



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 15, 2017 – 06:31 am GMT

PDB ID : 1VPX
Title : Crystal structure of Transaldolase (EC 2.2.1.2) (TM0295) from *Thermotoga maritima* at 2.40 Å resolution
Authors : Joint Center for Structural Genomics (JCSG)
Deposited on : 2004-11-23
Resolution : 2.40 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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : recalc28949

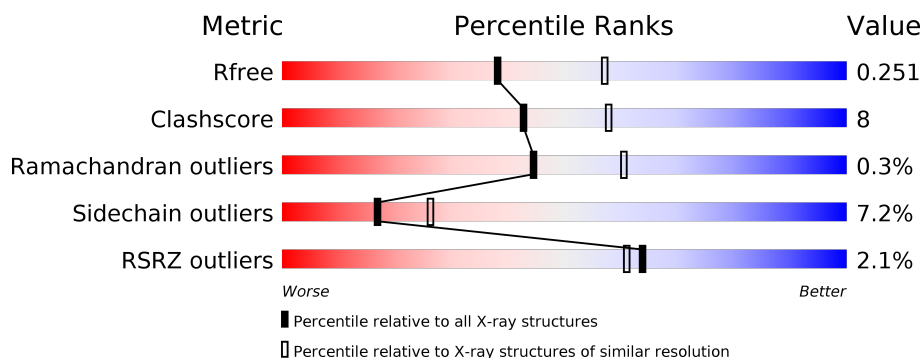
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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}	100719	3166 (2.40-2.40)
Clashscore	112137	3674 (2.40-2.40)
Ramachandran outliers	110173	3616 (2.40-2.40)
Sidechain outliers	110143	3617 (2.40-2.40)
RSRZ outliers	101464	3195 (2.40-2.40)

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	230	<div> <div>71%</div> <div>16%</div> <div>•</div> <div>10%</div> </div>
1	B	230	<div> <div>%</div> <div>71%</div> <div>17%</div> <div>•</div> <div>9%</div> </div>
1	C	230	<div> <div>%</div> <div>67%</div> <div>20%</div> <div>•</div> <div>10%</div> </div>
1	D	230	<div> <div>%</div> <div>73%</div> <div>17%</div> <div>•</div> <div>9%</div> </div>
1	E	230	<div> <div>72%</div> <div>20%</div> <div>•</div> <div>6%</div> </div>
1	F	230	<div> <div>%</div> <div>74%</div> <div>16%</div> <div>•</div> <div>7%</div> </div>

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	G	230	
1	H	230	
1	I	230	
1	J	230	
1	K	230	
1	L	230	
1	M	230	
1	N	230	
1	O	230	
1	P	230	
1	Q	230	
1	R	230	
1	S	230	
1	T	230	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	SO4	O	219	-	-	-	X
3	GOL	H	219	-	-	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 31916 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called PROTEIN (Transaldolase (EC 2.2.1.2)).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	207	Total	C	N	O	S	0	0	0
			1591	1022	258	299	12			
1	B	209	Total	C	N	O	S	0	0	0
			1584	1016	260	296	12			
1	C	208	Total	C	N	O	S	0	0	0
			1560	997	252	299	12			
1	D	210	Total	C	N	O	S	0	0	0
			1615	1034	264	305	12			
1	E	216	Total	C	N	O	S	0	0	0
			1674	1075	272	315	12			
1	F	213	Total	C	N	O	S	0	0	0
			1655	1064	270	309	12			
1	G	216	Total	C	N	O	S	0	0	0
			1667	1070	271	314	12			
1	H	205	Total	C	N	O	S	0	0	0
			1550	996	248	294	12			
1	I	211	Total	C	N	O	S	0	0	0
			1615	1034	264	305	12			
1	J	213	Total	C	N	O	S	0	0	0
			1619	1038	263	306	12			
1	K	216	Total	C	N	O	S	0	0	0
			1651	1059	265	315	12			
1	L	204	Total	C	N	O	S	0	0	0
			1530	980	249	289	12			
1	M	198	Total	C	N	O	S	0	0	0
			1457	928	240	278	11			
1	N	204	Total	C	N	O	S	0	0	0
			1475	939	243	281	12			
1	O	210	Total	C	N	O	S	0	0	0
			1604	1025	260	307	12			
1	P	209	Total	C	N	O	S	0	0	0
			1576	1010	258	296	12			

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Q	208	Total	C	N	O	S	0	1	0
			1596	1027	259	298	12			
1	R	210	Total	C	N	O	S	0	0	0
			1585	1014	259	300	12			
1	S	205	Total	C	N	O	S	0	0	0
			1533	978	254	290	11			
1	T	204	Total	C	N	O	S	0	0	0
			1541	987	249	293	12			

There are 240 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-11	MET	-	LEADER SEQUENCE	UNP Q9WYD1
A	-10	GLY	-	LEADER SEQUENCE	UNP Q9WYD1
A	-9	SER	-	LEADER SEQUENCE	UNP Q9WYD1
A	-8	ASP	-	LEADER SEQUENCE	UNP Q9WYD1
A	-7	LYS	-	LEADER SEQUENCE	UNP Q9WYD1
A	-6	ILE	-	LEADER SEQUENCE	UNP Q9WYD1
A	-5	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
A	-4	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
A	-3	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
A	-2	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
A	-1	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
A	0	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
B	-11	MET	-	LEADER SEQUENCE	UNP Q9WYD1
B	-10	GLY	-	LEADER SEQUENCE	UNP Q9WYD1
B	-9	SER	-	LEADER SEQUENCE	UNP Q9WYD1
B	-8	ASP	-	LEADER SEQUENCE	UNP Q9WYD1
B	-7	LYS	-	LEADER SEQUENCE	UNP Q9WYD1
B	-6	ILE	-	LEADER SEQUENCE	UNP Q9WYD1
B	-5	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
B	-4	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
B	-3	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
B	-2	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
B	-1	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
B	0	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
C	-11	MET	-	LEADER SEQUENCE	UNP Q9WYD1
C	-10	GLY	-	LEADER SEQUENCE	UNP Q9WYD1
C	-9	SER	-	LEADER SEQUENCE	UNP Q9WYD1
C	-8	ASP	-	LEADER SEQUENCE	UNP Q9WYD1
C	-7	LYS	-	LEADER SEQUENCE	UNP Q9WYD1
C	-6	ILE	-	LEADER SEQUENCE	UNP Q9WYD1
C	-5	HIS	-	LEADER SEQUENCE	UNP Q9WYD1

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
C	-4	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
C	-3	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
C	-2	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
C	-1	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
C	0	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
D	-11	MET	-	LEADER SEQUENCE	UNP Q9WYD1
D	-10	GLY	-	LEADER SEQUENCE	UNP Q9WYD1
D	-9	SER	-	LEADER SEQUENCE	UNP Q9WYD1
D	-8	ASP	-	LEADER SEQUENCE	UNP Q9WYD1
D	-7	LYS	-	LEADER SEQUENCE	UNP Q9WYD1
D	-6	ILE	-	LEADER SEQUENCE	UNP Q9WYD1
D	-5	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
D	-4	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
D	-3	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
D	-2	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
D	-1	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
D	0	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
E	-11	MET	-	LEADER SEQUENCE	UNP Q9WYD1
E	-10	GLY	-	LEADER SEQUENCE	UNP Q9WYD1
E	-9	SER	-	LEADER SEQUENCE	UNP Q9WYD1
E	-8	ASP	-	LEADER SEQUENCE	UNP Q9WYD1
E	-7	LYS	-	LEADER SEQUENCE	UNP Q9WYD1
E	-6	ILE	-	LEADER SEQUENCE	UNP Q9WYD1
E	-5	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
E	-4	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
E	-3	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
E	-2	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
E	-1	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
E	0	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
F	-11	MET	-	LEADER SEQUENCE	UNP Q9WYD1
F	-10	GLY	-	LEADER SEQUENCE	UNP Q9WYD1
F	-9	SER	-	LEADER SEQUENCE	UNP Q9WYD1
F	-8	ASP	-	LEADER SEQUENCE	UNP Q9WYD1
F	-7	LYS	-	LEADER SEQUENCE	UNP Q9WYD1
F	-6	ILE	-	LEADER SEQUENCE	UNP Q9WYD1
F	-5	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
F	-4	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
F	-3	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
F	-2	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
F	-1	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
F	0	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
G	-11	MET	-	LEADER SEQUENCE	UNP Q9WYD1

