



wwPDB X-ray Structure Validation Summary Report

Feb 28, 2014 – 01:43 PM GMT

PDB ID : 4BI5
Title : CRYSTAL STRUCTURE OF A DOUBLE MUTANT (C202A AND C222D)
OF TRIOSEPHOSPHATE ISOMERASE FROM GIARDIA LAMBLIA.
Authors : Torres-Larios, A.; Enriquez-Flores, S.; Reyes-Vivas, H.; Oria-Hernandez, J.;
Hernandez-Alcantara, G.
Deposited on : 2013-04-09
Resolution : 2.70 Å(reported)

This is a wwPDB validation summary 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/ValidationPDFNotes.html>

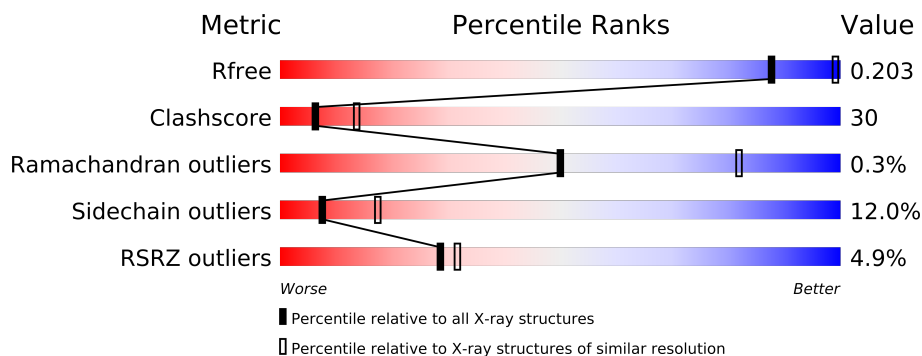
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.70 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.





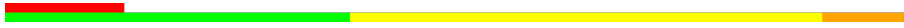


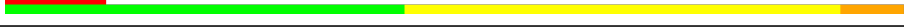
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	66092	1557 (2.70-2.70)
Clashscore	79885	1939 (2.70-2.70)
Ramachandran outliers	78287	1905 (2.70-2.70)
Sidechain outliers	78261	1905 (2.70-2.70)
RSRZ outliers	66119	1559 (2.70-2.70)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	255	
1	B	255	
1	C	255	
1	D	255	
1	E	255	
1	F	255	
1	G	255	
1	H	255	
1	I	255	
1	J	255	
1	K	255	
1	L	255	
1	M	255	
1	N	255	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	O	255	
1	P	255	
1	Q	255	
1	R	255	
1	S	255	
1	T	255	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 38560 atoms, of which 0 are hydrogen and 0 are deuterium.

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	254	Total	C	N	O	S	0	0	0
			1928	1212	341	364	11			
1	B	254	Total	C	N	O	S	0	0	0
			1928	1212	341	364	11			
1	C	254	Total	C	N	O	S	0	0	0
			1928	1212	341	364	11			
1	D	254	Total	C	N	O	S	0	0	0
			1928	1212	341	364	11			
1	E	254	Total	C	N	O	S	0	0	0
			1928	1212	341	364	11			
1	F	254	Total	C	N	O	S	0	0	0
			1928	1212	341	364	11			
1	G	254	Total	C	N	O	S	0	0	0
			1928	1212	341	364	11			
1	H	254	Total	C	N	O	S	0	0	0
			1928	1212	341	364	11			
1	I	254	Total	C	N	O	S	0	0	0
			1928	1212	341	364	11			
1	J	254	Total	C	N	O	S	0	0	0
			1928	1212	341	364	11			
1	K	254	Total	C	N	O	S	0	0	0
			1928	1212	341	364	11			
1	L	254	Total	C	N	O	S	0	0	0
			1928	1212	341	364	11			
1	M	254	Total	C	N	O	S	0	0	0
			1928	1212	341	364	11			
1	N	254	Total	C	N	O	S	0	0	0
			1928	1212	341	364	11			
1	O	254	Total	C	N	O	S	0	0	0
			1928	1212	341	364	11			
1	P	254	Total	C	N	O	S	0	0	0
			1928	1212	341	364	11			

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Q	254	Total 1928	C 1212	N 341	O 364	S 11	0	0	0
1	R	254	Total 1928	C 1212	N 341	O 364	S 11	0	0	0
1	S	254	Total 1928	C 1212	N 341	O 364	S 11	0	0	0
1	T	254	Total 1928	C 1212	N 341	O 364	S 11	0	0	0

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	202	ALA	CYS	ENGINEERED MUTATION	UNP P36186
A	222	ASP	CYS	ENGINEERED MUTATION	UNP P36186
B	202	ALA	CYS	ENGINEERED MUTATION	UNP P36186
B	222	ASP	CYS	ENGINEERED MUTATION	UNP P36186
C	202	ALA	CYS	ENGINEERED MUTATION	UNP P36186
C	222	ASP	CYS	ENGINEERED MUTATION	UNP P36186
D	202	ALA	CYS	ENGINEERED MUTATION	UNP P36186
D	222	ASP	CYS	ENGINEERED MUTATION	UNP P36186
E	202	ALA	CYS	ENGINEERED MUTATION	UNP P36186
E	222	ASP	CYS	ENGINEERED MUTATION	UNP P36186
F	202	ALA	CYS	ENGINEERED MUTATION	UNP P36186
F	222	ASP	CYS	ENGINEERED MUTATION	UNP P36186
G	202	ALA	CYS	ENGINEERED MUTATION	UNP P36186
G	222	ASP	CYS	ENGINEERED MUTATION	UNP P36186
H	202	ALA	CYS	ENGINEERED MUTATION	UNP P36186
H	222	ASP	CYS	ENGINEERED MUTATION	UNP P36186
I	202	ALA	CYS	ENGINEERED MUTATION	UNP P36186
I	222	ASP	CYS	ENGINEERED MUTATION	UNP P36186
J	202	ALA	CYS	ENGINEERED MUTATION	UNP P36186
J	222	ASP	CYS	ENGINEERED MUTATION	UNP P36186
K	202	ALA	CYS	ENGINEERED MUTATION	UNP P36186
K	222	ASP	CYS	ENGINEERED MUTATION	UNP P36186
L	202	ALA	CYS	ENGINEERED MUTATION	UNP P36186
L	222	ASP	CYS	ENGINEERED MUTATION	UNP P36186
M	202	ALA	CYS	ENGINEERED MUTATION	UNP P36186
M	222	ASP	CYS	ENGINEERED MUTATION	UNP P36186
N	202	ALA	CYS	ENGINEERED MUTATION	UNP P36186
N	222	ASP	CYS	ENGINEERED MUTATION	UNP P36186
O	202	ALA	CYS	ENGINEERED MUTATION	UNP P36186
O	222	ASP	CYS	ENGINEERED MUTATION	UNP P36186
P	202	ALA	CYS	ENGINEERED MUTATION	UNP P36186

