



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 03:12 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 X-ray Structure 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/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

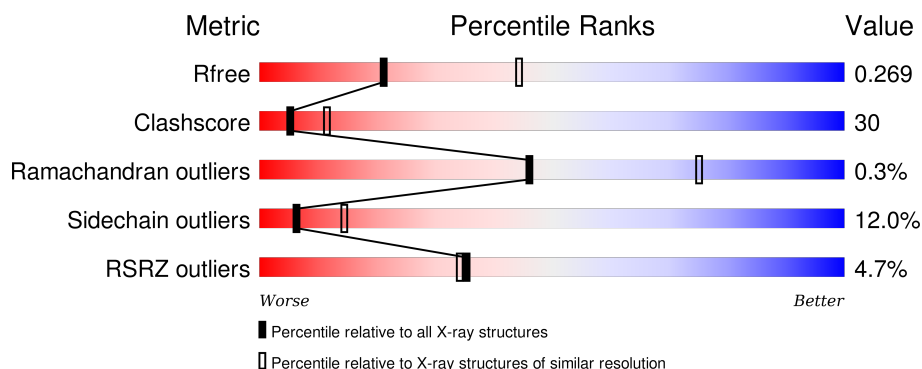
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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}	91344	2103 (2.70-2.70)
Clashscore	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (2.70-2.70)
RSRZ outliers	91569	2107 (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. 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	255	<div> <div>4%</div> <div>56%</div> <div>37%</div> <div>7%</div> </div>
1	B	255	<div> <div>3%</div> <div>62%</div> <div>33%</div> <div>.</div> </div>
1	C	255	<div> <div>3%</div> <div>54%</div> <div>40%</div> <div>5%</div> </div>
1	D	255	<div> <div>2%</div> <div>56%</div> <div>36%</div> <div>8%</div> </div>
1	E	255	<div> <div>4%</div> <div>52%</div> <div>41%</div> <div>6%</div> </div>

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Mol	Chain	Length	Quality of chain
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	
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 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	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			

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

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

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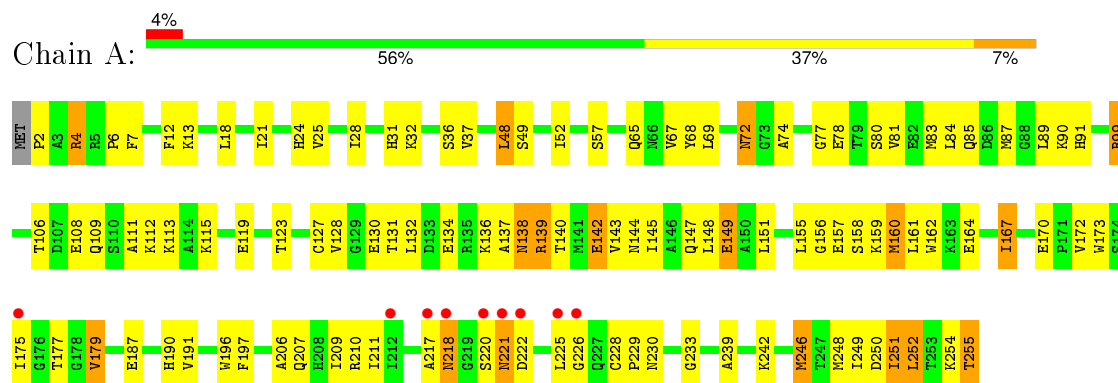
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Chain	Residue	Modelled	Actual	Comment	Reference
P	222	ASP	CYS	ENGINEERED MUTATION	UNP P36186
Q	202	ALA	CYS	ENGINEERED MUTATION	UNP P36186
Q	222	ASP	CYS	ENGINEERED MUTATION	UNP P36186
R	202	ALA	CYS	ENGINEERED MUTATION	UNP P36186
R	222	ASP	CYS	ENGINEERED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

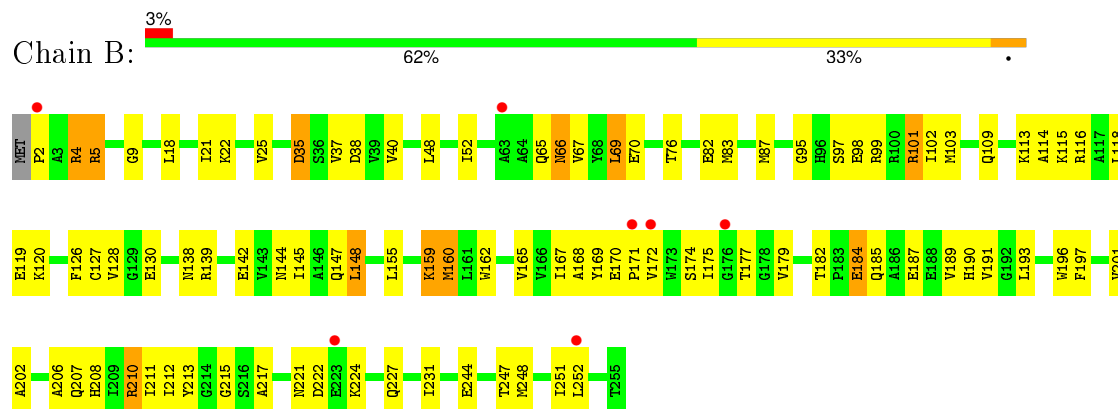
3 Residue-property plots [i](#)

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.