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
G	-10	GLY	-	LEADER SEQUENCE	UNP Q9WYD1
G	-9	SER	-	LEADER SEQUENCE	UNP Q9WYD1
G	-8	ASP	-	LEADER SEQUENCE	UNP Q9WYD1
G	-7	LYS	-	LEADER SEQUENCE	UNP Q9WYD1
G	-6	ILE	-	LEADER SEQUENCE	UNP Q9WYD1
G	-5	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
G	-4	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
G	-3	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
G	-2	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
G	-1	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
G	0	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
H	-11	MET	-	LEADER SEQUENCE	UNP Q9WYD1
H	-10	GLY	-	LEADER SEQUENCE	UNP Q9WYD1
H	-9	SER	-	LEADER SEQUENCE	UNP Q9WYD1
H	-8	ASP	-	LEADER SEQUENCE	UNP Q9WYD1
H	-7	LYS	-	LEADER SEQUENCE	UNP Q9WYD1
H	-6	ILE	-	LEADER SEQUENCE	UNP Q9WYD1
H	-5	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
H	-4	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
H	-3	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
H	-2	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
H	-1	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
H	0	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
I	-11	MET	-	LEADER SEQUENCE	UNP Q9WYD1
I	-10	GLY	-	LEADER SEQUENCE	UNP Q9WYD1
I	-9	SER	-	LEADER SEQUENCE	UNP Q9WYD1
I	-8	ASP	-	LEADER SEQUENCE	UNP Q9WYD1
I	-7	LYS	-	LEADER SEQUENCE	UNP Q9WYD1
I	-6	ILE	-	LEADER SEQUENCE	UNP Q9WYD1
I	-5	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
I	-4	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
I	-3	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
I	-2	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
I	-1	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
I	0	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
J	-11	MET	-	LEADER SEQUENCE	UNP Q9WYD1
J	-10	GLY	-	LEADER SEQUENCE	UNP Q9WYD1
J	-9	SER	-	LEADER SEQUENCE	UNP Q9WYD1
J	-8	ASP	-	LEADER SEQUENCE	UNP Q9WYD1
J	-7	LYS	-	LEADER SEQUENCE	UNP Q9WYD1
J	-6	ILE	-	LEADER SEQUENCE	UNP Q9WYD1
J	-5	HIS	-	LEADER SEQUENCE	UNP Q9WYD1

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
J	-4	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
J	-3	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
J	-2	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
J	-1	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
J	0	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
K	-11	MET	-	LEADER SEQUENCE	UNP Q9WYD1
K	-10	GLY	-	LEADER SEQUENCE	UNP Q9WYD1
K	-9	SER	-	LEADER SEQUENCE	UNP Q9WYD1
K	-8	ASP	-	LEADER SEQUENCE	UNP Q9WYD1
K	-7	LYS	-	LEADER SEQUENCE	UNP Q9WYD1
K	-6	ILE	-	LEADER SEQUENCE	UNP Q9WYD1
K	-5	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
K	-4	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
K	-3	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
K	-2	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
K	-1	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
K	0	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
L	-11	MET	-	LEADER SEQUENCE	UNP Q9WYD1
L	-10	GLY	-	LEADER SEQUENCE	UNP Q9WYD1
L	-9	SER	-	LEADER SEQUENCE	UNP Q9WYD1
L	-8	ASP	-	LEADER SEQUENCE	UNP Q9WYD1
L	-7	LYS	-	LEADER SEQUENCE	UNP Q9WYD1
L	-6	ILE	-	LEADER SEQUENCE	UNP Q9WYD1
L	-5	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
L	-4	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
L	-3	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
L	-2	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
L	-1	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
L	0	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
M	-11	MET	-	LEADER SEQUENCE	UNP Q9WYD1
M	-10	GLY	-	LEADER SEQUENCE	UNP Q9WYD1
M	-9	SER	-	LEADER SEQUENCE	UNP Q9WYD1
M	-8	ASP	-	LEADER SEQUENCE	UNP Q9WYD1
M	-7	LYS	-	LEADER SEQUENCE	UNP Q9WYD1
M	-6	ILE	-	LEADER SEQUENCE	UNP Q9WYD1
M	-5	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
M	-4	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
M	-3	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
M	-2	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
M	-1	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
M	0	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
N	-11	MET	-	LEADER SEQUENCE	UNP Q9WYD1

Continued on next page...

Continued from previous page...

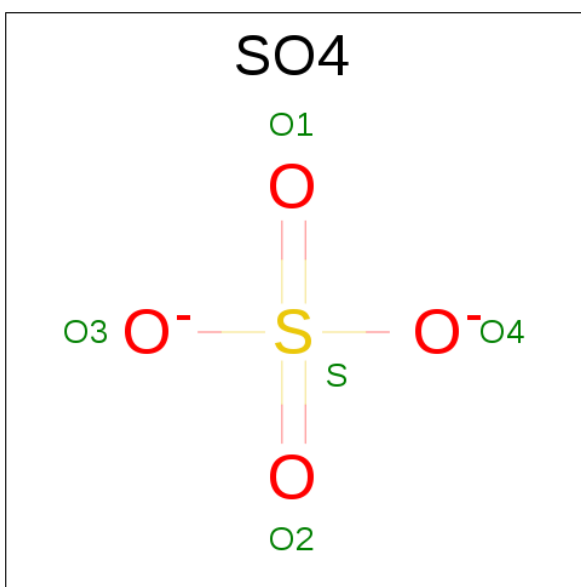
Chain	Residue	Modelled	Actual	Comment	Reference
N	-10	GLY	-	LEADER SEQUENCE	UNP Q9WYD1
N	-9	SER	-	LEADER SEQUENCE	UNP Q9WYD1
N	-8	ASP	-	LEADER SEQUENCE	UNP Q9WYD1
N	-7	LYS	-	LEADER SEQUENCE	UNP Q9WYD1
N	-6	ILE	-	LEADER SEQUENCE	UNP Q9WYD1
N	-5	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
N	-4	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
N	-3	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
N	-2	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
N	-1	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
N	0	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
O	-11	MET	-	LEADER SEQUENCE	UNP Q9WYD1
O	-10	GLY	-	LEADER SEQUENCE	UNP Q9WYD1
O	-9	SER	-	LEADER SEQUENCE	UNP Q9WYD1
O	-8	ASP	-	LEADER SEQUENCE	UNP Q9WYD1
O	-7	LYS	-	LEADER SEQUENCE	UNP Q9WYD1
O	-6	ILE	-	LEADER SEQUENCE	UNP Q9WYD1
O	-5	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
O	-4	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
O	-3	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
O	-2	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
O	-1	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
O	0	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
P	-11	MET	-	LEADER SEQUENCE	UNP Q9WYD1
P	-10	GLY	-	LEADER SEQUENCE	UNP Q9WYD1
P	-9	SER	-	LEADER SEQUENCE	UNP Q9WYD1
P	-8	ASP	-	LEADER SEQUENCE	UNP Q9WYD1
P	-7	LYS	-	LEADER SEQUENCE	UNP Q9WYD1
P	-6	ILE	-	LEADER SEQUENCE	UNP Q9WYD1
P	-5	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
P	-4	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
P	-3	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
P	-2	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
P	-1	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
P	0	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
Q	-11	MET	-	LEADER SEQUENCE	UNP Q9WYD1
Q	-10	GLY	-	LEADER SEQUENCE	UNP Q9WYD1
Q	-9	SER	-	LEADER SEQUENCE	UNP Q9WYD1
Q	-8	ASP	-	LEADER SEQUENCE	UNP Q9WYD1
Q	-7	LYS	-	LEADER SEQUENCE	UNP Q9WYD1
Q	-6	ILE	-	LEADER SEQUENCE	UNP Q9WYD1
Q	-5	HIS	-	LEADER SEQUENCE	UNP Q9WYD1

Continued on next page...