Continued on next page...

Continued from previous page...

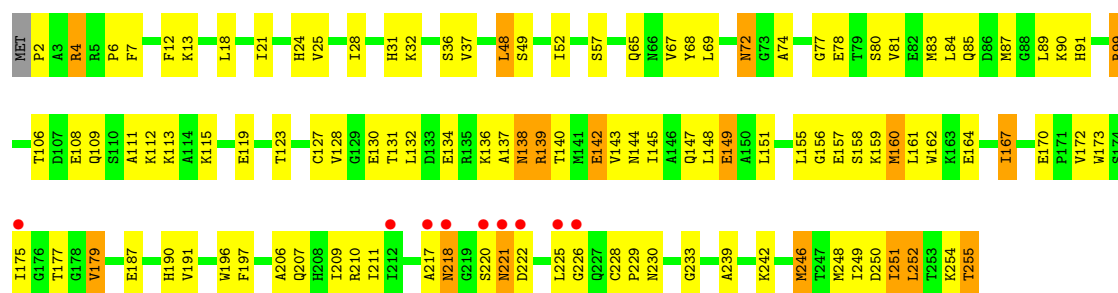
Chain	Residue	Modelled	Actual	Comment	Reference
P	222	ASP	CYS	ENGINEERED MUTATION	UNP P36186
Q	202	ALA	CYS	ENGINEERED MUTATION	UNP P36186
Q	222	ASP	CYS	ENGINEERED MUTATION	UNP P36186
R	202	ALA	CYS	ENGINEERED MUTATION	UNP P36186
R	222	ASP	CYS	ENGINEERED MUTATION	UNP P36186
S	202	ALA	CYS	ENGINEERED MUTATION	UNP P36186
S	222	ASP	CYS	ENGINEERED MUTATION	UNP P36186
T	202	ALA	CYS	ENGINEERED MUTATION	UNP P36186
T	222	ASP	CYS	ENGINEERED MUTATION	UNP P36186

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.

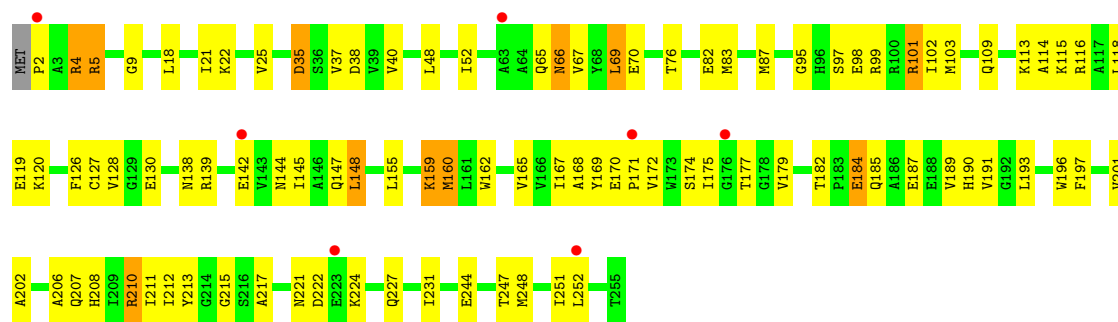
• Molecule 1: TRIOSEPHOSPHATE ISOMERASE

Chain A:



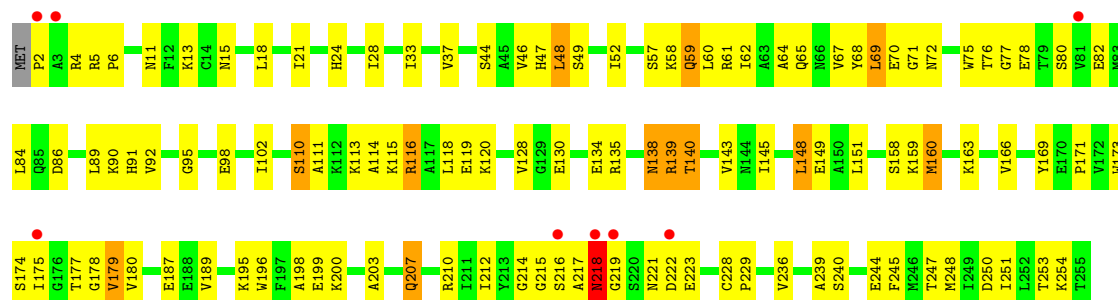
• Molecule 1: TRIOSEPHOSPHATE ISOMERASE

Chain B:



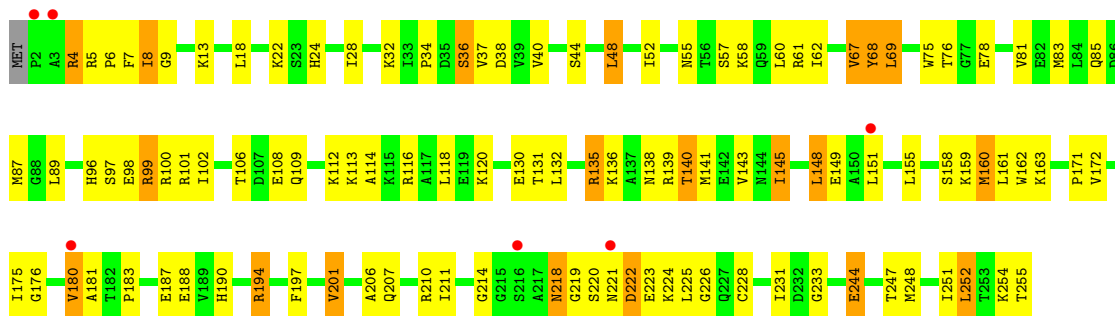
• Molecule 1: TRIOSEPHOSPHATE ISOMERASE

Chain C:



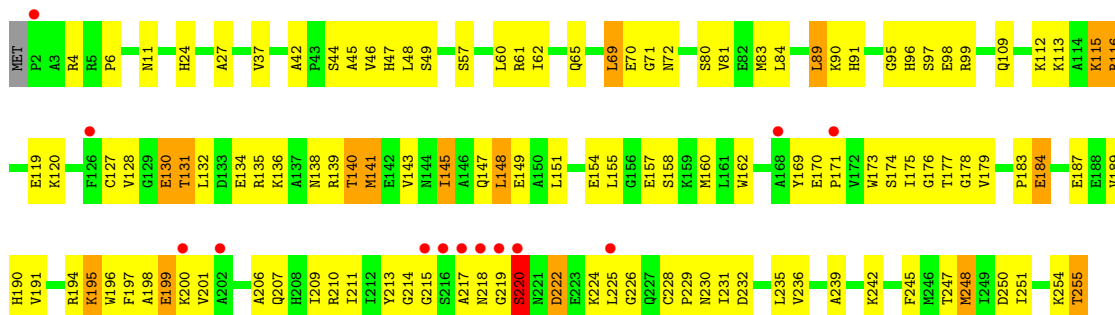
- Molecule 1: TRIOSEPHOSPHATE ISOMERASE

Chain D:



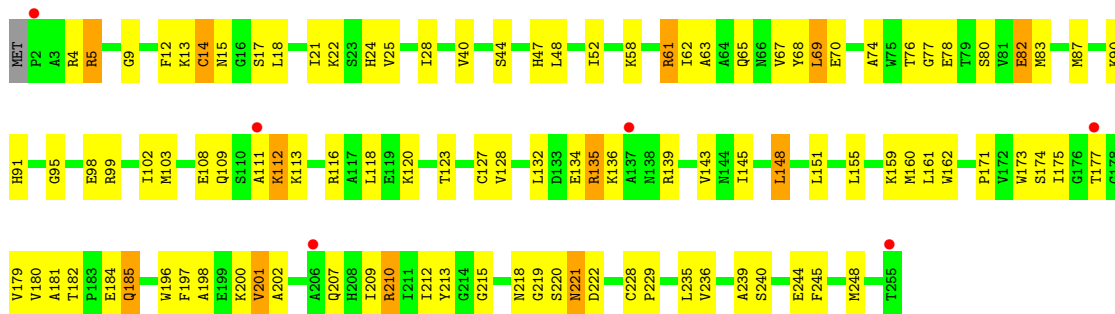
- Molecule 1: TRIOSEPHOSPHATE ISOMERASE

Chain E:



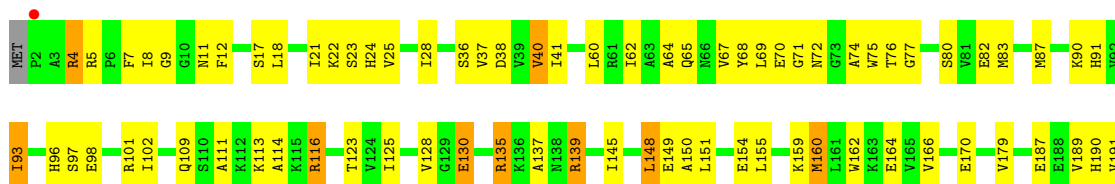
- Molecule 1: TRIOSEPHOSPHATE ISOMERASE

Chain F:



- Molecule 1: TRIOSEPHOSPHATE ISOMERASE

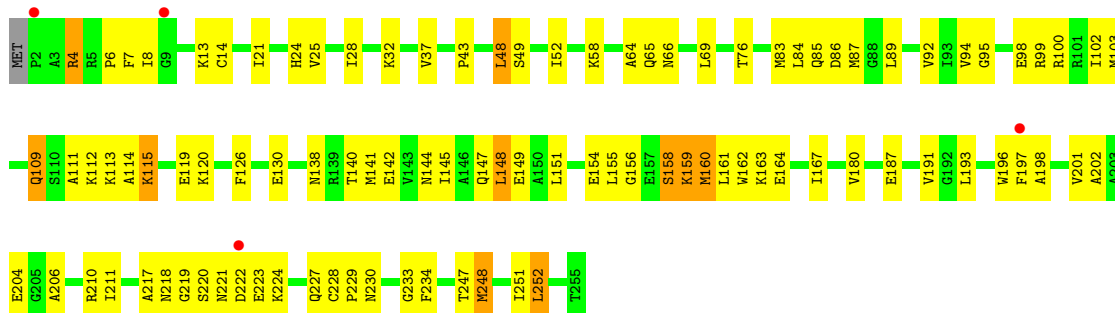
Chain G:





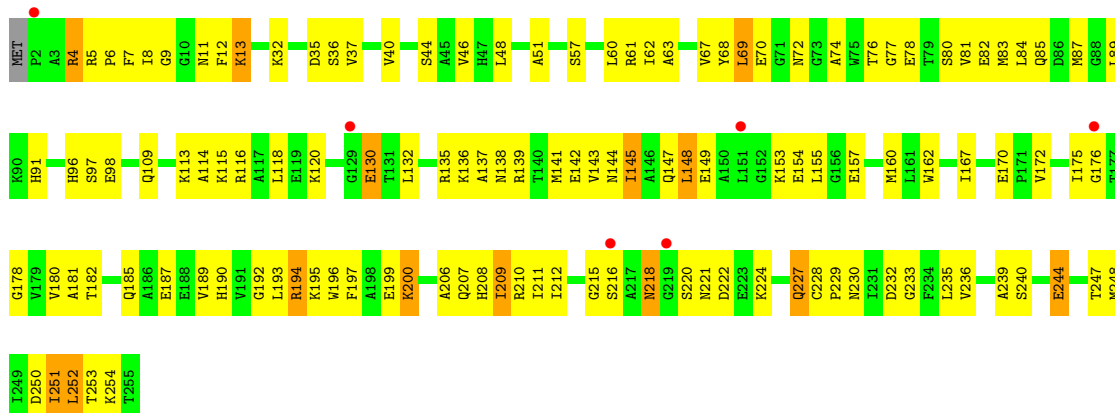
• Molecule 1: TRIOSEPHOSPHATE ISOMERASE

Chain H:



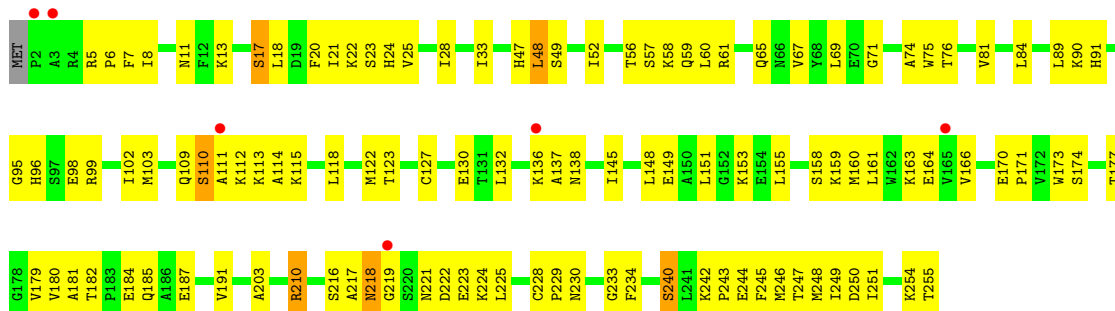
• Molecule 1: TRIOSEPHOSPHATE ISOMERASE

Chain I:



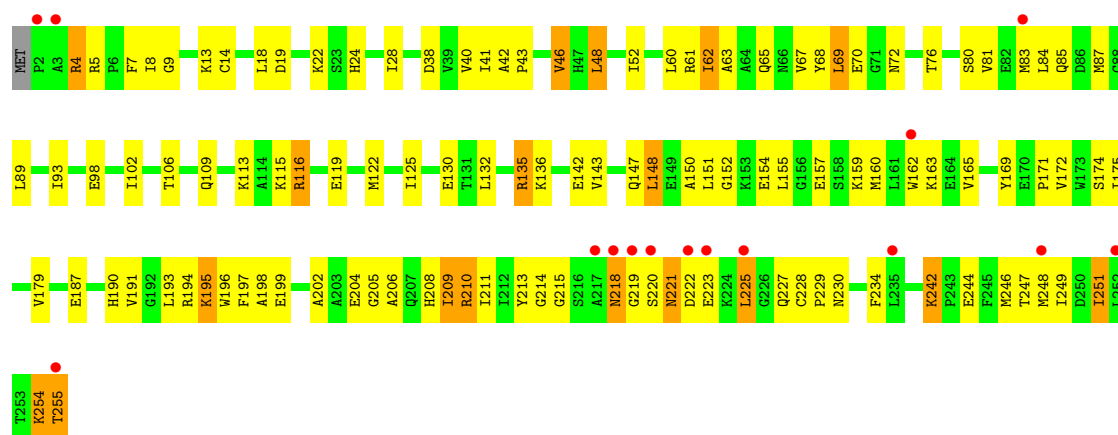
• Molecule 1: TRIOSEPHOSPHATE ISOMERASE

Chain J:



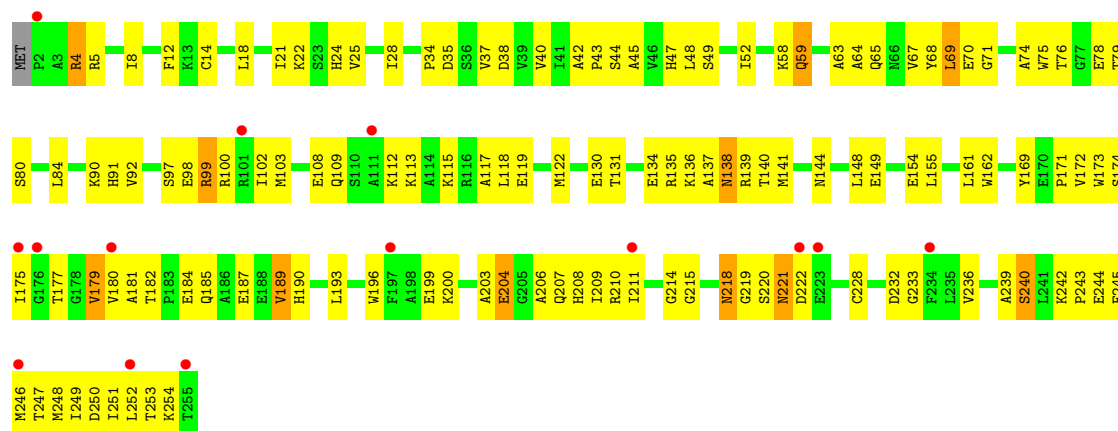
• Molecule 1: TRIOSEPHOSPHATE ISOMERASE

Chain K:



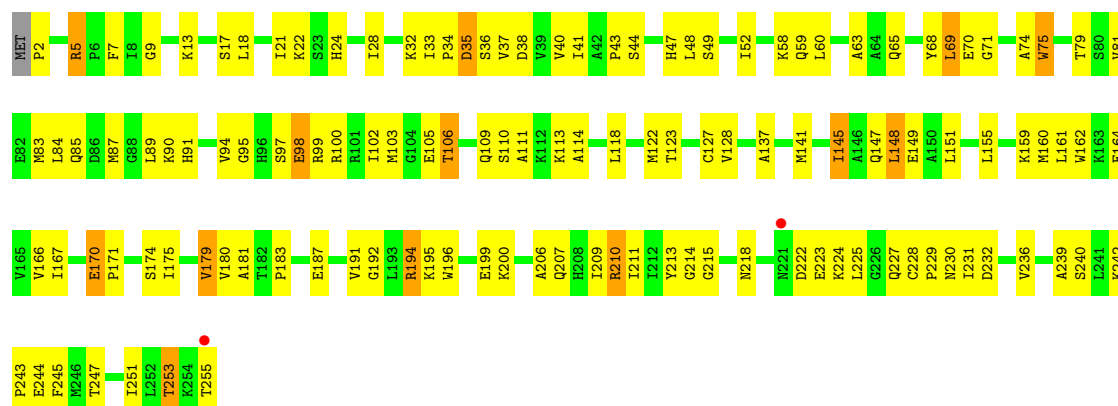
• Molecule 1: TRIOSEPHOSPHATE ISOMERASE

Chain L:



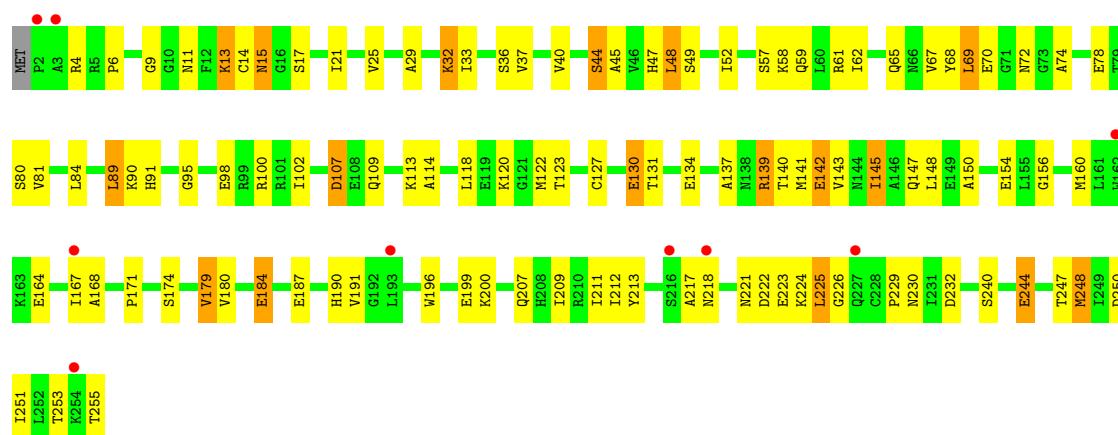
• Molecule 1: TRIOSEPHOSPHATE ISOMERASE

Chain M:



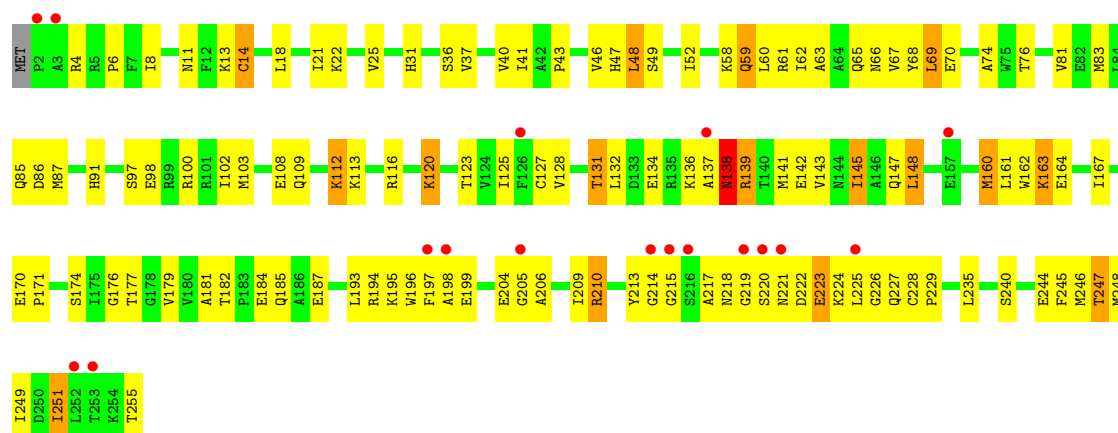
• Molecule 1: TRIOSEPHOSPHATE ISOMERASE

Chain N:



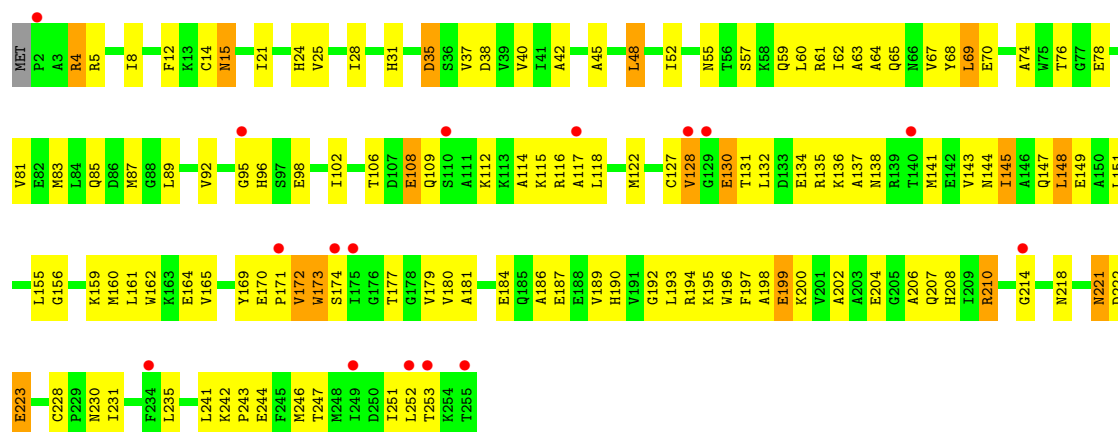
• Molecule 1: TRIOSEPHOSPHATE ISOMERASE

Chain O:



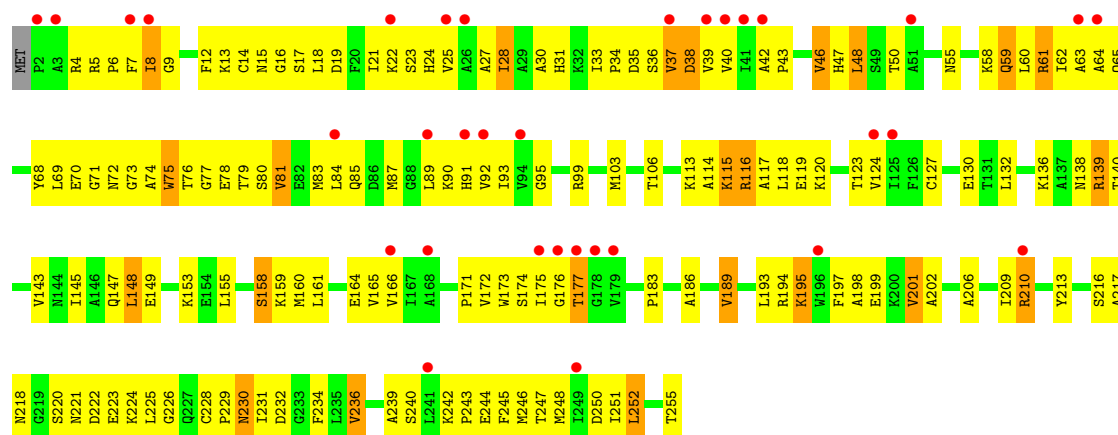
• Molecule 1: TRIOSEPHOSPHATE ISOMERASE

Chain P:



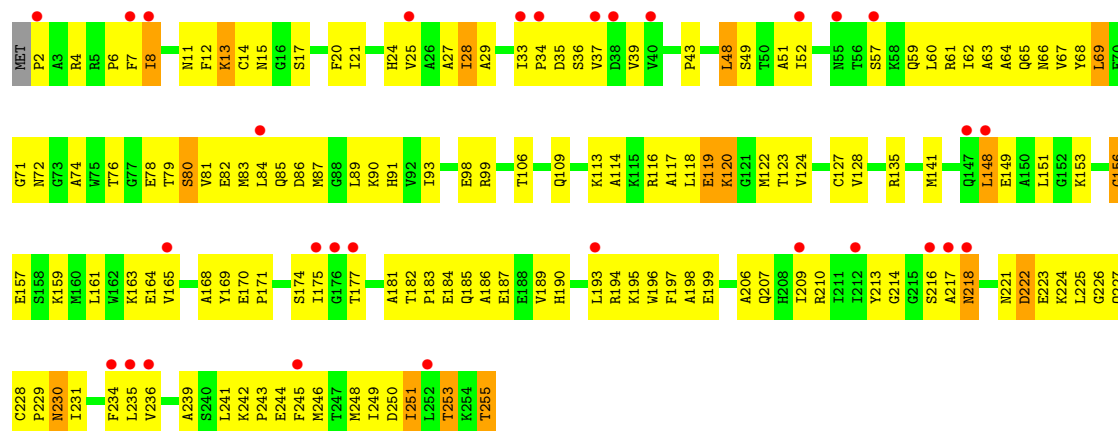
• Molecule 1: TRIOSEPHOSPHATE ISOMERASE

Chain Q:



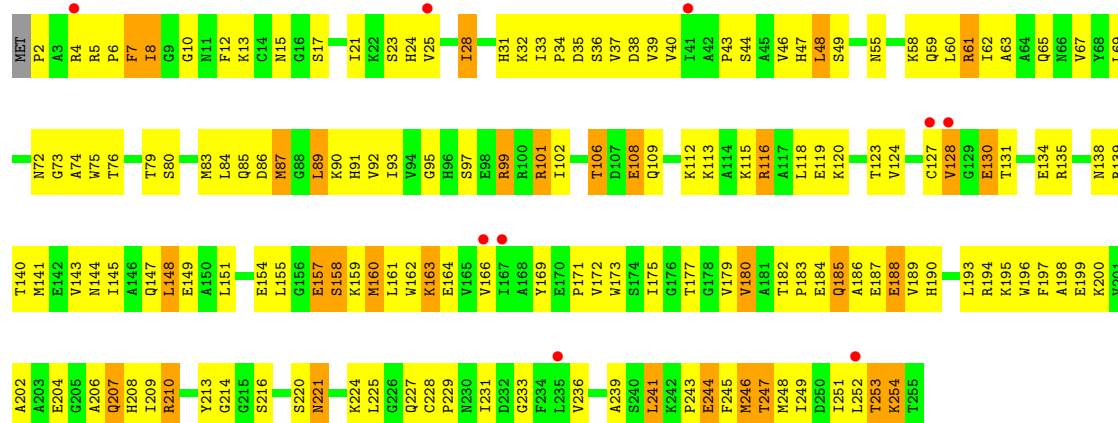
• Molecule 1: TRIOSEPHOSPHATE ISOMERASE

Chain R:



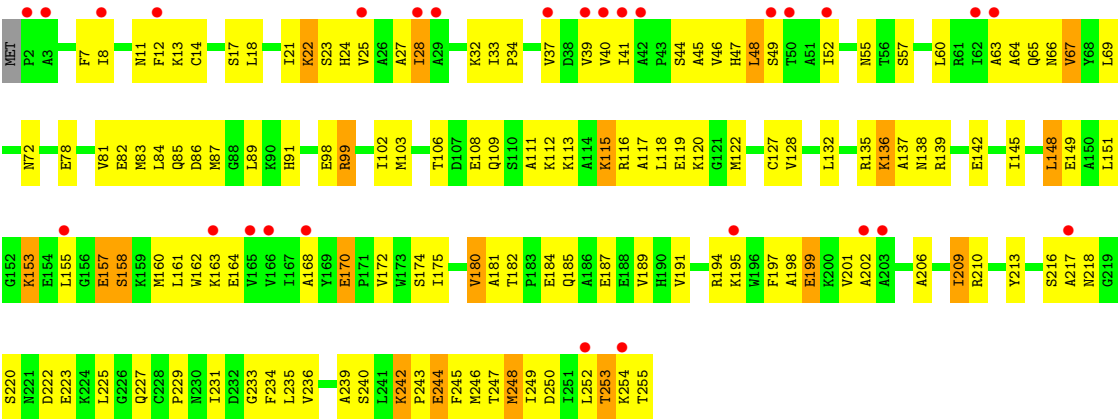
• Molecule 1: TRIOSEPHOSPHATE ISOMERASE

Chain S:



• Molecule 1: TRIOSEPHOSPHATE ISOMERASE

Chain T:



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	105.22Å 131.57Å 132.55Å 115.73° 89.81° 90.24°	Depositor
Resolution (Å)	78.87 – 2.70 78.88 – 2.70	Depositor EDS
% Data completeness (in resolution range)	82.0 (78.87-2.70) 79.8 (78.88-2.70)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.46 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.239 , 0.272 0.201 , 0.203	Depositor DCC
R_{free} test set	7212 reflections (5.26%)	DCC
Wilson B-factor (Å ²)	50.3	Xtriage
Anisotropy	0.256	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 21.6	EDS
Estimated twinning fraction	0.418 for h,-k,-l 0.197 for -h,-l,-k 0.197 for -h,l,k	Xtriage
L-test for twinning	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.25$	Xtriage
Outliers	0 of 144197 reflections	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	38560	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.64% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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	0.48	0/1960	0.49	0/2644
1	B	0.58	2/1960 (0.1%)	0.50	0/2644
1	C	0.55	0/1960	0.53	0/2644
1	D	0.40	0/1960	0.48	0/2644
1	E	0.63	0/1960	0.53	0/2644
1	F	0.49	1/1960 (0.1%)	0.52	0/2644
1	G	0.62	2/1960 (0.1%)	0.52	0/2644
1	H	0.58	0/1960	0.52	0/2644
1	I	0.37	0/1960	0.50	0/2644
1	J	0.44	0/1960	0.49	0/2644
1	K	0.34	0/1960	0.51	0/2644
1	L	0.55	0/1960	0.56	0/2644
1	M	0.34	0/1960	0.47	0/2644
1	N	0.27	0/1960	0.46	0/2644
1	O	0.30	0/1960	0.50	0/2644
1	P	0.28	0/1960	0.49	0/2644
1	Q	0.33	0/1960	0.49	0/2644
1	R	0.37	0/1960	0.50	0/2644
1	S	0.32	0/1960	0.50	0/2644
1	T	0.28	0/1960	0.50	0/2644
All	All	0.44	5/39200 (0.0%)	0.50	0/52880

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	14	CYS	CB-SG	-5.68	1.72	1.81
1	B	169	TYR	CE2-CZ	-5.38	1.31	1.38
1	G	68	TYR	CD2-CE2	-5.31	1.31	1.39
1	G	68	TYR	CE1-CZ	-5.25	1.31	1.38
1	B	169	TYR	CD2-CE2	-5.00	1.31	1.39

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1928	0	1949	111	0
1	B	1928	0	1949	82	0
1	C	1928	0	1949	95	0
1	D	1928	0	1949	103	0
1	E	1928	0	1949	136	0
1	F	1928	0	1949	93	0
1	G	1928	0	1949	98	0
1	H	1928	0	1949	80	0
1	I	1928	0	1949	137	0
1	J	1928	0	1949	104	0
1	K	1928	0	1949	113	0
1	L	1928	0	1949	141	0
1	M	1928	0	1949	104	0
1	N	1928	0	1949	110	0
1	O	1928	0	1949	141	0
1	P	1928	0	1949	127	0
1	Q	1928	0	1949	195	0
1	R	1928	0	1949	184	0
1	S	1928	0	1949	184	0
1	T	1928	0	1949	130	0
All	All	38560	0	38980	2346	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 30.

The worst 5 of 2346 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:76:THR:CG2	1:D:98:GLU:OE1	1.67	1.42
1:T:115:LYS:HG2	1:T:155:LEU:CD2	1.47	1.41
1:B:66:ASN:HD22	1:B:67:VAL:N	1.25	1.31
1:L:177:THR:HG22	1:L:179:VAL:CG2	1.60	1.30
1:B:66:ASN:ND2	1:B:67:VAL:H	1.30	1.27

