



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 05:22 AM GMT

PDB ID : 2Q50  
Title : Ensemble refinement of the protein crystal structure of a glyoxylate/hydroxy pyruvate reductase from Homo sapiens  
Authors : Levin, E.J.; Kondrashov, D.A.; Wesenberg, G.E.; Phillips Jr., G.N.; Center for Eukaryotic Structural Genomics (CESG)  
Deposited on : 2007-05-31  
Resolution : 2.45 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](mailto: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.

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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

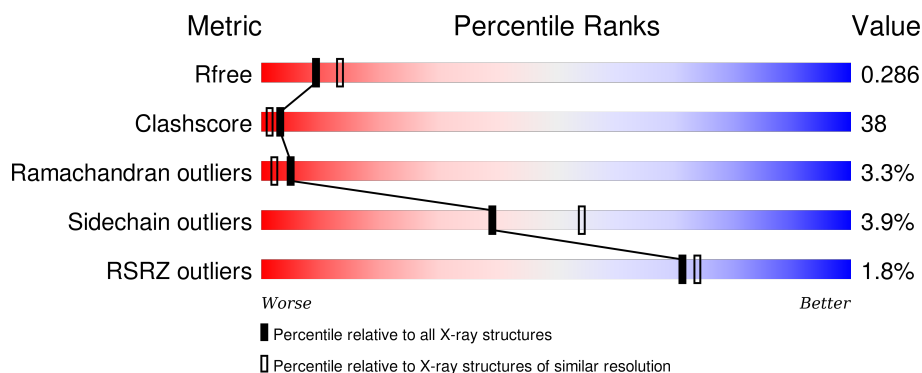
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.45 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	4776 (2.50-2.42)
Clashscore	102246	1030 (2.48-2.44)
Ramachandran outliers	100387	1024 (2.48-2.44)
Sidechain outliers	100360	1024 (2.48-2.44)
RSRZ outliers	91569	4787 (2.50-2.42)

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  $\geq 3$ , 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	1-A	328	
1	1-B	328	
1	1-C	328	
1	1-D	328	
1	2-A	328	

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Mol	Chain	Length	Quality of chain
1	2-B	328	
1	2-C	328	
1	2-D	328	
1	3-A	328	
1	3-B	328	
1	3-C	328	
1	3-D	328	
1	4-A	328	
1	4-B	328	
1	4-C	328	
1	4-D	328	
1	5-A	328	
1	5-B	328	
1	5-C	328	
1	5-D	328	
1	6-A	328	
1	6-B	328	
1	6-C	328	
1	6-D	328	
1	7-A	328	
1	7-B	328	
1	7-C	328	
1	7-D	328	
1	8-A	328	
1	8-B	328	

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Mol	Chain	Length	Quality of chain
1	8-C	328	 2% 46% 46% 6%
1	8-D	328	 1% 51% 45% 3%

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 81744 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 Glyoxylate reductase/hydroxypyruvate reductase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	1-A	321	Total	C	N	O	S	Se	0	0	0
			2442	1542	431	457	7	5			
1	2-A	321	Total	C	N	O	S	Se	0	0	0
			2442	1542	431	457	7	5			
1	3-A	321	Total	C	N	O	S	Se	0	0	0
			2442	1542	431	457	7	5			
1	4-A	321	Total	C	N	O	S	Se	0	0	0
			2442	1542	431	457	7	5			
1	5-A	321	Total	C	N	O	S	Se	0	0	0
			2442	1542	431	457	7	5			
1	6-A	321	Total	C	N	O	S	Se	0	0	0
			2442	1542	431	457	7	5			
1	7-A	321	Total	C	N	O	S	Se	0	0	0
			2442	1542	431	457	7	5			
1	8-A	321	Total	C	N	O	S	Se	0	0	0
			2442	1542	431	457	7	5			
1	1-B	321	Total	C	N	O	S	Se	0	0	0
			2442	1542	431	457	7	5			
1	2-B	321	Total	C	N	O	S	Se	0	0	0
			2442	1542	431	457	7	5			
1	3-B	321	Total	C	N	O	S	Se	0	0	0
			2442	1542	431	457	7	5			
1	4-B	321	Total	C	N	O	S	Se	0	0	0
			2442	1542	431	457	7	5			
1	5-B	321	Total	C	N	O	S	Se	0	0	0
			2442	1542	431	457	7	5			
1	6-B	321	Total	C	N	O	S	Se	0	0	0
			2442	1542	431	457	7	5			
1	7-B	321	Total	C	N	O	S	Se	0	0	0
			2442	1542	431	457	7	5			
1	8-B	321	Total	C	N	O	S	Se	0	0	0
			2442	1542	431	457	7	5			

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Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	1-C	321	Total	C	N	O	S	Se	0	0	0
			2442	1542	431	457	7	5			
1	2-C	321	Total	C	N	O	S	Se	0	0	0
			2442	1542	431	457	7	5			
1	3-C	321	Total	C	N	O	S	Se	0	0	0
			2442	1542	431	457	7	5			
1	4-C	321	Total	C	N	O	S	Se	0	0	0
			2442	1542	431	457	7	5			
1	5-C	321	Total	C	N	O	S	Se	0	0	0
			2442	1542	431	457	7	5			
1	6-C	321	Total	C	N	O	S	Se	0	0	0
			2442	1542	431	457	7	5			
1	7-C	321	Total	C	N	O	S	Se	0	0	0
			2442	1542	431	457	7	5			
1	8-C	321	Total	C	N	O	S	Se	0	0	0
			2442	1542	431	457	7	5			
1	1-D	321	Total	C	N	O	S	Se	0	0	0
			2442	1542	431	457	7	5			
1	2-D	321	Total	C	N	O	S	Se	0	0	0
			2442	1542	431	457	7	5			
1	3-D	321	Total	C	N	O	S	Se	0	0	0
			2442	1542	431	457	7	5			
1	4-D	321	Total	C	N	O	S	Se	0	0	0
			2442	1542	431	457	7	5			
1	5-D	321	Total	C	N	O	S	Se	0	0	0
			2442	1542	431	457	7	5			
1	6-D	321	Total	C	N	O	S	Se	0	0	0
			2442	1542	431	457	7	5			
1	7-D	321	Total	C	N	O	S	Se	0	0	0
			2442	1542	431	457	7	5			
1	8-D	321	Total	C	N	O	S	Se	0	0	0
			2442	1542	431	457	7	5			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	SER	-	EXPRESSION TAG	UNP Q9UBQ7
A	7	MSE	MET	MODIFIED RESIDUE	UNP Q9UBQ7
A	81	MSE	MET	MODIFIED RESIDUE	UNP Q9UBQ7
A	234	MSE	MET	MODIFIED RESIDUE	UNP Q9UBQ7
A	305	MSE	MET	MODIFIED RESIDUE	UNP Q9UBQ7
A	322	MSE	MET	MODIFIED RESIDUE	UNP Q9UBQ7
B	1	SER	-	EXPRESSION TAG	UNP Q9UBQ7