Continued from previous page...

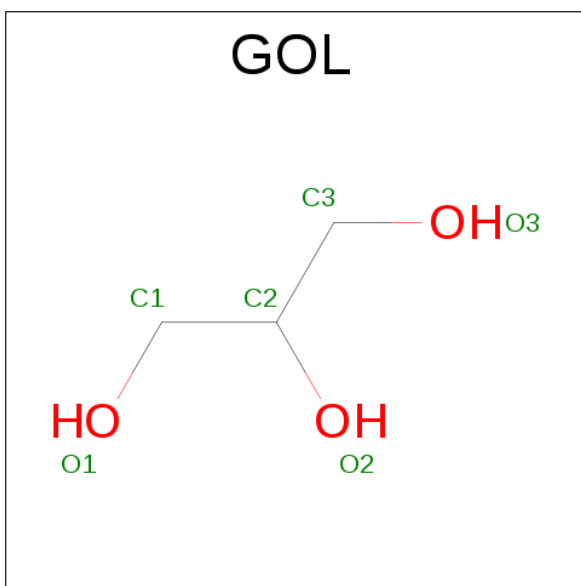
Chain	Residue	Modelled	Actual	Comment	Reference
Q	-4	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
Q	-3	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
Q	-2	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
Q	-1	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
Q	0	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
R	-11	MET	-	LEADER SEQUENCE	UNP Q9WYD1
R	-10	GLY	-	LEADER SEQUENCE	UNP Q9WYD1
R	-9	SER	-	LEADER SEQUENCE	UNP Q9WYD1
R	-8	ASP	-	LEADER SEQUENCE	UNP Q9WYD1
R	-7	LYS	-	LEADER SEQUENCE	UNP Q9WYD1
R	-6	ILE	-	LEADER SEQUENCE	UNP Q9WYD1
R	-5	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
R	-4	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
R	-3	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
R	-2	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
R	-1	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
R	0	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
S	-11	MET	-	LEADER SEQUENCE	UNP Q9WYD1
S	-10	GLY	-	LEADER SEQUENCE	UNP Q9WYD1
S	-9	SER	-	LEADER SEQUENCE	UNP Q9WYD1
S	-8	ASP	-	LEADER SEQUENCE	UNP Q9WYD1
S	-7	LYS	-	LEADER SEQUENCE	UNP Q9WYD1
S	-6	ILE	-	LEADER SEQUENCE	UNP Q9WYD1
S	-5	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
S	-4	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
S	-3	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
S	-2	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
S	-1	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
S	0	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
T	-11	MET	-	LEADER SEQUENCE	UNP Q9WYD1
T	-10	GLY	-	LEADER SEQUENCE	UNP Q9WYD1
T	-9	SER	-	LEADER SEQUENCE	UNP Q9WYD1
T	-8	ASP	-	LEADER SEQUENCE	UNP Q9WYD1
T	-7	LYS	-	LEADER SEQUENCE	UNP Q9WYD1
T	-6	ILE	-	LEADER SEQUENCE	UNP Q9WYD1
T	-5	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
T	-4	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
T	-3	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
T	-2	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
T	-1	HIS	-	LEADER SEQUENCE	UNP Q9WYD1
T	0	HIS	-	LEADER SEQUENCE	UNP Q9WYD1

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	O	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	C	O	0	0
			6	3	3		
3	C	1	Total	C	O	0	0
			6	3	3		
3	R	1	Total	C	O	0	0
			6	3	3		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	S	1	Total	C	O	0	0
			6	3	3		
3	K	1	Total	C	O	0	1
			10	5	5		
3	N	1	Total	C	O	0	0
			6	3	3		
3	O	1	Total	C	O	0	0
			6	3	3		
3	F	1	Total	C	O	0	0
			6	3	3		
3	G	1	Total	C	O	0	0
			6	3	3		
3	H	1	Total	C	O	0	0
			6	3	3		
3	I	1	Total	C	O	0	0
			6	3	3		
3	J	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
3	D	1	Total	C	O	0	0
			6	3	3		
3	E	1	Total	C	O	0	0
			6	3	3		
3	P	1	Total	C	O	0	0
			6	3	3		
3	Q	1	Total	C	O	0	0
			6	3	3		
3	T	1	Total	C	O	0	0
			6	3	3		
3	L	1	Total	C	O	0	0
			6	3	3		
3	M	1	Total	C	O	0	0
			6	3	3		
3	P	1	Total	C	O	0	0
			6	3	3		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	5	Total	O	0	0
			5	5		

Continued on next page...

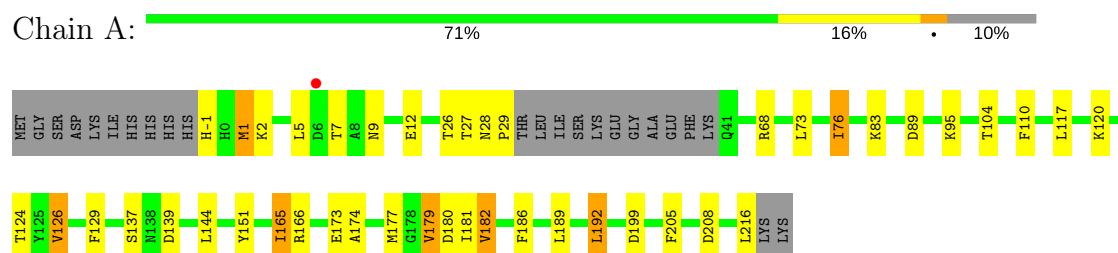
Continued from previous page...

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	6	Total O 6 6	0	0
4	C	7	Total O 7 7	0	0
4	D	16	Total O 16 16	0	0
4	E	7	Total O 7 7	0	0
4	F	5	Total O 5 5	0	0
4	G	17	Total O 17 17	0	0
4	H	3	Total O 3 3	0	0
4	I	4	Total O 4 4	0	0
4	J	7	Total O 7 7	0	0
4	K	3	Total O 3 3	0	0
4	L	1	Total O 1 1	0	0
4	M	2	Total O 2 2	0	0
4	O	5	Total O 5 5	0	0
4	P	3	Total O 3 3	0	0
4	Q	7	Total O 7 7	0	0
4	R	2	Total O 2 2	0	0
4	S	2	Total O 2 2	0	0
4	T	1	Total O 1 1	0	0

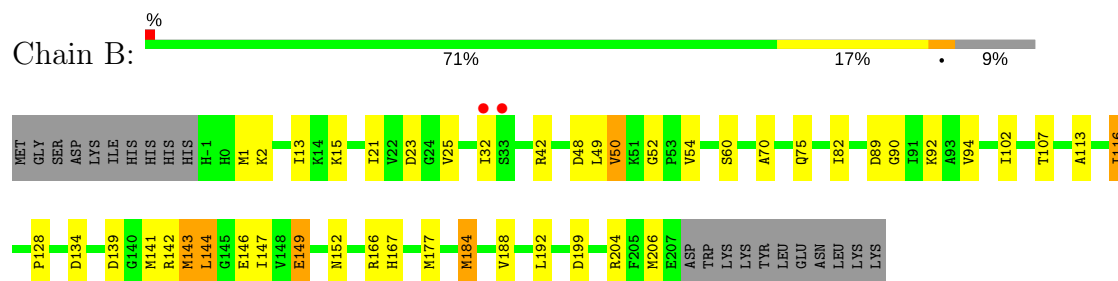
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