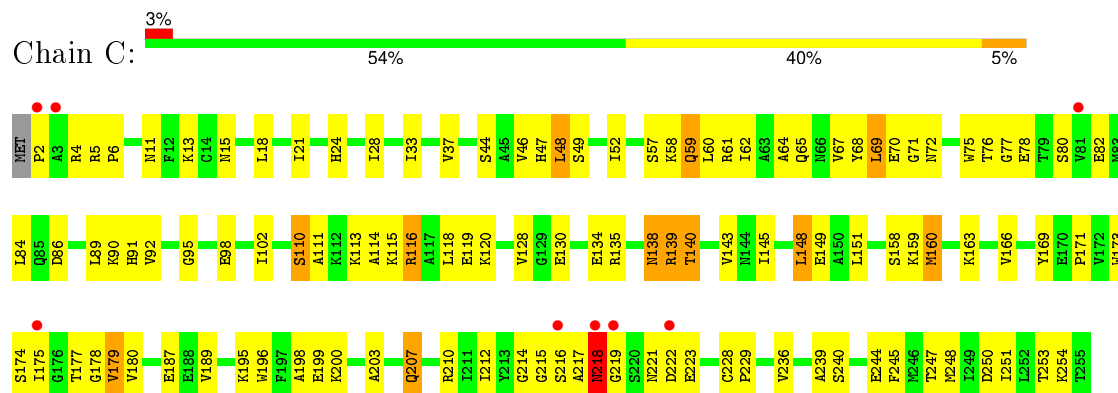
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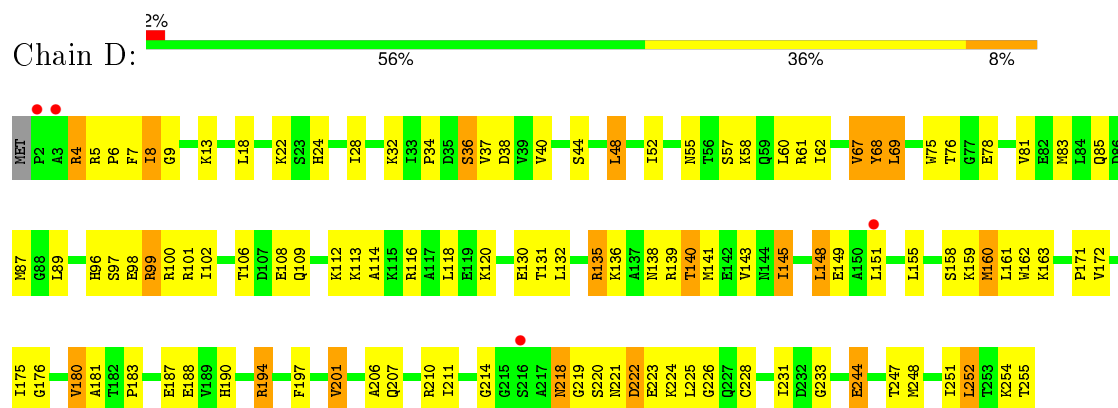
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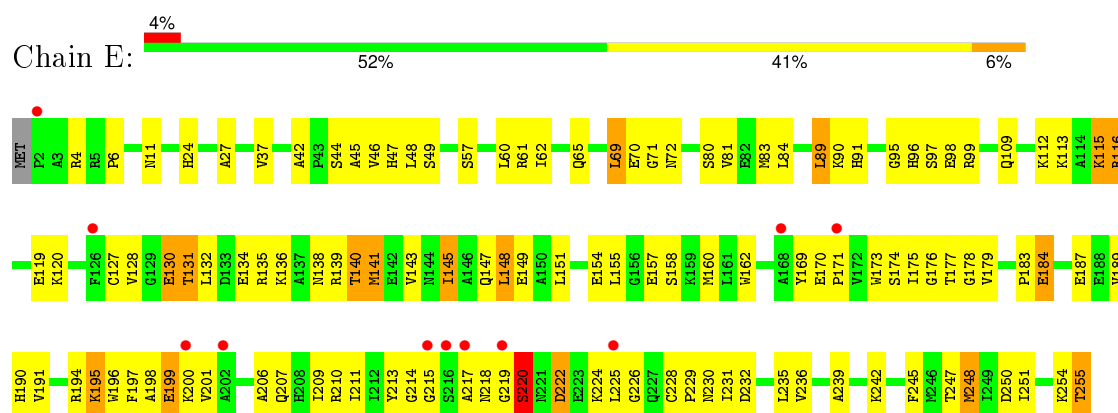
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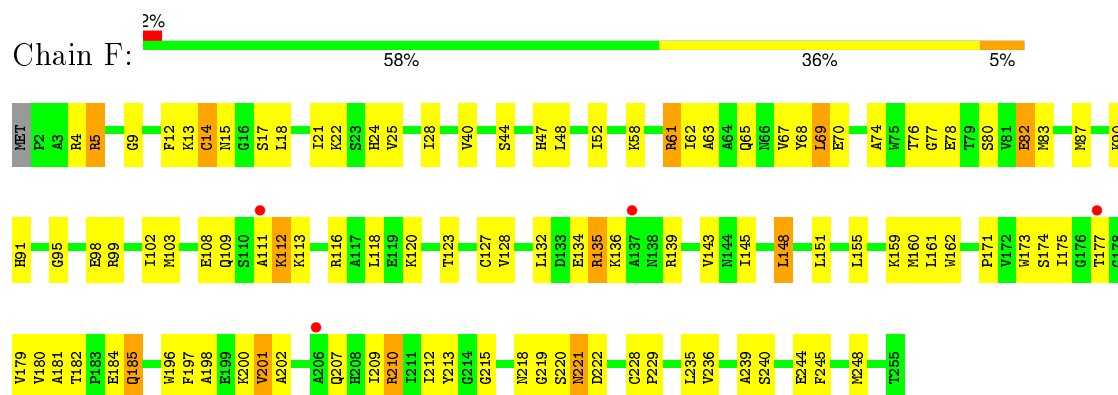
• Molecule 1: TRIOSEPHOSPHATE ISOMERASE