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Chain	Residue	Modelled	Actual	Comment	Reference
B	7	MSE	MET	MODIFIED RESIDUE	UNP Q9UBQ7
B	81	MSE	MET	MODIFIED RESIDUE	UNP Q9UBQ7
B	234	MSE	MET	MODIFIED RESIDUE	UNP Q9UBQ7
B	305	MSE	MET	MODIFIED RESIDUE	UNP Q9UBQ7
B	322	MSE	MET	MODIFIED RESIDUE	UNP Q9UBQ7
C	1	SER	-	EXPRESSION TAG	UNP Q9UBQ7
C	7	MSE	MET	MODIFIED RESIDUE	UNP Q9UBQ7
C	81	MSE	MET	MODIFIED RESIDUE	UNP Q9UBQ7
C	234	MSE	MET	MODIFIED RESIDUE	UNP Q9UBQ7
C	305	MSE	MET	MODIFIED RESIDUE	UNP Q9UBQ7
C	322	MSE	MET	MODIFIED RESIDUE	UNP Q9UBQ7
D	1	SER	-	EXPRESSION TAG	UNP Q9UBQ7
D	7	MSE	MET	MODIFIED RESIDUE	UNP Q9UBQ7
D	81	MSE	MET	MODIFIED RESIDUE	UNP Q9UBQ7
D	234	MSE	MET	MODIFIED RESIDUE	UNP Q9UBQ7
D	305	MSE	MET	MODIFIED RESIDUE	UNP Q9UBQ7
D	322	MSE	MET	MODIFIED RESIDUE	UNP Q9UBQ7

- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	1-A	103	Total O 103 103	0	0
2	2-A	104	Total O 104 104	0	0
2	3-A	104	Total O 104 104	0	0
2	4-A	104	Total O 104 104	0	0
2	5-A	111	Total O 111 111	0	0
2	6-A	107	Total O 107 107	0	0
2	7-A	106	Total O 106 106	0	0
2	8-A	108	Total O 108 108	0	0
2	1-B	130	Total O 130 130	0	0
2	2-B	128	Total O 128 128	0	0
2	3-B	128	Total O 128 128	0	0

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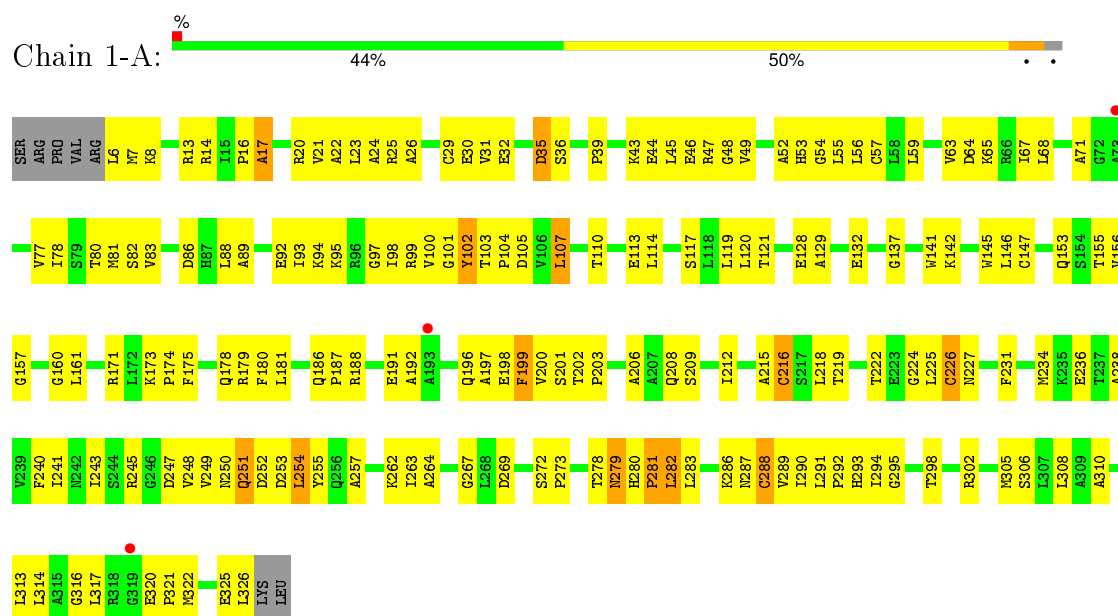
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	4-B	128	Total 128	O 128	0	0
2	5-B	121	Total 121	O 121	0	0
2	6-B	125	Total 125	O 125	0	0
2	7-B	126	Total 126	O 126	0	0
2	8-B	124	Total 124	O 124	0	0
2	1-C	122	Total 122	O 122	0	0
2	2-C	122	Total 122	O 122	0	0
2	3-C	121	Total 121	O 121	0	0
2	4-C	122	Total 122	O 122	0	0
2	5-C	121	Total 121	O 121	0	0
2	6-C	120	Total 120	O 120	0	0
2	7-C	119	Total 119	O 119	0	0
2	8-C	119	Total 119	O 119	0	0
2	1-D	95	Total 95	O 95	0	0
2	2-D	96	Total 96	O 96	0	0
2	3-D	97	Total 97	O 97	0	0
2	4-D	96	Total 96	O 96	0	0
2	5-D	97	Total 97	O 97	0	0
2	6-D	98	Total 98	O 98	0	0
2	7-D	99	Total 99	O 99	0	0
2	8-D	99	Total 99	O 99	0	0