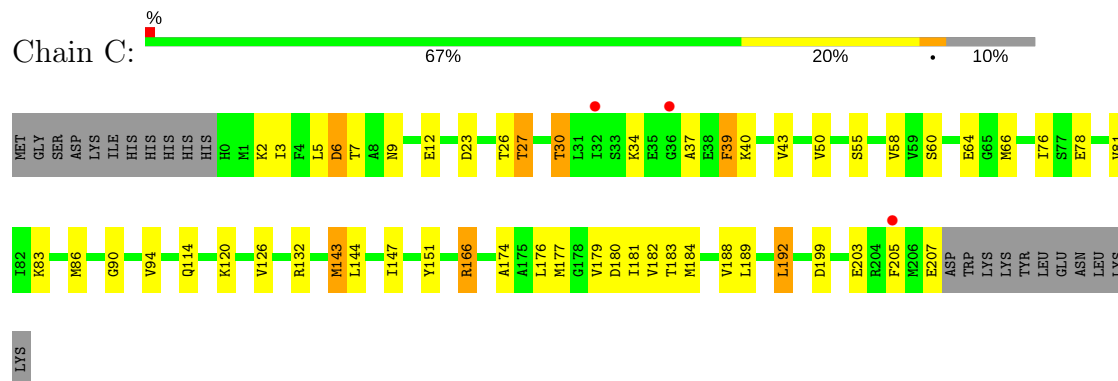
- Molecule 1: PROTEIN (Transaldolase (EC 2.2.1.2))



- Molecule 1: PROTEIN (Transaldolase (EC 2.2.1.2))

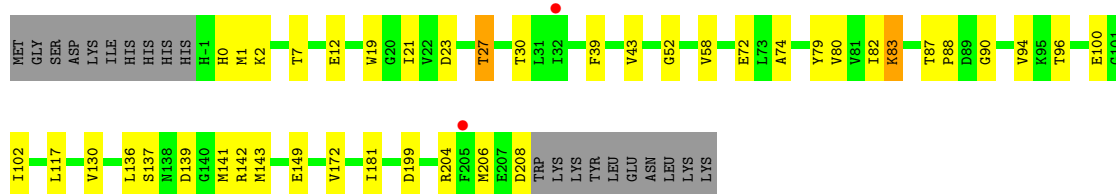


- Molecule 1: PROTEIN (Transaldolase (EC 2.2.1.2))



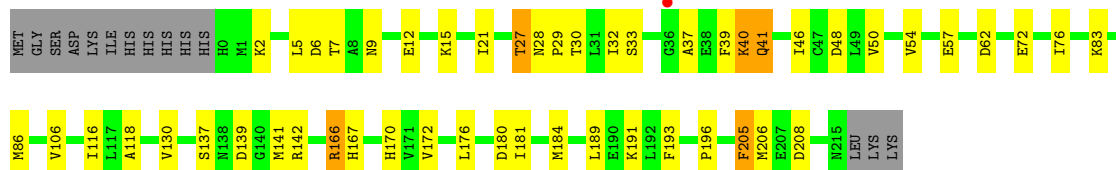
- Molecule 1: PROTEIN (Transaldolase (EC 2.2.1.2))





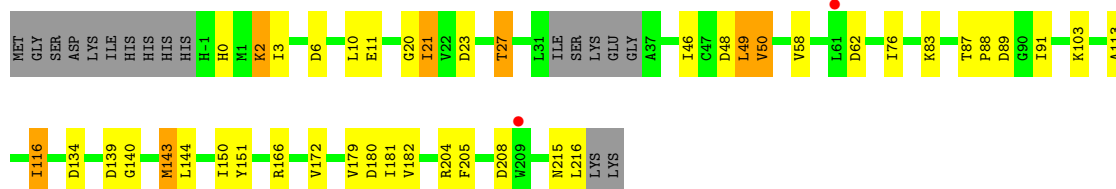
- Molecule 1: PROTEIN (Transaldolase (EC 2.2.1.2))

Chain E: 72% 20% 6%



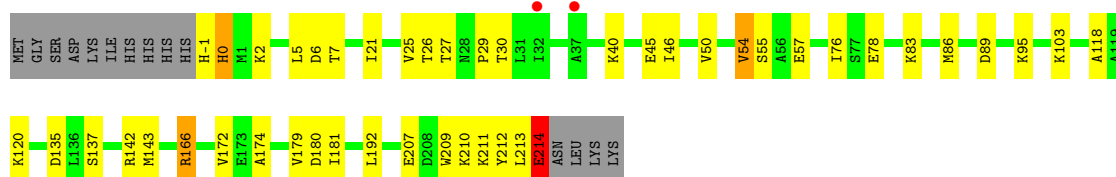
- Molecule 1: PROTEIN (Transaldolase (EC 2.2.1.2))

Chain F: 74% 16% 7%



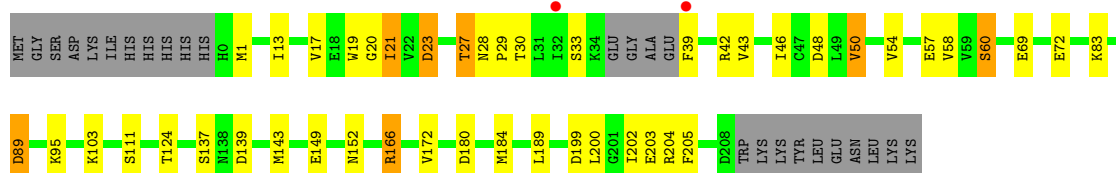
- Molecule 1: PROTEIN (Transaldolase (EC 2.2.1.2))

Chain G: 74% 18% 6%

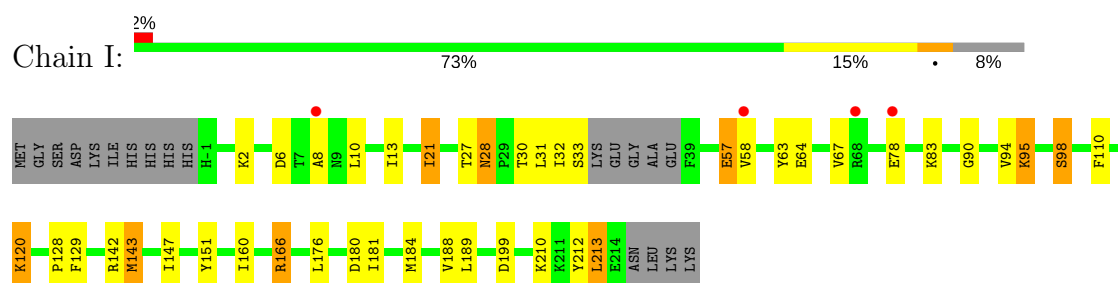


- Molecule 1: PROTEIN (Transaldolase (EC 2.2.1.2))

