU:HB3	2:B:522:HOH:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:240:LYS:HD2	1:A:240:LYS:N	2.33	0.42
1:A:96:GLY:CA	1:A:111:ILE:HD13	2.50	0.42
1:A:233:LEU:HD12	1:A:233:LEU:HA	1.80	0.42
1:B:4:ARG:HD3	1:B:206:GLN:HA	2.01	0.42
1:B:249:LYS:HB3	2:B:353:HOH:O	2.19	0.42
1:B:142:GLU:HB3	1:B:191:PHE:CZ	2.54	0.42
1:B:217:ALA:HB2	1:B:246:VAL:HG21	2.01	0.42
1:B:61:ILE:HD12	1:B:62:MET:O	2.19	0.42
1:A:173:ALA:HA	1:A:176:THR:HG1	1.85	0.42
1:B:158:ALA:O	1:B:161:PHE:HB2	2.20	0.42
1:B:216:ASN:N	1:B:219:ASN:OD1	2.30	0.42
1:B:178:LYS:HA	1:B:178:LYS:HD3	1.54	0.42
1:B:153:LEU:HD12	1:B:153:LEU:HA	1.61	0.42
1:A:64:GLY:HA2	1:A:92:TYR:O	2.20	0.42
1:B:171:VAL:H	1:B:171:VAL:HG23	1.49	0.41
1:A:77:THR:O	1:B:100:ARG:HD2	2.19	0.41
1:B:132:THR:HG23	2:B:523:HOH:O	2.20	0.41
1:A:42:ILE:O	1:A:64:GLY:N	2.54	0.41
1:A:110:LEU:O	1:A:113:LYS:HB2	2.20	0.41
1:A:202:ASN:O	1:A:206:GLN:OE1	2.38	0.41
1:B:12:TRP:N	1:B:12:TRP:CD1	2.86	0.41
1:B:150:ASP:O	1:B:154:LYS:HB2	2.19	0.41
1:A:8:VAL:HG23	1:A:38:CYS:SG	2.60	0.41
1:B:207:VAL:HG12	1:B:208:ILE:N	2.36	0.41
1:A:45:PRO:CB	1:A:47:MET:CE	2.99	0.41
1:A:23:GLU:O	1:A:26:SER:HB2	2.21	0.41
1:B:133:GLU:HA	1:B:172:TRP:CB	2.52	0.40
1:B:154:LYS:HZ1	1:B:155:THR:HG22	1.85	0.40
1:A:49:ILE:O	1:A:53:LYS:N	2.55	0.40
1:A:6:PRO:HG3	1:A:255:LYS:HG3	2.04	0.40
1:B:98:SER:N	1:B:169:GLU:OE2	2.51	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	253/255 (99%)	232 (92%)	20 (8%)	1 (0%)	39 65
1	B	251/255 (98%)	243 (97%)	7 (3%)	1 (0%)	39 65
All	All	504/510 (99%)	475 (94%)	27 (5%)	2 (0%)	39 65

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	141	THR
1	A	49	ILE

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	188/188 (100%)	165 (88%)	23 (12%)	6 11
1	B	187/188 (100%)	154 (82%)	33 (18%)	2 3
All	All	375/376 (100%)	319 (85%)	56 (15%)	4 6

All (56) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	MET
1	A	20	MET
1	A	28	LEU
1	A	42	ILE
1	A	47	MET
1	A	53	LYS
1	A	63	LEU
1	A	68	VAL
1	A	86	LYS
1	A	109	GLU
1	A	120	GLU

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Mol	Chain	Res	Type
1	A	127	LEU
1	A	140	LYS
1	A	142	GLU
1	A	149	ILE
1	A	154	LYS
1	A	178	LYS
1	A	207	VAL
1	A	215	VAL
1	A	219	ASN
1	A	230	ASP
1	A	239	LEU
1	A	255	LYS
1	B	3	MET
1	B	18	ARG
1	B	29	ARG
1	B	47	MET
1	B	51	MET
1	B	61	ILE
1	B	68	VAL
1	B	88	ILE
1	B	100	ARG
1	B	105	LYS
1	B	109	GLU
1	B	113	LYS
1	B	117	VAL
1	B	119	LYS
1	B	120	GLU
1	B	137	GLU
1	B	143	GLU
1	B	147	ARG
1	B	154	LYS
1	B	162	GLU
1	B	178	LYS
1	B	179	SER
1	B	190	LYS
1	B	198	LYS
1	B	202	ASN
1	B	206	GLN
1	B	209	ILE
1	B	218	SER
1	B	239	LEU
1	B	240	LYS

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Mol	Chain	Res	Type
1	B	246	VAL
1	B	249	LYS
1	B	255	LYS

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	5	HIS
1	A	22	HIS
1	A	71	ASN
1	A	148	GLN
1	A	219	ASN
1	A	226	GLN
1	B	69	ASN
1	B	71	ASN
1	B	91	GLN
1	B	202	ASN

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 carbohydrates in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

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, 95^{th} 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	255/255 (100%)	-0.51	4 (1%)	74	69	9, 29, 57, 94	0
1	B	253/255 (99%)	-0.60	1 (0%)	93	91	11, 27, 57, 89	0
All	All	508/510 (99%)	-0.56	5 (0%)	84	81	9, 28, 57, 94	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	257	ALA	5.3
1	A	3	MET	3.0
1	A	175	GLY	2.8
1	B	3	MET	2.1
1	A	137	GLU	2.0

6.2 Non-standard residues in protein, DNA, RNA chains

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

6.3 Carbohydrates

There are no carbohydrates in this entry.

6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.