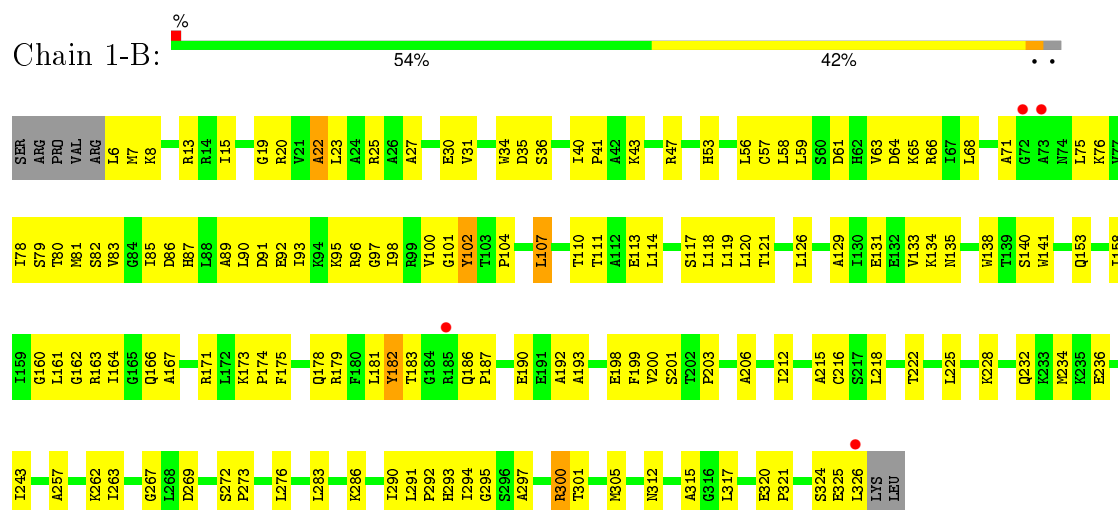
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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.

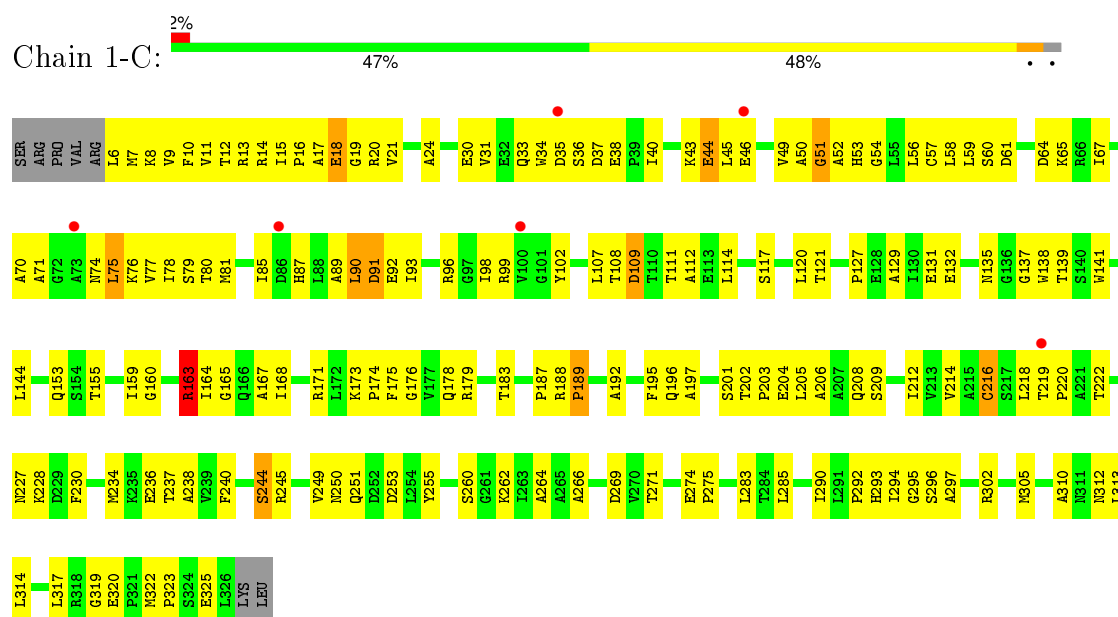
- Molecule 1: Glyoxylate reductase/hydroxypyruvate reductase



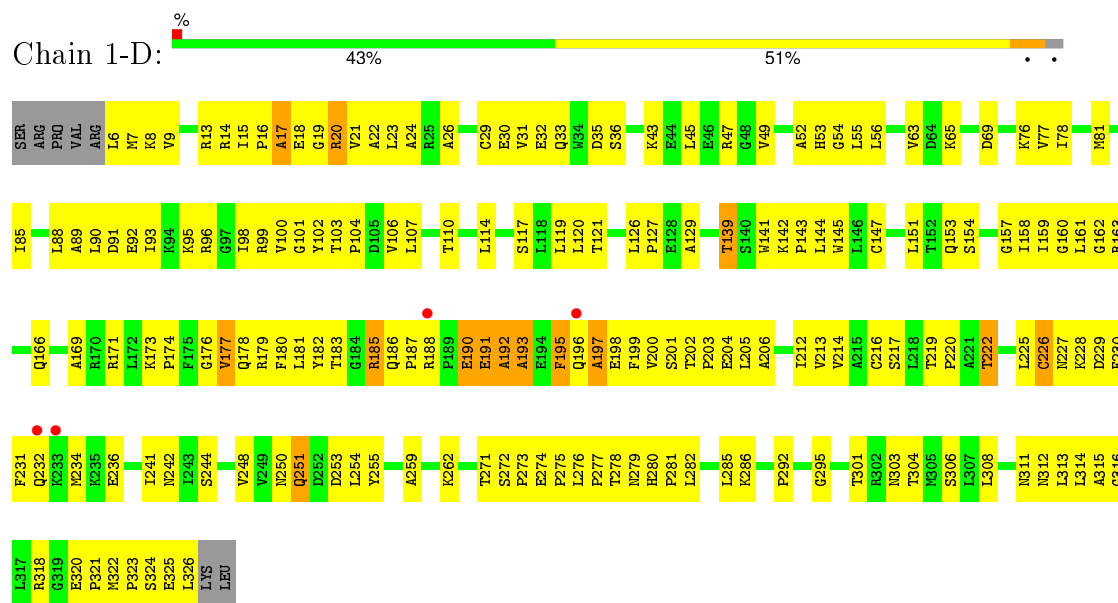
- Molecule 1: Glyoxylate reductase/hydroxypyruvate reductase