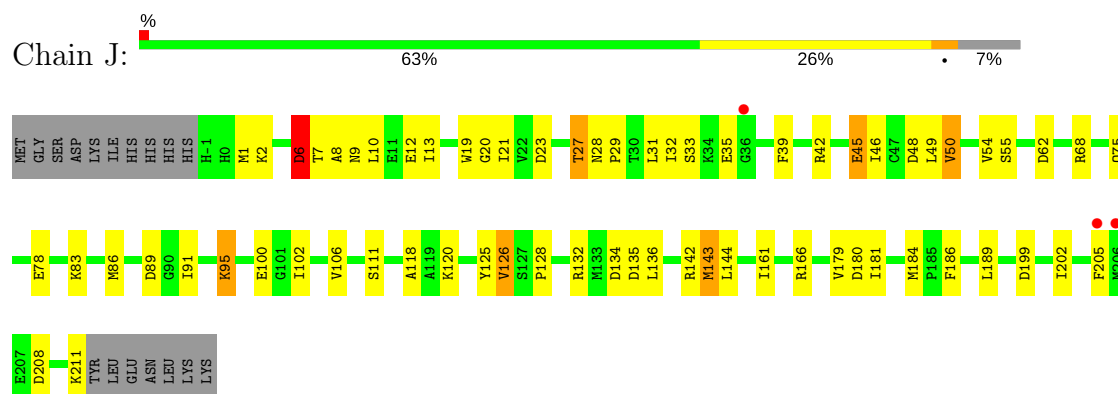
Chain H: 69% 17% 11%



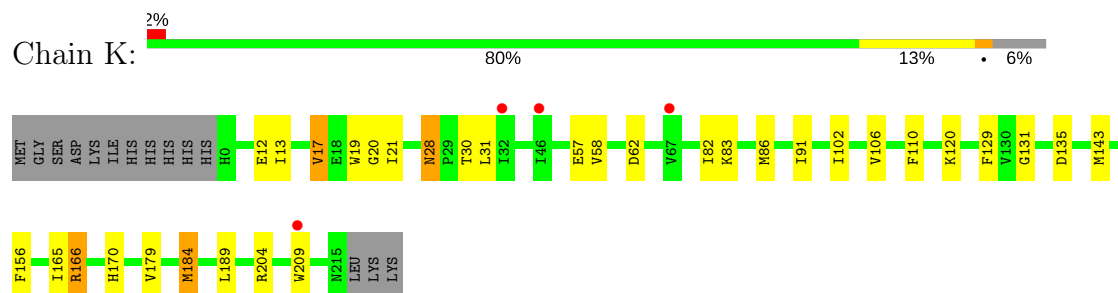
- Molecule 1: PROTEIN (Transaldolase (EC 2.2.1.2))



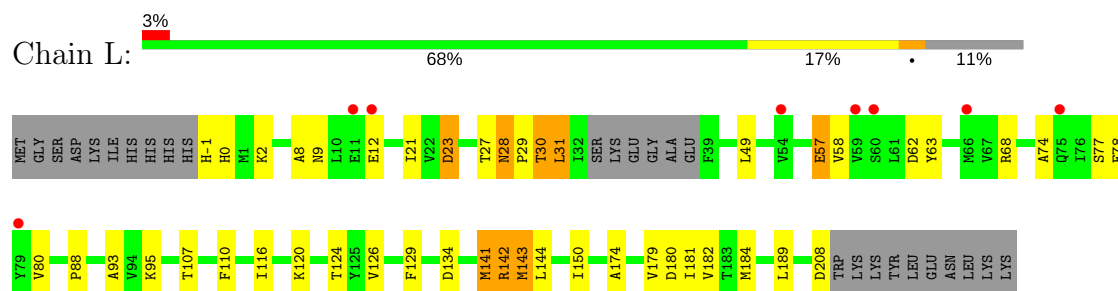
• Molecule 1: PROTEIN (Transaldolase (EC 2.2.1.2))



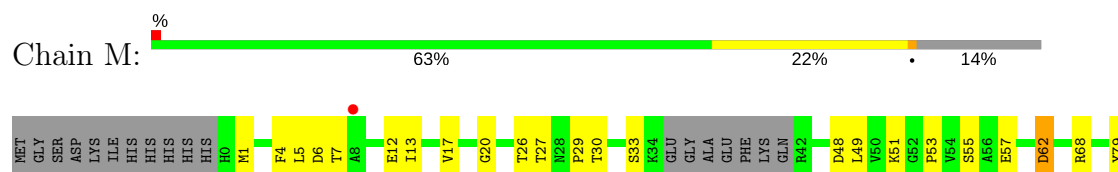
• Molecule 1: PROTEIN (Transaldolase (EC 2.2.1.2))

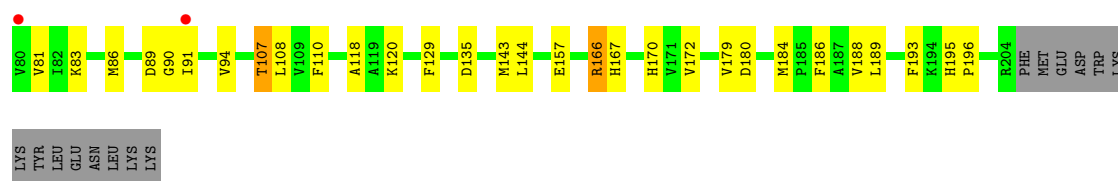


• Molecule 1: PROTEIN (Transaldolase (EC 2.2.1.2))

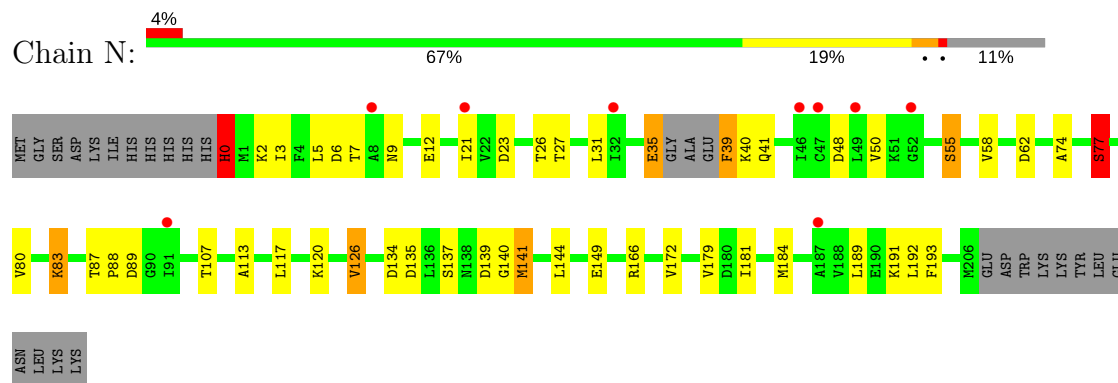


• Molecule 1: PROTEIN (Transaldolase (EC 2.2.1.2))