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

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	252/255 (99%)	241 (96%)	10 (4%)	1 (0%)	43	76
1	B	252/255 (99%)	247 (98%)	5 (2%)	0	100	100
1	C	252/255 (99%)	240 (95%)	11 (4%)	1 (0%)	43	76
1	D	252/255 (99%)	244 (97%)	7 (3%)	1 (0%)	43	76
1	E	252/255 (99%)	240 (95%)	11 (4%)	1 (0%)	43	76
1	F	252/255 (99%)	244 (97%)	7 (3%)	1 (0%)	43	76
1	G	252/255 (99%)	243 (96%)	8 (3%)	1 (0%)	43	76
1	H	252/255 (99%)	240 (95%)	12 (5%)	0	100	100
1	I	252/255 (99%)	243 (96%)	9 (4%)	0	100	100
1	J	252/255 (99%)	244 (97%)	8 (3%)	0	100	100
1	K	252/255 (99%)	240 (95%)	11 (4%)	1 (0%)	43	76
1	L	252/255 (99%)	239 (95%)	13 (5%)	0	100	100
1	M	252/255 (99%)	244 (97%)	8 (3%)	0	100	100
1	N	252/255 (99%)	239 (95%)	11 (4%)	2 (1%)	27	58
1	O	252/255 (99%)	237 (94%)	14 (6%)	1 (0%)	43	76
1	P	252/255 (99%)	233 (92%)	18 (7%)	1 (0%)	43	76
1	Q	252/255 (99%)	237 (94%)	14 (6%)	1 (0%)	43	76
1	R	252/255 (99%)	242 (96%)	7 (3%)	3 (1%)	19	45
1	S	252/255 (99%)	238 (94%)	14 (6%)	0	100	100
1	T	252/255 (99%)	246 (98%)	6 (2%)	0	100	100
All	All	5040/5100 (99%)	4821 (96%)	204 (4%)	15 (0%)	50	82

5 of 15 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	218	ASN
1	E	220	SER
1	G	219	GLY
1	R	218	ASN
1	Q	201	VAL

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	202/203 (100%)	178 (88%)	24 (12%)	8	18
1	B	202/203 (100%)	187 (93%)	15 (7%)	20	43
1	C	202/203 (100%)	180 (89%)	22 (11%)	9	21
1	D	202/203 (100%)	176 (87%)	26 (13%)	6	15
1	E	202/203 (100%)	177 (88%)	25 (12%)	7	16
1	F	202/203 (100%)	186 (92%)	16 (8%)	18	39
1	G	202/203 (100%)	181 (90%)	21 (10%)	10	23
1	H	202/203 (100%)	180 (89%)	22 (11%)	9	21
1	I	202/203 (100%)	177 (88%)	25 (12%)	7	16
1	J	202/203 (100%)	184 (91%)	18 (9%)	14	31
1	K	202/203 (100%)	181 (90%)	21 (10%)	10	23
1	L	202/203 (100%)	184 (91%)	18 (9%)	14	31
1	M	202/203 (100%)	176 (87%)	26 (13%)	6	15
1	N	202/203 (100%)	176 (87%)	26 (13%)	6	15
1	O	202/203 (100%)	176 (87%)	26 (13%)	6	15
1	P	202/203 (100%)	180 (89%)	22 (11%)	9	21
1	Q	202/203 (100%)	169 (84%)	33 (16%)	3	9
1	R	202/203 (100%)	181 (90%)	21 (10%)	10	23
1	S	202/203 (100%)	160 (79%)	42 (21%)	2	4
1	T	202/203 (100%)	168 (83%)	34 (17%)	3	8
All	All	4040/4060 (100%)	3557 (88%)	483 (12%)	7	17

5 of 483 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	K	69	LEU
1	M	170	GLU
1	S	247	THR
1	K	209	ILE
1	L	189	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 112 such sidechains are listed below:

Mol	Chain	Res	Type
1	L	47	HIS
1	N	15	ASN
1	S	221	ASN
1	L	72	ASN
1	L	221	ASN

5.3.3 RNA ⓘ

There are no RNA chains 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, 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	254/255 (99%)	0.15	9 (3%) 42 47	26, 40, 72, 88	0
1	B	254/255 (99%)	0.16	7 (2%) 50 56	21, 37, 70, 89	0
1	C	254/255 (99%)	0.17	8 (3%) 47 52	22, 39, 72, 93	0
1	D	254/255 (99%)	0.12	6 (2%) 56 62	25, 40, 71, 84	0
1	E	254/255 (99%)	0.23	13 (5%) 27 30	24, 44, 75, 90	0
1	F	254/255 (99%)	0.15	6 (2%) 56 62	23, 39, 71, 88	0
1	G	254/255 (99%)	0.24	10 (3%) 37 42	24, 38, 70, 92	0
1	H	254/255 (99%)	0.12	4 (1%) 68 74	24, 39, 73, 91	0
1	I	254/255 (99%)	0.19	6 (2%) 56 62	25, 40, 70, 85	0
1	J	254/255 (99%)	0.11	6 (2%) 56 62	24, 38, 72, 93	0
1	K	254/255 (99%)	0.32	15 (5%) 22 23	25, 48, 76, 93	0
1	L	254/255 (99%)	0.42	14 (5%) 24 26	27, 52, 79, 90	0
1	M	254/255 (99%)	0.17	2 (0%) 83 87	24, 42, 75, 87	0
1	N	254/255 (99%)	0.20	9 (3%) 42 47	23, 43, 76, 92	0
1	O	254/255 (99%)	0.39	17 (6%) 17 19	24, 45, 77, 93	0
1	P	254/255 (99%)	0.36	16 (6%) 19 21	27, 51, 80, 95	0
1	Q	254/255 (99%)	0.70	33 (12%) 4 4	40, 65, 86, 96	0
1	R	254/255 (99%)	0.60	30 (11%) 5 5	35, 64, 87, 95	0
1	S	254/255 (99%)	0.38	9 (3%) 42 47	41, 64, 85, 96	0
1	T	254/255 (99%)	0.57	28 (11%) 6 6	36, 62, 87, 96	0
All	All	5080/5100 (99%)	0.29	248 (4%) 28 31	21, 46, 79, 96	0

The worst 5 of 248 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	N	2	PRO	11.4
1	R	217	ALA	11.1
1	K	219	GLY	9.6
1	Q	40	VAL	8.2
1	A	217	ALA	7.9

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.