- Molecule 1: Glyoxylate reductase/hydroxypyruvate reductase

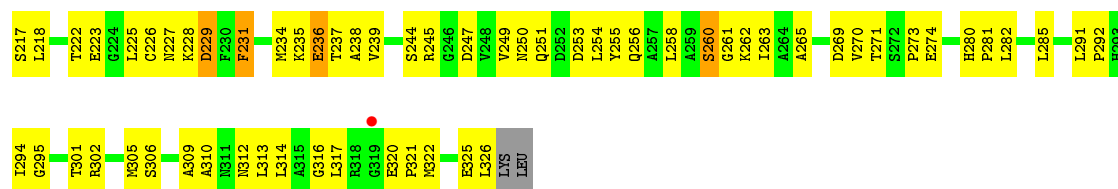


- Molecule 1: Glyoxylate reductase/hydroxypyruvate reductase

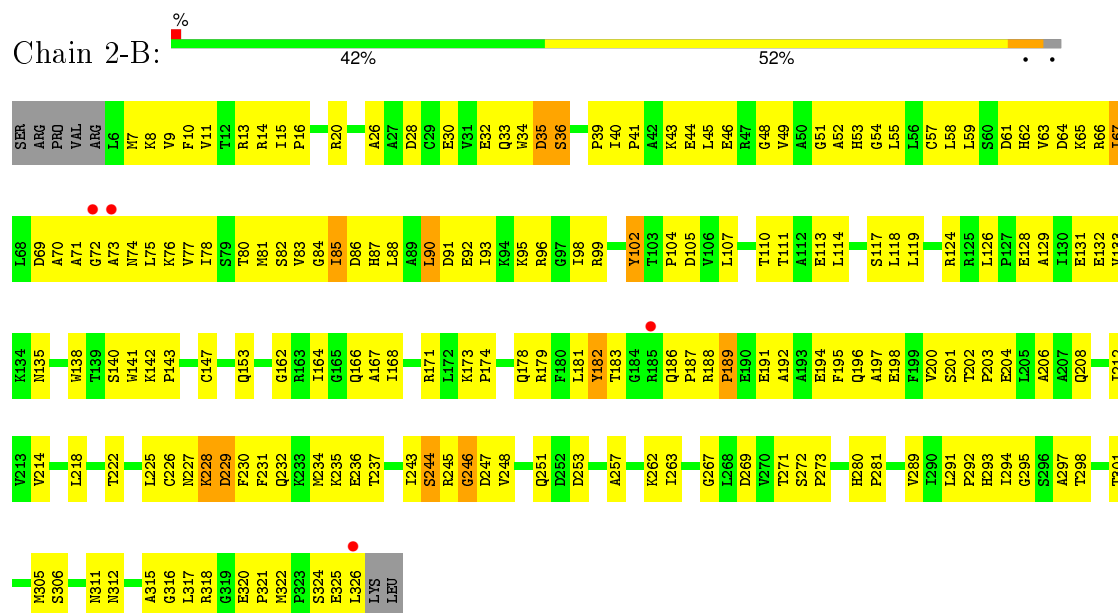


- Molecule 1: Glyoxylate reductase/hydroxypyruvate reductase

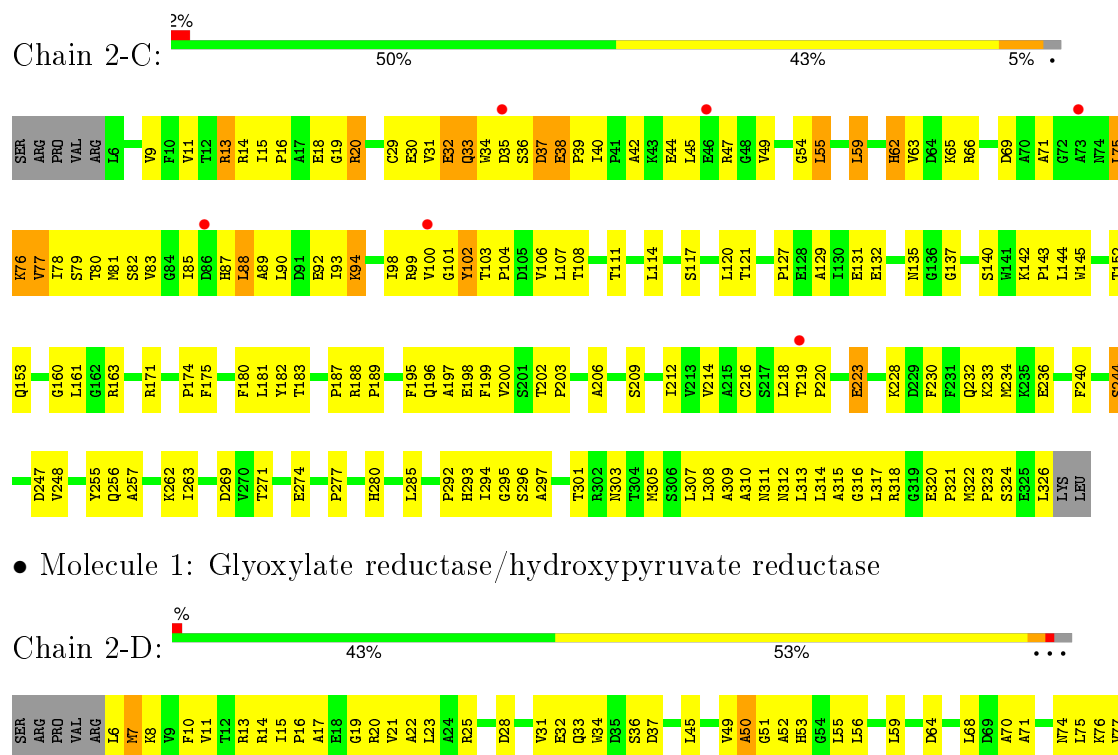




- Molecule 1: Glyoxylate reductase/hydroxypyruvate reductase