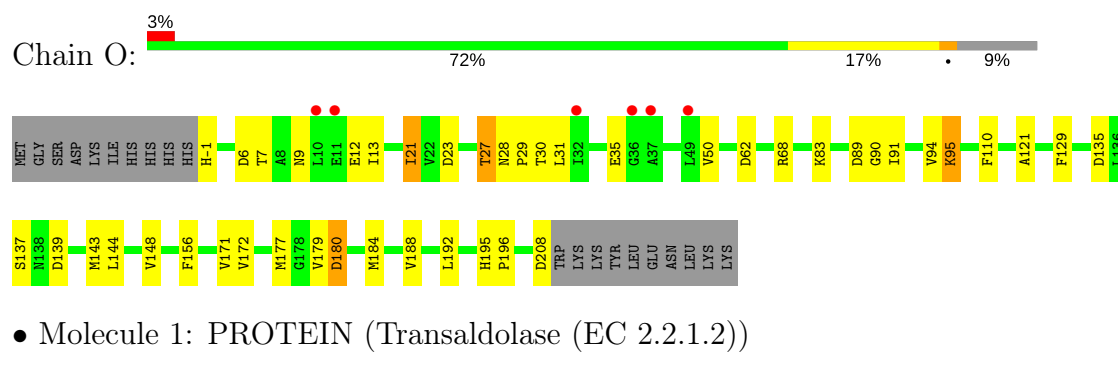




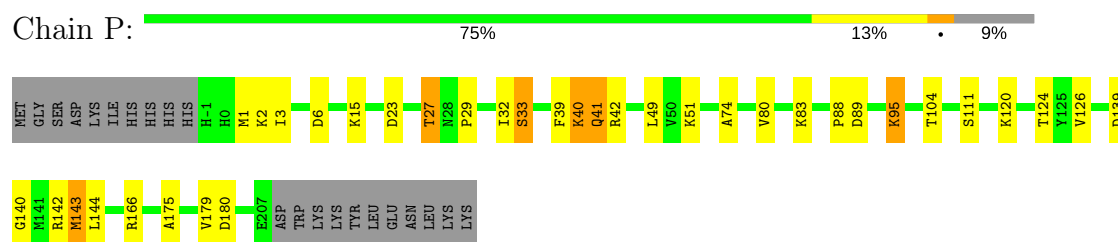
- Molecule 1: PROTEIN (Transaldolase (EC 2.2.1.2))



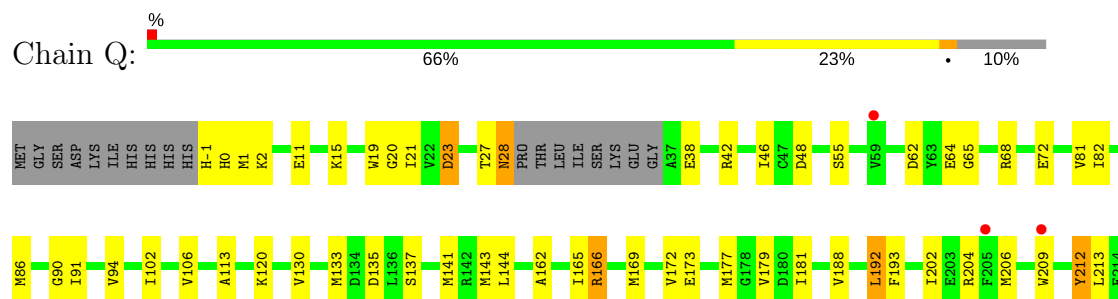
- Molecule 1: PROTEIN (Transaldolase (EC 2.2.1.2))



- Molecule 1: PROTEIN (Transaldolase (EC 2.2.1.2))



- Molecule 1: PROTEIN (Transaldolase (EC 2.2.1.2))



ASN
LEU
LYS
LYS

- Molecule 1: PROTEIN (Transaldolase (EC 2.2.1.2))

Chain R: 

MET GLY SER ASP LYS ILE HIS HIS HIS HIS HO M1 K2 D6 N9 E12 I13 W19 G20 G21 I21 V22 D23 G24 V25 T26 T27 N28 P29 T30 LEU ILE SER LYS GLY A37 E38 F39 V43 V50 E57 V58 V59 S60 R68 E69 A70 R71 E72 L73 A74

Q75 Y79 K83 M86 T87 I102 T107 L108 I116 K120 T124 F129 R132 S137 R142 G143 M144 Y154 R166 V172 E173 A174 V179 D180 I181 V182 T183 M184 L192 D199 F205 M206 E207 D208 W209 Y212 L213 E214 N215

LEU
LYS
LYS

- Molecule 1: PROTEIN (Transaldolase (EC 2.2.1.2))

Chain S: 

MET GLY SER ASP LYS ILE HIS HIS HIS HIS HO M1 K2 I3 F4 L5 E12 I13 V17 D23 T27 N28 G29 T30 L31 I32 G36 A37 E38 F39 I46 V50 S55 D62 R68 S77 V80 K83 M86 D89 G90 I91 K95

Q114 L117 K120 A121 V126 S137 R142 M143 L144 R166 A174 M177 G178 V179 D180 I181 M184 F185 F186 L189 T198 R204 PHE MET GLU ASP TRP LYS TYR LEU GLU ASN LEU LYS LYS

- Molecule 1: PROTEIN (Transaldolase (EC 2.2.1.2))

Chain T: 

MET GLY SER ASP LYS ILE HIS HIS HIS HIS HO M1 K2 A8 N9 E12 I13 W19 G20 I21 V22 D23 G24 V25 T26 T27 N28 P29 T30 LEU ILE SER LYS GLY ALA GLU PHE LYS GLN ARG V43 I46 L49 V50 K51 G52 S60 L61 D62 Q75

Y79 D89 K95 K103 T104 K120 T124 M143 L144 I161 I165 R166 H167 P168 M169 H170 A174 V179 D180 M184 V188 D199 R204 P205 D208 W209 Y212 N215 LEU LYS LYS

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	145.30Å 104.42Å 171.12Å 90.00° 108.99° 90.00°	Depositor
Resolution (Å)	83.13 – 2.40 83.13 – 2.40	Depositor EDS
% Data completeness (in resolution range)	85.9 (83.13-2.40) 85.5 (83.13-2.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.68 (at 2.40Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.196 , 0.247 0.204 , 0.251	Depositor DCC
R_{free} test set	8140 reflections (5.29%)	DCC
Wilson B-factor (Å ²)	46.6	Xtriage
Anisotropy	0.567	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 66.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	31916	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.38% 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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, SO4

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	0.72	0/1620	0.89	5/2194 (0.2%)
1	B	0.74	0/1612	0.85	5/2182 (0.2%)
1	C	0.77	1/1586 (0.1%)	0.87	6/2147 (0.3%)
1	D	0.84	0/1643	0.88	3/2223 (0.1%)
1	E	0.83	0/1704	0.91	7/2305 (0.3%)
1	F	0.76	0/1685	0.94	9/2280 (0.4%)
1	G	1.05	2/1698 (0.1%)	0.96	6/2300 (0.3%)
1	H	0.74	0/1576	0.90	8/2136 (0.4%)
1	I	0.85	3/1643 (0.2%)	0.90	5/2226 (0.2%)
1	J	1.33	4/1649 (0.2%)	0.94	10/2236 (0.4%)
1	K	0.68	0/1681	0.80	1/2279 (0.0%)
1	L	0.60	0/1556	0.83	4/2111 (0.2%)
1	M	0.59	0/1481	0.79	6/2009 (0.3%)
1	N	1.17	11/1498 (0.7%)	0.93	14/2027 (0.7%)
1	O	0.77	0/1632	0.86	5/2209 (0.2%)
1	P	0.69	0/1603	0.88	5/2172 (0.2%)
1	Q	0.75	3/1625 (0.2%)	0.85	6/2200 (0.3%)
1	R	0.70	3/1613 (0.2%)	0.84	4/2188 (0.2%)
1	S	0.63	0/1559	0.85	5/2112 (0.2%)
1	T	0.61	0/1569	0.78	3/2128 (0.1%)
All	All	0.81	27/32233 (0.1%)	0.88	117/43664 (0.3%)

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	G	0	1
1	N	0	1
1	R	0	1

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
All	All	0	3

The worst 5 of 27 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	J	45	GLU	CD-OE2	31.92	1.60	1.25
1	J	45	GLU	CD-OE1	28.67	1.57	1.25
1	G	214	GLU	C-O	23.22	1.67	1.23
1	N	35	GLU	CD-OE1	19.15	1.46	1.25
1	N	39	PHE	N-CA	15.11	1.76	1.46

The worst 5 of 117 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	166	ARG	NE-CZ-NH2	-9.84	115.38	120.30
1	G	166	ARG	NE-CZ-NH1	9.14	124.87	120.30
1	G	214	GLU	CA-C-O	-8.57	102.11	120.10
1	P	89	ASP	CB-CG-OD2	7.95	125.45	118.30
1	F	48	ASP	CB-CG-OD2	7.90	125.41	118.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	G	-1	HIS	Peptide
1	N	35	GLU	Sidechain
1	R	37	ALA	Mainchain