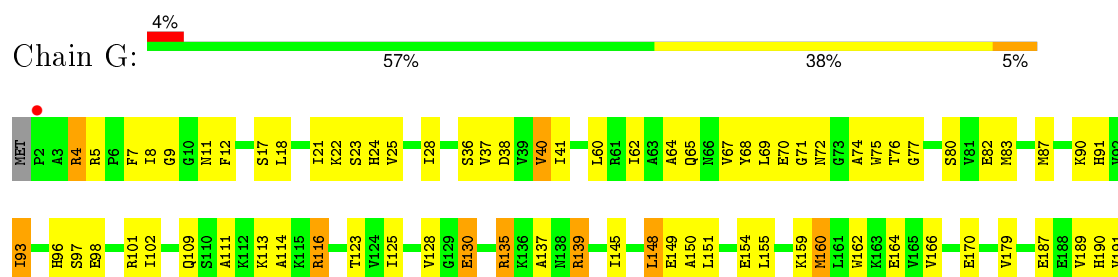
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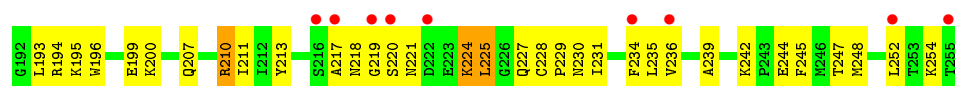


• Molecule 1: TRIOSEPHOSPHATE ISOMERASE

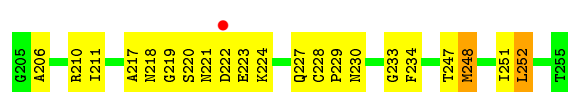
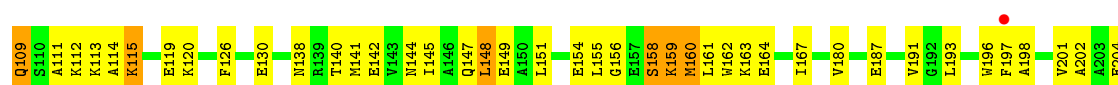
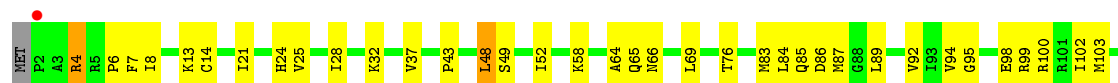


• Molecule 1: TRIOSEPHOSPHATE ISOMERASE

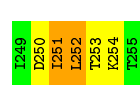
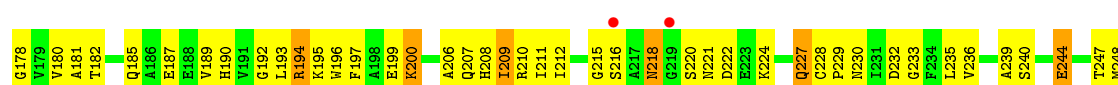
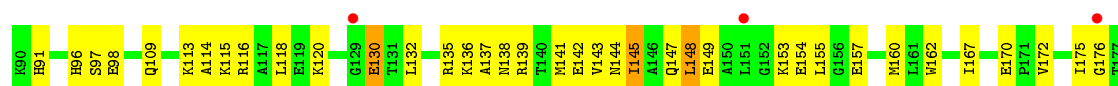