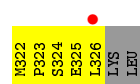


- Molecule 1: Glyoxylate reductase/hydroxypyruvate reductase

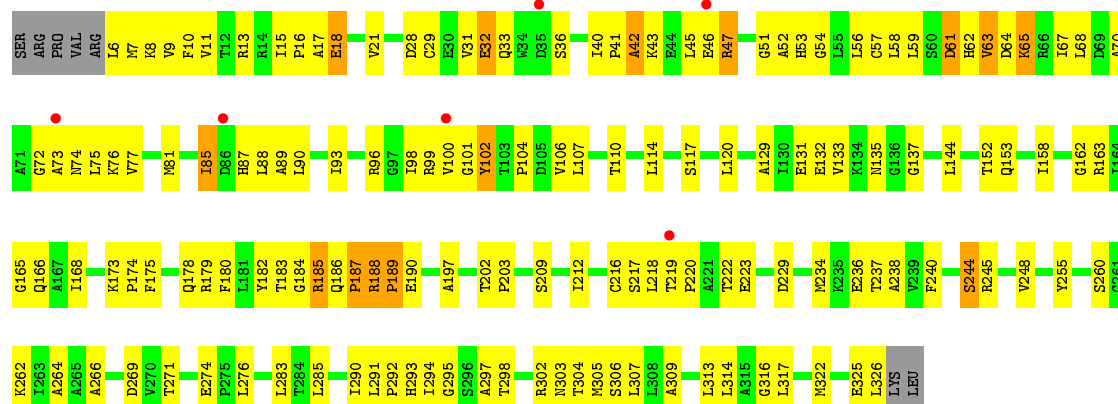


- Molecule 1: Glyoxylate reductase/hydroxypyruvate reductase

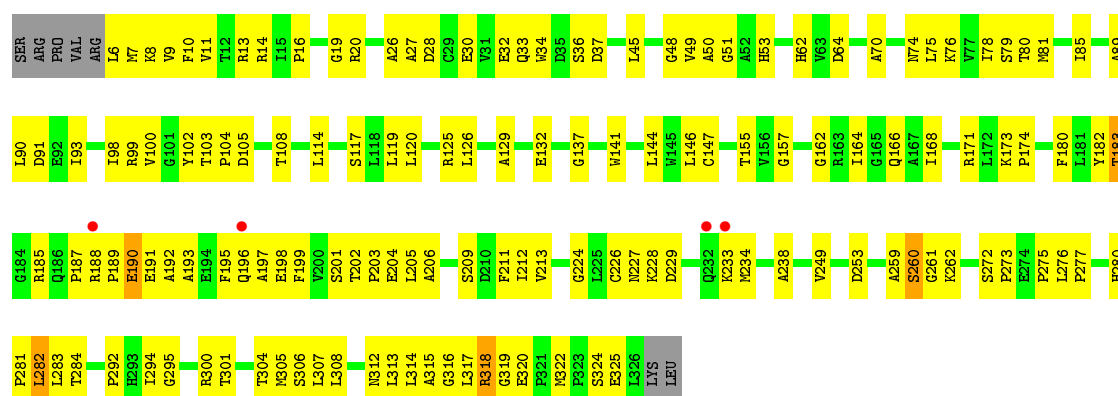




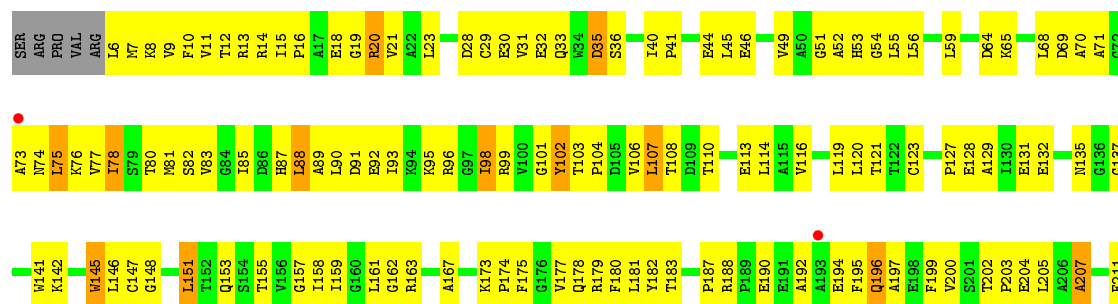
• Molecule 1: Glyoxylate reductase/hydroxypyruvate reductase