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	1591	0	1601	32	0
1	B	1584	0	1598	31	0
1	C	1560	0	1561	32	0
1	D	1615	0	1642	29	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	1674	0	1703	35	0
1	F	1655	0	1680	18	0
1	G	1667	0	1680	27	0
1	H	1550	0	1557	28	0
1	I	1615	0	1623	29	0
1	J	1619	0	1617	51	0
1	K	1651	0	1648	23	0
1	L	1530	0	1521	27	0
1	M	1457	0	1439	32	0
1	N	1475	0	1446	29	0
1	O	1604	0	1613	30	0
1	P	1576	0	1590	21	0
1	Q	1596	0	1594	32	0
1	R	1585	0	1569	28	0
1	S	1533	0	1538	27	0
1	T	1541	0	1521	19	0
2	O	5	0	0	0	0
3	A	6	0	8	1	0
3	B	6	0	8	1	0
3	C	6	0	8	1	0
3	D	6	0	8	0	0
3	E	6	0	8	0	0
3	F	6	0	8	1	0
3	G	6	0	8	0	0
3	H	6	0	8	2	0
3	I	6	0	8	0	0
3	J	6	0	8	0	0
3	K	10	0	16	0	0
3	L	6	0	8	0	0
3	M	6	0	8	0	0
3	N	6	0	8	0	0
3	O	6	0	8	3	0
3	P	12	0	16	1	0
3	Q	6	0	8	0	0
3	R	6	0	8	0	0
3	S	6	0	8	0	0
3	T	6	0	8	0	0
4	A	5	0	0	0	0
4	B	6	0	0	1	0
4	C	7	0	0	0	0
4	D	16	0	0	2	0
4	E	7	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	F	5	0	0	0	0
4	G	17	0	0	1	0
4	H	3	0	0	0	0
4	I	4	0	0	0	0
4	J	7	0	0	0	0
4	K	3	0	0	0	0
4	L	1	0	0	0	0
4	M	2	0	0	0	0
4	O	5	0	0	0	0
4	P	3	0	0	0	0
4	Q	7	0	0	0	0
4	R	2	0	0	0	0
4	S	2	0	0	0	0
4	T	1	0	0	0	0
All	All	31916	0	31917	496	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 8.

The worst 5 of 496 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:N:39:PHE:CA	1:N:39:PHE:N	1.76	1.48
1:G:214:GLU:C	1:G:214:GLU:O	1.67	1.30
1:O:156:PHE:O	3:O:220:GOL:H31	1.63	0.96
1:L:142:ARG:CZ	1:S:142:ARG:HD2	2.10	0.80
1:K:184:MET:CE	1:K:189:LEU:HB2	2.12	0.79

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	203/230 (88%)	198 (98%)	5 (2%)	0	100	100
1	B	207/230 (90%)	205 (99%)	2 (1%)	0	100	100
1	C	206/230 (90%)	202 (98%)	3 (2%)	1 (0%)	32	46
1	D	208/230 (90%)	204 (98%)	3 (1%)	1 (0%)	32	46
1	E	214/230 (93%)	210 (98%)	2 (1%)	2 (1%)	20	29
1	F	209/230 (91%)	204 (98%)	5 (2%)	0	100	100
1	G	214/230 (93%)	210 (98%)	3 (1%)	1 (0%)	32	46
1	H	201/230 (87%)	196 (98%)	4 (2%)	1 (0%)	32	46
1	I	207/230 (90%)	202 (98%)	4 (2%)	1 (0%)	32	46
1	J	211/230 (92%)	207 (98%)	4 (2%)	0	100	100
1	K	214/230 (93%)	212 (99%)	2 (1%)	0	100	100
1	L	200/230 (87%)	194 (97%)	5 (2%)	1 (0%)	32	46
1	M	194/230 (84%)	191 (98%)	3 (2%)	0	100	100
1	N	200/230 (87%)	195 (98%)	5 (2%)	0	100	100
1	O	208/230 (90%)	204 (98%)	4 (2%)	0	100	100
1	P	207/230 (90%)	201 (97%)	5 (2%)	1 (0%)	32	46
1	Q	205/230 (89%)	201 (98%)	3 (2%)	1 (0%)	32	46
1	R	206/230 (90%)	200 (97%)	5 (2%)	1 (0%)	32	46
1	S	203/230 (88%)	199 (98%)	2 (1%)	2 (1%)	18	26
1	T	200/230 (87%)	197 (98%)	2 (1%)	1 (0%)	32	46
All	All	4117/4600 (90%)	4032 (98%)	71 (2%)	14 (0%)	44	60

5 of 14 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	G	0	HIS
1	P	41	GLN
1	S	38	GLU
1	E	41	GLN
1	H	204	ARG

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	171/196 (87%)	158 (92%)	13 (8%)	15	24
1	B	168/196 (86%)	154 (92%)	14 (8%)	13	20
1	C	165/196 (84%)	152 (92%)	13 (8%)	14	22
1	D	175/196 (89%)	166 (95%)	9 (5%)	28	44
1	E	181/196 (92%)	171 (94%)	10 (6%)	25	40
1	F	179/196 (91%)	163 (91%)	16 (9%)	11	17
1	G	179/196 (91%)	170 (95%)	9 (5%)	28	45
1	H	166/196 (85%)	152 (92%)	14 (8%)	13	19
1	I	173/196 (88%)	164 (95%)	9 (5%)	27	43
1	J	172/196 (88%)	157 (91%)	15 (9%)	12	18
1	K	176/196 (90%)	165 (94%)	11 (6%)	21	33
1	L	161/196 (82%)	144 (89%)	17 (11%)	8	11
1	M	152/196 (78%)	141 (93%)	11 (7%)	17	26
1	N	151/196 (77%)	140 (93%)	11 (7%)	16	26
1	O	173/196 (88%)	162 (94%)	11 (6%)	20	32
1	P	167/196 (85%)	155 (93%)	12 (7%)	17	26
1	Q	168/196 (86%)	161 (96%)	7 (4%)	34	53
1	R	167/196 (85%)	152 (91%)	15 (9%)	11	16
1	S	162/196 (83%)	146 (90%)	16 (10%)	9	13
1	T	162/196 (83%)	151 (93%)	11 (7%)	18	29
All	All	3368/3920 (86%)	3124 (93%)	244 (7%)	17	26

5 of 244 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	J	42	ARG
1	L	30	THR
1	S	120	LYS
1	J	50	VAL
1	K	17	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	L	28	ASN
1	N	167	HIS
1	M	170	HIS
1	K	28	ASN
1	N	0	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