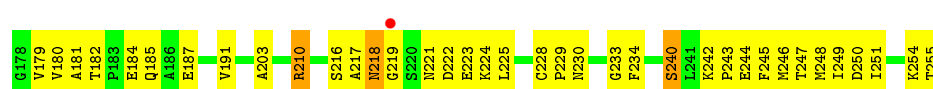
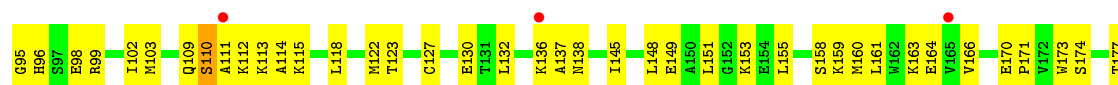
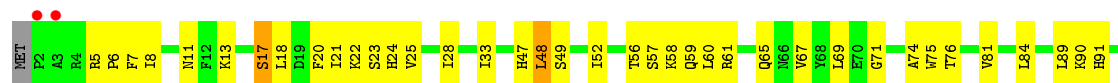
• Molecule 1: TRIOSEPHOSPHATE ISOMERASE



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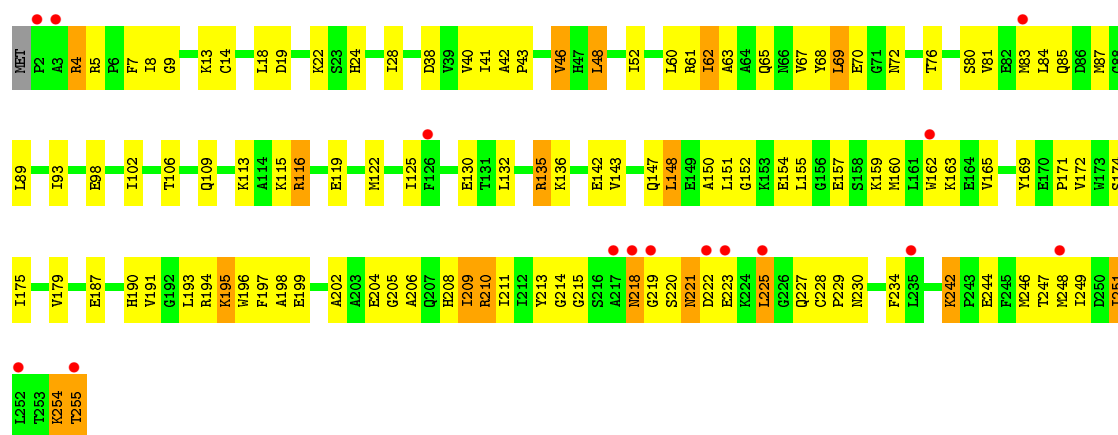


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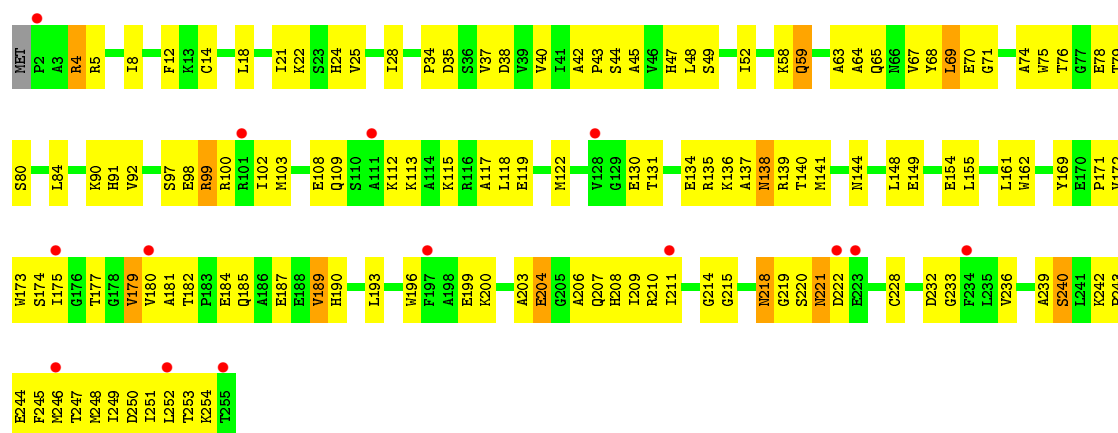