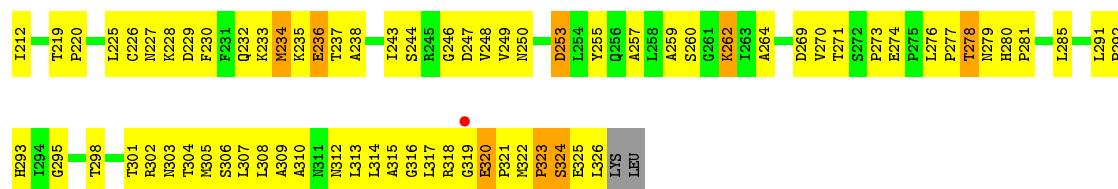


• Molecule 1: Glyoxylate reductase/hydroxypyruvate reductase

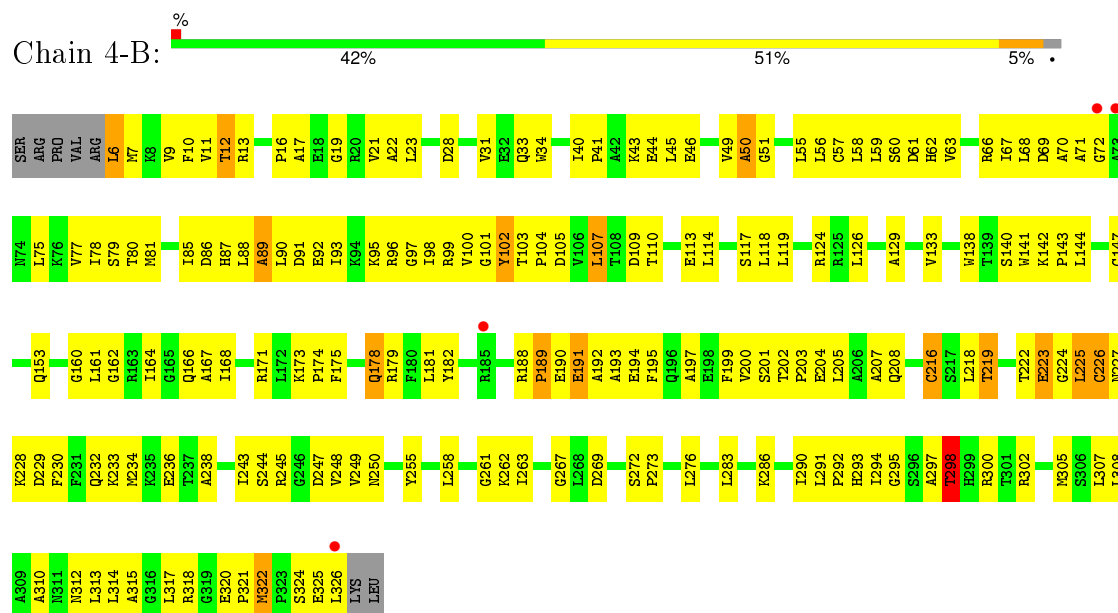


• Molecule 1: Glyoxylate reductase/hydroxypyruvate reductase

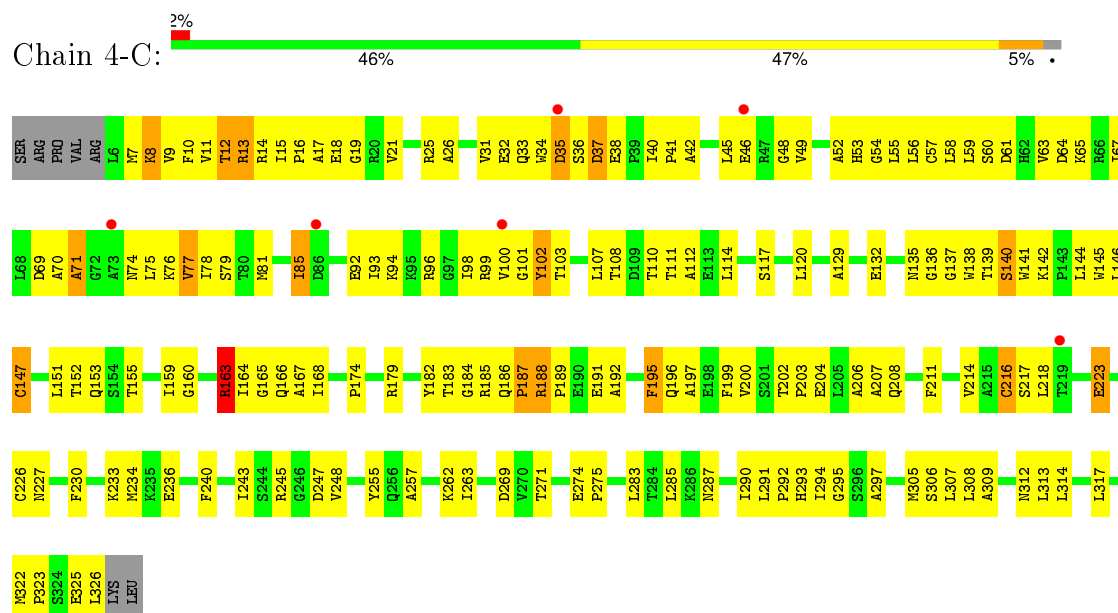




- Molecule 1: Glyoxylate reductase/hydroxypyruvate reductase

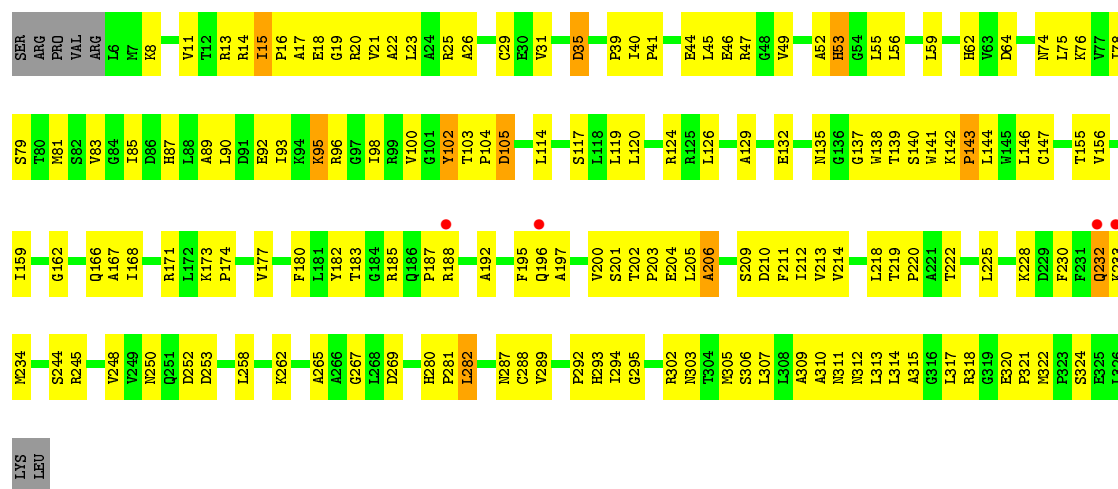