23 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	GOL	A	219	-	5,5,5	0.54	0	5,5,5	1.07	0
3	GOL	B	219	-	5,5,5	0.39	0	5,5,5	0.78	0
3	GOL	C	219	-	5,5,5	0.44	0	5,5,5	1.16	0
3	GOL	D	219	-	5,5,5	0.27	0	5,5,5	0.98	0
3	GOL	E	219	-	5,5,5	0.24	0	5,5,5	0.80	0
3	GOL	F	219	-	5,5,5	0.36	0	5,5,5	0.32	0
3	GOL	G	219	-	5,5,5	0.78	0	5,5,5	1.22	1 (20%)
3	GOL	H	219	-	5,5,5	0.39	0	5,5,5	0.99	0
3	GOL	I	219	-	5,5,5	0.18	0	5,5,5	0.57	0
3	GOL	J	219	-	5,5,5	0.13	0	5,5,5	0.67	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	GOL	K	219[A]	-	5,5,5	0.21	0	5,5,5	0.58	0
3	GOL	K	219[B]	-	5,5,5	0.38	0	5,5,5	0.29	0
3	GOL	L	219	-	5,5,5	0.28	0	5,5,5	0.24	0
3	GOL	M	219	-	5,5,5	0.38	0	5,5,5	0.81	0
3	GOL	N	219	-	5,5,5	0.16	0	5,5,5	0.63	0
2	SO4	O	219	-	4,4,4	0.32	0	6,6,6	0.16	0
3	GOL	O	220	-	5,5,5	0.51	0	5,5,5	1.41	1 (20%)
3	GOL	P	219	-	5,5,5	0.30	0	5,5,5	0.40	0
3	GOL	P	220	-	5,5,5	0.24	0	5,5,5	0.77	0
3	GOL	Q	219	-	5,5,5	0.41	0	5,5,5	0.82	0
3	GOL	R	219	-	5,5,5	0.29	0	5,5,5	0.76	0
3	GOL	S	219	-	5,5,5	0.37	0	5,5,5	0.60	0
3	GOL	T	219	-	5,5,5	0.41	0	5,5,5	0.89	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	A	219	-	-	0/4/4/4	0/0/0/0
3	GOL	B	219	-	-	0/4/4/4	0/0/0/0
3	GOL	C	219	-	-	0/4/4/4	0/0/0/0
3	GOL	D	219	-	-	0/4/4/4	0/0/0/0
3	GOL	E	219	-	-	0/4/4/4	0/0/0/0
3	GOL	F	219	-	-	0/4/4/4	0/0/0/0
3	GOL	G	219	-	-	0/4/4/4	0/0/0/0
3	GOL	H	219	-	-	0/4/4/4	0/0/0/0
3	GOL	I	219	-	-	0/4/4/4	0/0/0/0
3	GOL	J	219	-	-	0/4/4/4	0/0/0/0
3	GOL	K	219[A]	-	-	0/4/4/4	0/0/0/0
3	GOL	K	219[B]	-	-	0/4/4/4	0/0/0/0
3	GOL	L	219	-	-	0/4/4/4	0/0/0/0
3	GOL	M	219	-	-	0/4/4/4	0/0/0/0
3	GOL	N	219	-	-	0/4/4/4	0/0/0/0
2	SO4	O	219	-	-	0/0/0/0	0/0/0/0
3	GOL	O	220	-	-	0/4/4/4	0/0/0/0
3	GOL	P	219	-	-	0/4/4/4	0/0/0/0
3	GOL	P	220	-	-	0/4/4/4	0/0/0/0
3	GOL	Q	219	-	-	0/4/4/4	0/0/0/0
3	GOL	R	219	-	-	0/4/4/4	0/0/0/0
3	GOL	S	219	-	-	0/4/4/4	0/0/0/0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	T	219	-	-	0/4/4/4	0/0/0/0

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	O	220	GOL	C3-C2-C1	-2.36	102.14	111.52
3	G	219	GOL	O1-C1-C2	2.28	121.56	110.07

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

7 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	219	GOL	1	0
3	B	219	GOL	1	0
3	C	219	GOL	1	0
3	F	219	GOL	1	0
3	H	219	GOL	2	0
3	O	220	GOL	3	0
3	P	220	GOL	1	0

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	207/230 (90%)	0.21	1 (0%) 90 89	36, 49, 59, 81	0
1	B	209/230 (90%)	0.07	2 (0%) 82 80	39, 49, 67, 79	0
1	C	208/230 (90%)	0.06	3 (1%) 75 74	40, 49, 60, 73	0
1	D	210/230 (91%)	0.09	2 (0%) 82 80	40, 49, 65, 86	0
1	E	216/230 (93%)	0.07	1 (0%) 90 89	41, 49, 60, 75	0
1	F	213/230 (92%)	0.05	2 (0%) 84 82	39, 49, 61, 87	0
1	G	216/230 (93%)	0.10	2 (0%) 84 82	40, 49, 61, 89	0
1	H	205/230 (89%)	0.03	2 (0%) 82 80	38, 49, 60, 70	0
1	I	211/230 (91%)	0.12	4 (1%) 67 64	41, 48, 60, 83	0
1	J	213/230 (92%)	0.19	3 (1%) 75 74	37, 49, 72, 83	0
1	K	216/230 (93%)	0.18	4 (1%) 67 64	39, 48, 61, 69	0
1	L	204/230 (88%)	0.28	8 (3%) 40 39	37, 48, 57, 85	0
1	M	198/230 (86%)	0.16	3 (1%) 74 72	40, 48, 60, 68	0
1	N	204/230 (88%)	0.21	9 (4%) 35 33	40, 48, 57, 66	0
1	O	210/230 (91%)	0.19	6 (2%) 52 50	39, 48, 65, 82	0
1	P	209/230 (90%)	0.02	0 100 100	39, 49, 60, 84	0
1	Q	208/230 (90%)	0.08	3 (1%) 75 74	39, 48, 60, 74	0
1	R	210/230 (91%)	0.39	16 (7%) 15 13	40, 49, 61, 74	0
1	S	205/230 (89%)	0.21	3 (1%) 74 72	40, 48, 60, 72	0
1	T	204/230 (88%)	0.35	12 (5%) 23 22	40, 48, 57, 66	0
All	All	4176/4600 (90%)	0.15	86 (2%) 64 61	36, 49, 61, 89	0

The worst 5 of 86 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	Q	209	TRP	8.7
1	H	32	ILE	5.8
1	T	205	PHE	5.3
1	M	91	ILE	5.3
1	R	209	TRP	4.7

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](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
2	SO4	O	219	5/5	0.80	0.27	10.21	91,92,96,103	0
3	GOL	H	219	6/6	0.81	0.23	2.03	49,55,58,65	0
3	GOL	R	219	6/6	0.83	0.21	1.70	61,70,76,81	0
3	GOL	C	219	6/6	0.85	0.19	1.58	58,60,68,71	0
3	GOL	N	219	6/6	0.79	0.17	1.41	61,67,68,74	0
3	GOL	E	219	6/6	0.85	0.19	1.14	33,49,51,65	0
3	GOL	D	219	6/6	0.88	0.19	1.01	52,58,64,65	0
3	GOL	F	219	6/6	0.84	0.19	0.80	60,62,62,69	0
3	GOL	K	219[A]	6/6	0.89	0.18	0.74	38,46,48,53	4
3	GOL	P	219	6/6	0.87	0.18	0.53	54,73,81,85	0
3	GOL	O	220	6/6	0.86	0.17	0.45	47,49,53,62	0
3	GOL	G	219	6/6	0.78	0.19	0.44	34,49,53,57	0
3	GOL	K	219[B]	6/6	0.89	0.18	0.30	34,45,48,53	4
3	GOL	Q	219	6/6	0.86	0.17	0.11	44,52,62,64	0
3	GOL	L	219	6/6	0.85	0.17	0.07	85,90,93,94	0
3	GOL	M	219	6/6	0.84	0.15	-0.09	74,77,77,81	0
3	GOL	T	219	6/6	0.92	0.15	-0.14	54,67,71,74	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	GOL	B	219	6/6	0.92	0.15	-0.32	41,55,67,68	0
3	GOL	S	219	6/6	0.86	0.13	-0.84	61,65,67,70	0
3	GOL	J	219	6/6	0.92	0.13	-1.21	42,53,62,68	0
3	GOL	A	219	6/6	0.94	0.12	-1.63	42,57,58,58	0
3	GOL	P	220	6/6	0.89	0.14	-1.65	45,54,59,59	0
3	GOL	I	219	6/6	0.94	0.08	-3.11	51,56,59,62	0

6.5 Other polymers [i](#)

There are no such residues in this entry.