• Molecule 1: TRIOSEPHOSPHATE ISOMERASE

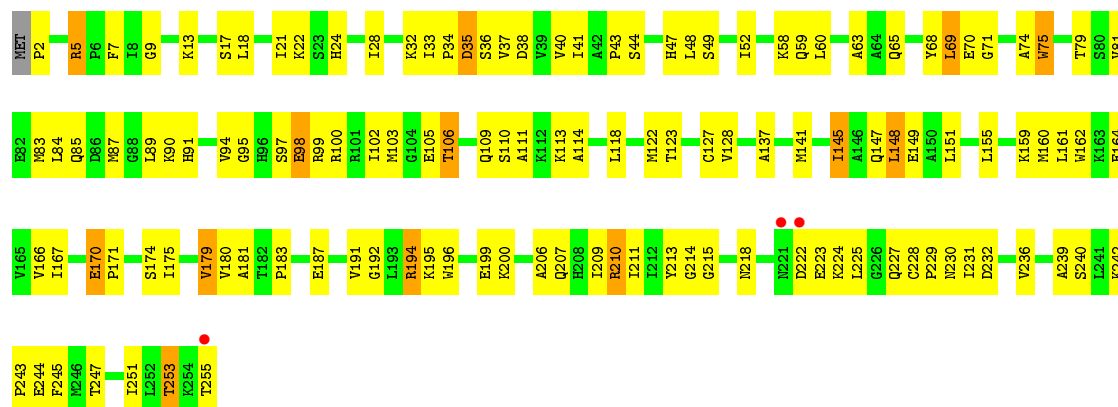




• Molecule 1: TRIOSEPHOSPHATE ISOMERASE

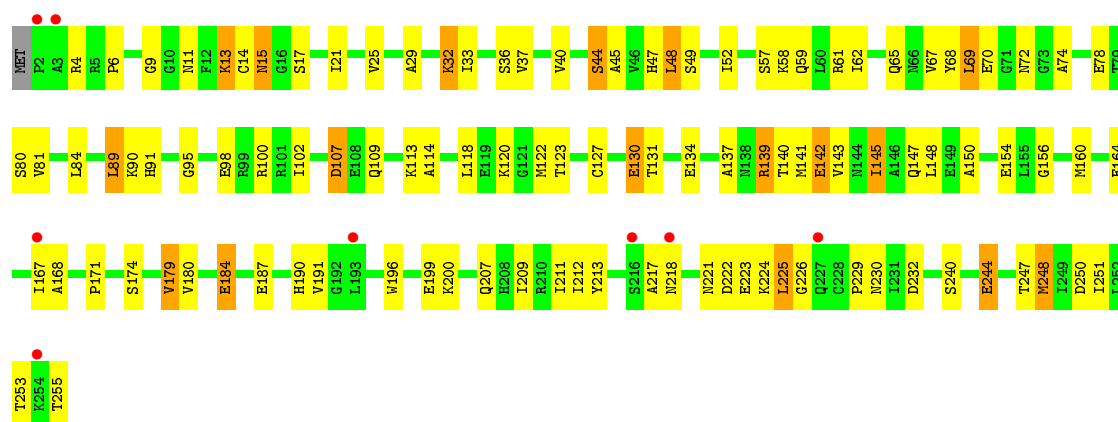


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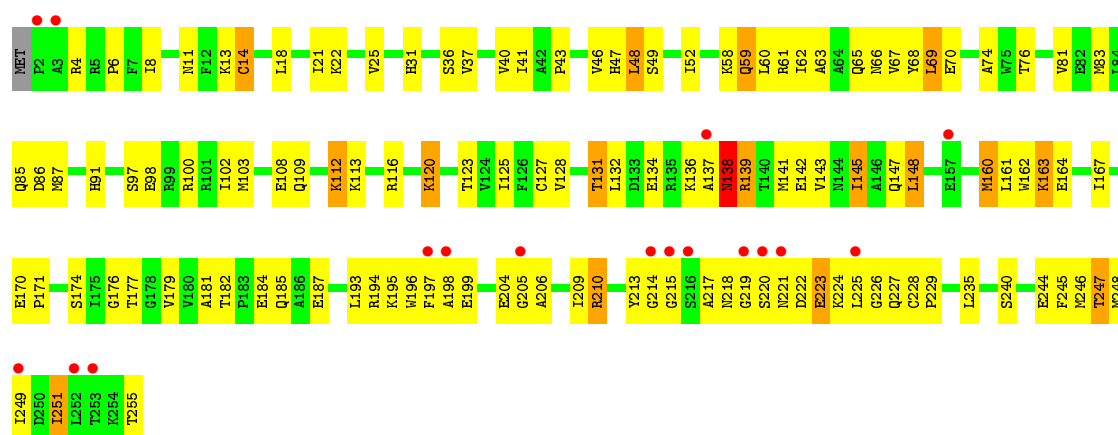