- Molecule 1: Glyoxylate reductase/hydroxypyruvate reductase

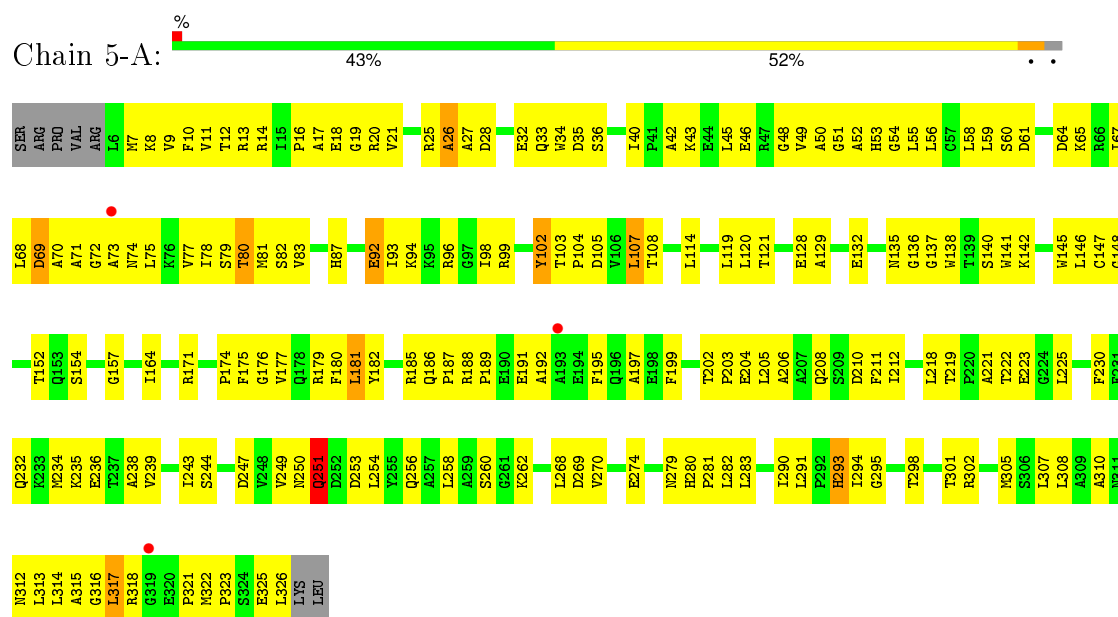


- Molecule 1: Glyoxylate reductase/hydroxypyruvate reductase

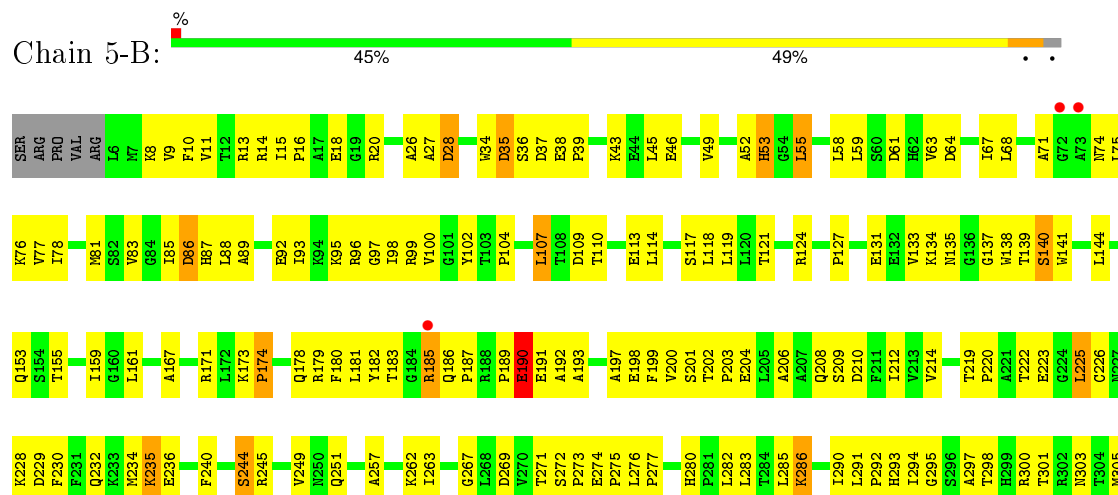




• Molecule 1: Glyoxylate reductase/hydroxypyruvate reductase

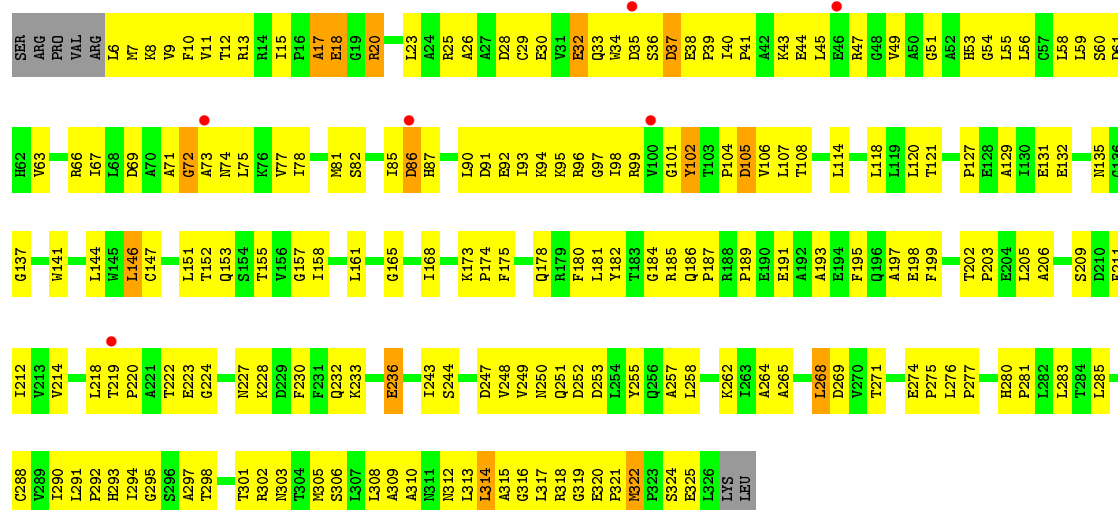


• Molecule 1: Glyoxylate reductase/hydroxypyruvate reductase