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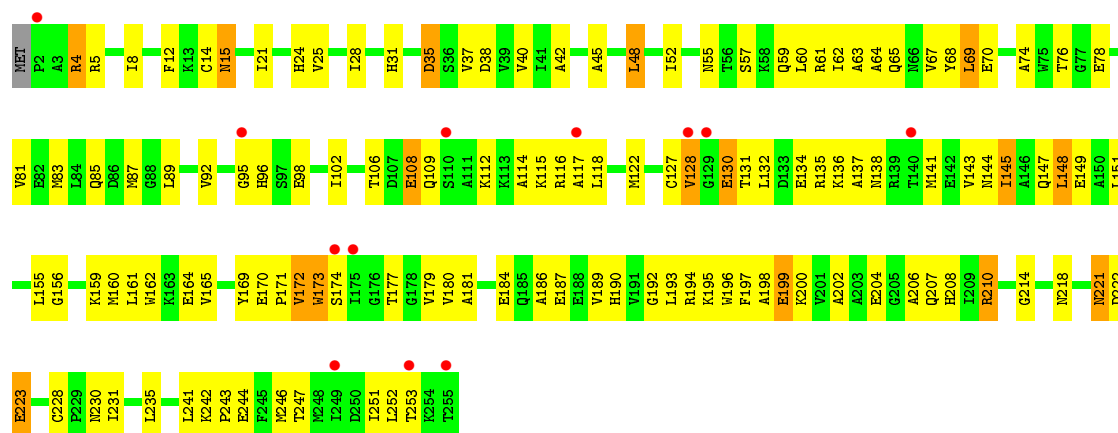




● Molecule 1: TRIOSEPHOSPHATE ISOMERASE

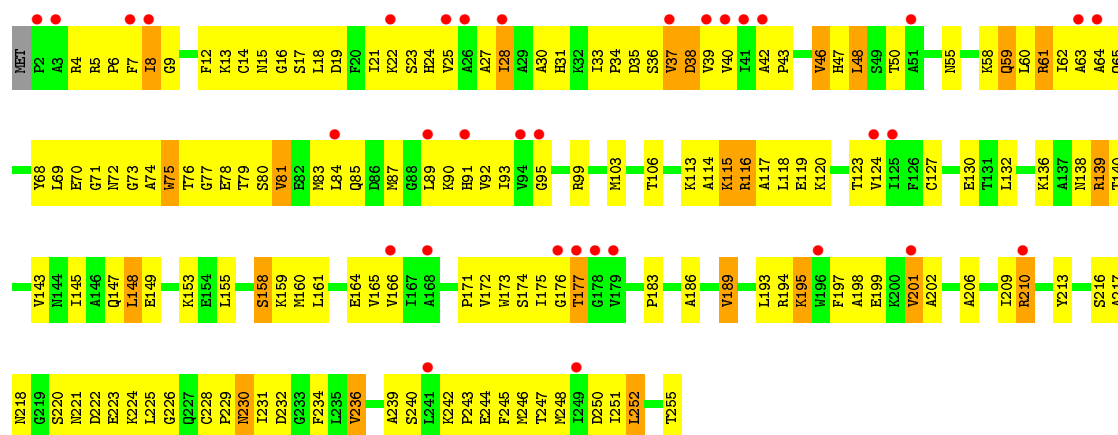


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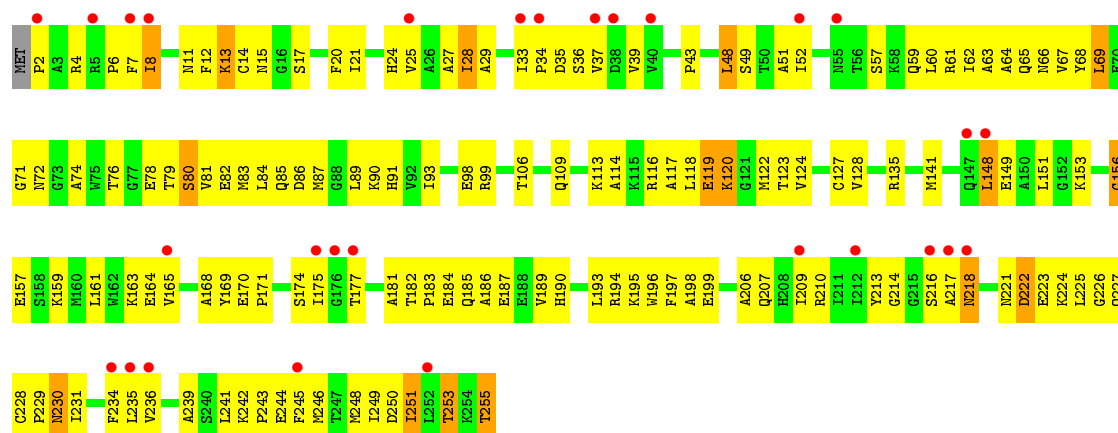
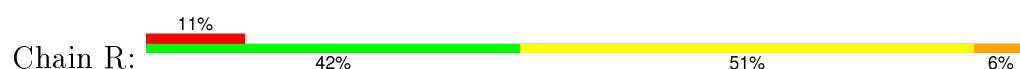


● Molecule 1: TRIOSEPHOSPHATE ISOMERASE

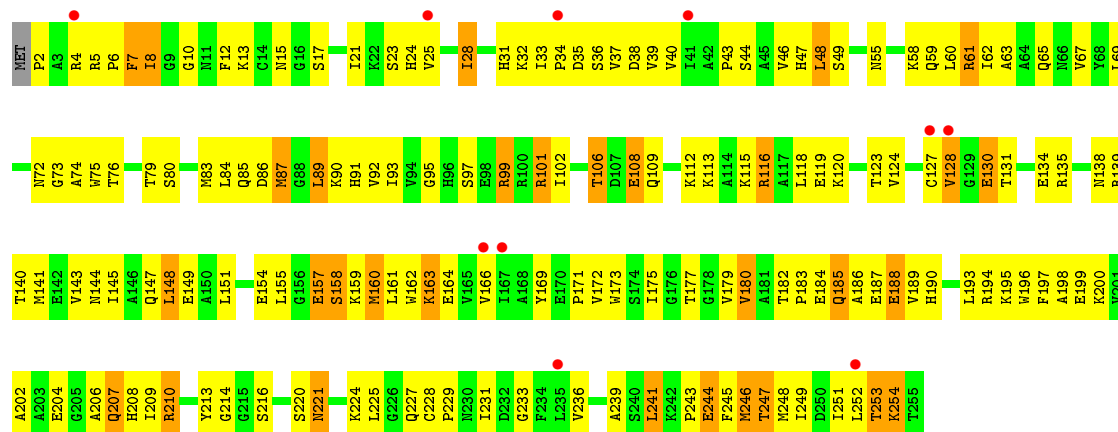




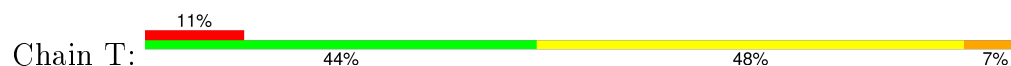
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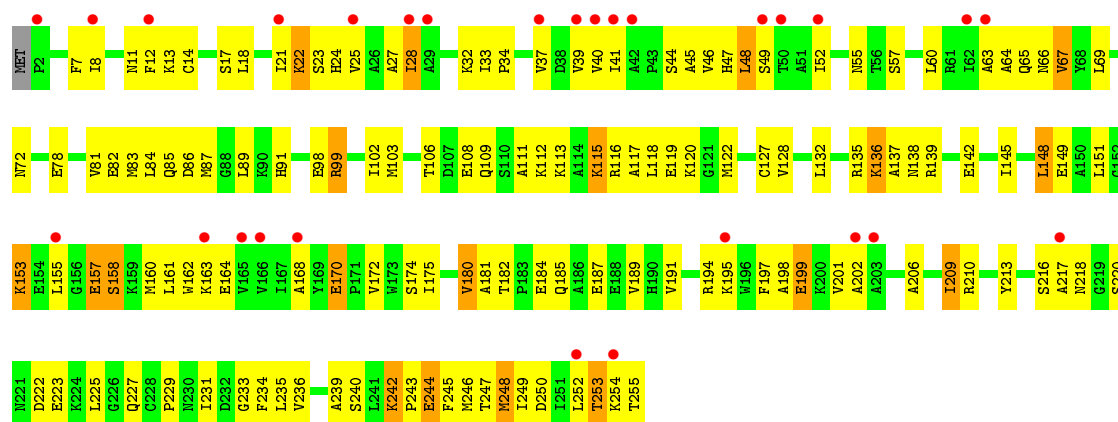


• Molecule 1: TRIOSEPHOSPHATE ISOMERASE



• Molecule 1: TRIOSEPHOSPHATE ISOMERASE





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) 65.6 (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 0.236 , 0.269	Depositor DCC
R_{free} test set	8804 reflections (6.43%)	DCC
Wilson B-factor (Å ²)	50.3	Xtriage
Anisotropy	0.256	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	(Not available) , (Not available)	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 ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.25$	Xtriage
Outliers	0 of 144197 reflections	Xtriage
F_o, F_c correlation	0.91	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.

²Theoretical 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	0.48	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 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	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

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 30.

The worst 5 of 2346 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C: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 [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	252/255 (99%)	241 (96%)	10 (4%)	1 (0%)	39	69
1	B	252/255 (99%)	247 (98%)	5 (2%)	0	100	100
1	C	252/255 (99%)	240 (95%)	11 (4%)	1 (0%)	39	69
1	D	252/255 (99%)	244 (97%)	7 (3%)	1 (0%)	39	69
1	E	252/255 (99%)	240 (95%)	11 (4%)	1 (0%)	39	69
1	F	252/255 (99%)	244 (97%)	7 (3%)	1 (0%)	39	69
1	G	252/255 (99%)	243 (96%)	8 (3%)	1 (0%)	39	69
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%)	39	69
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%)	24	51
1	O	252/255 (99%)	237 (94%)	14 (6%)	1 (0%)	39	69
1	P	252/255 (99%)	233 (92%)	18 (7%)	1 (0%)	39	69
1	Q	252/255 (99%)	237 (94%)	14 (6%)	1 (0%)	39	69
1	R	252/255 (99%)	242 (96%)	7 (3%)	3 (1%)	16	39
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%)	46	75

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%)	6	15
1	B	202/203 (100%)	187 (93%)	15 (7%)	17	39
1	C	202/203 (100%)	180 (89%)	22 (11%)	8	18
1	D	202/203 (100%)	176 (87%)	26 (13%)	5	12
1	E	202/203 (100%)	177 (88%)	25 (12%)	6	13
1	F	202/203 (100%)	186 (92%)	16 (8%)	15	34
1	G	202/203 (100%)	181 (90%)	21 (10%)	9	20
1	H	202/203 (100%)	180 (89%)	22 (11%)	8	18
1	I	202/203 (100%)	177 (88%)	25 (12%)	6	13
1	J	202/203 (100%)	184 (91%)	18 (9%)	12	27
1	K	202/203 (100%)	181 (90%)	21 (10%)	9	20
1	L	202/203 (100%)	184 (91%)	18 (9%)	12	27
1	M	202/203 (100%)	176 (87%)	26 (13%)	5	12
1	N	202/203 (100%)	176 (87%)	26 (13%)	5	12
1	O	202/203 (100%)	176 (87%)	26 (13%)	5	12
1	P	202/203 (100%)	180 (89%)	22 (11%)	8	18
1	Q	202/203 (100%)	169 (84%)	33 (16%)	3	7
1	R	202/203 (100%)	181 (90%)	21 (10%)	9	20
1	S	202/203 (100%)	160 (79%)	42 (21%)	1	4
1	T	202/203 (100%)	168 (83%)	34 (17%)	2	6

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	4040/4060 (100%)	3557 (88%)	483 (12%)	6 14

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 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 [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, 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%)	0.10	9 (3%) 48 48	26, 40, 72, 88	0
1	B	254/255 (99%)	0.11	7 (2%) 56 57	21, 37, 70, 89	0
1	C	254/255 (99%)	0.11	8 (3%) 52 52	22, 39, 72, 93	0
1	D	254/255 (99%)	0.08	4 (1%) 74 75	25, 40, 71, 84	0
1	E	254/255 (99%)	0.18	11 (4%) 39 38	24, 44, 75, 90	0
1	F	254/255 (99%)	0.09	4 (1%) 74 75	23, 39, 71, 88	0
1	G	254/255 (99%)	0.18	10 (3%) 43 43	24, 38, 70, 92	0
1	H	254/255 (99%)	0.07	3 (1%) 81 81	24, 39, 73, 91	0
1	I	254/255 (99%)	0.13	6 (2%) 62 62	25, 40, 70, 85	0
1	J	254/255 (99%)	0.05	6 (2%) 62 62	24, 38, 72, 93	0
1	K	254/255 (99%)	0.26	15 (5%) 26 24	25, 48, 76, 93	0
1	L	254/255 (99%)	0.36	14 (5%) 29 27	27, 52, 79, 90	0
1	M	254/255 (99%)	0.12	3 (1%) 81 81	24, 42, 75, 87	0
1	N	254/255 (99%)	0.16	8 (3%) 52 52	23, 43, 76, 92	0
1	O	254/255 (99%)	0.35	17 (6%) 21 19	24, 45, 77, 93	0
1	P	254/255 (99%)	0.30	12 (4%) 35 34	27, 51, 80, 95	0
1	Q	254/255 (99%)	0.65	34 (13%) 4 3	40, 65, 86, 96	0
1	R	254/255 (99%)	0.56	28 (11%) 7 5	35, 64, 87, 95	0
1	S	254/255 (99%)	0.34	10 (3%) 43 43	41, 64, 85, 96	0
1	T	254/255 (99%)	0.51	28 (11%) 7 5	36, 62, 87, 96	0
All	All	5080/5100 (99%)	0.23	237 (4%) 35 34	21, 46, 79, 96	0

The worst 5 of 237 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	N	2	PRO	11.8
1	R	217	ALA	11.0
1	K	219	GLY	9.2
1	Q	40	VAL	7.9
1	A	217	ALA	7.8

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.