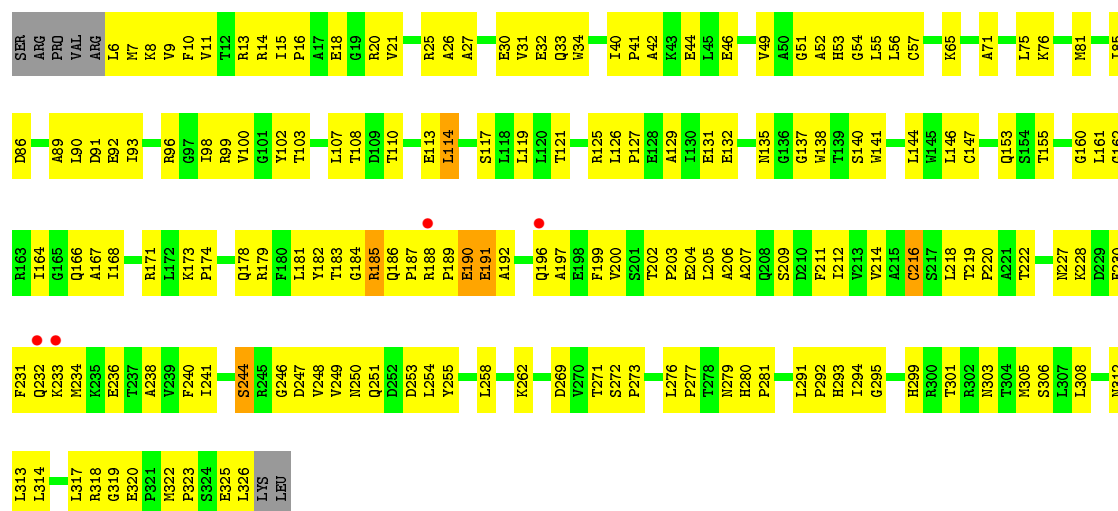




- Molecule 1: Glyoxylate reductase/hydroxypyruvate reductase



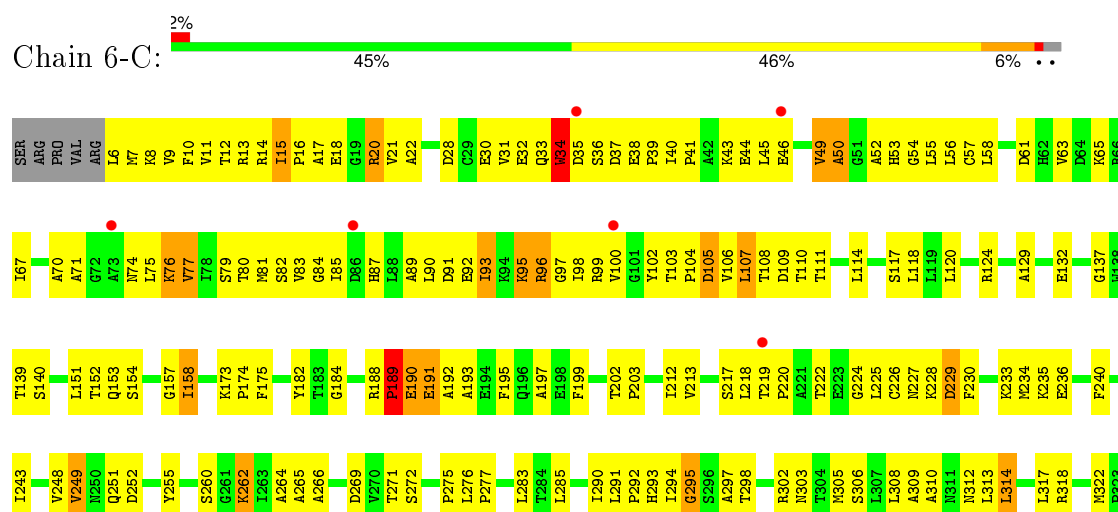
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- Molecule 1: Glyoxylate reductase/hydroxypyruvate reductase



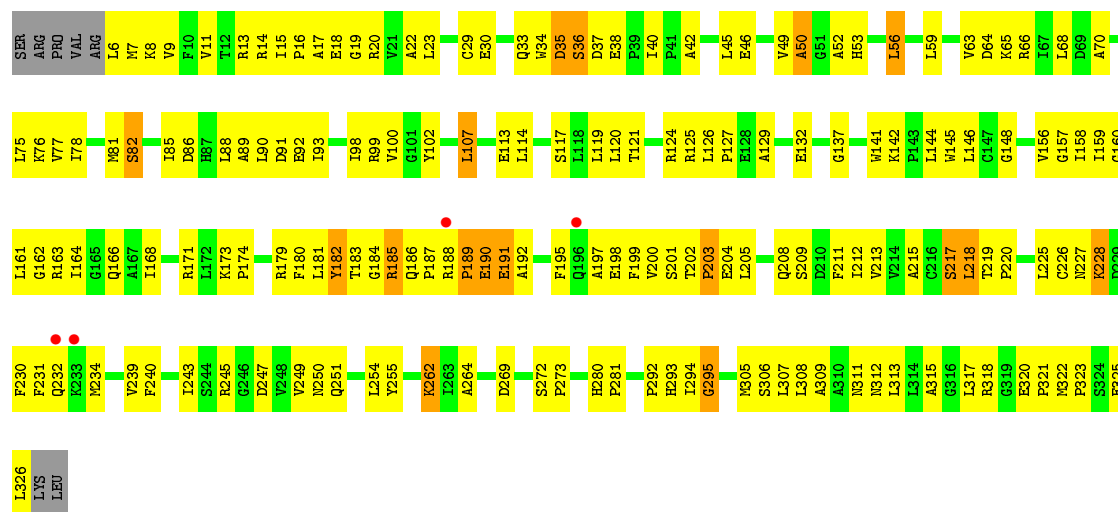




S324  
E325  
L326  
LYS  
LEU

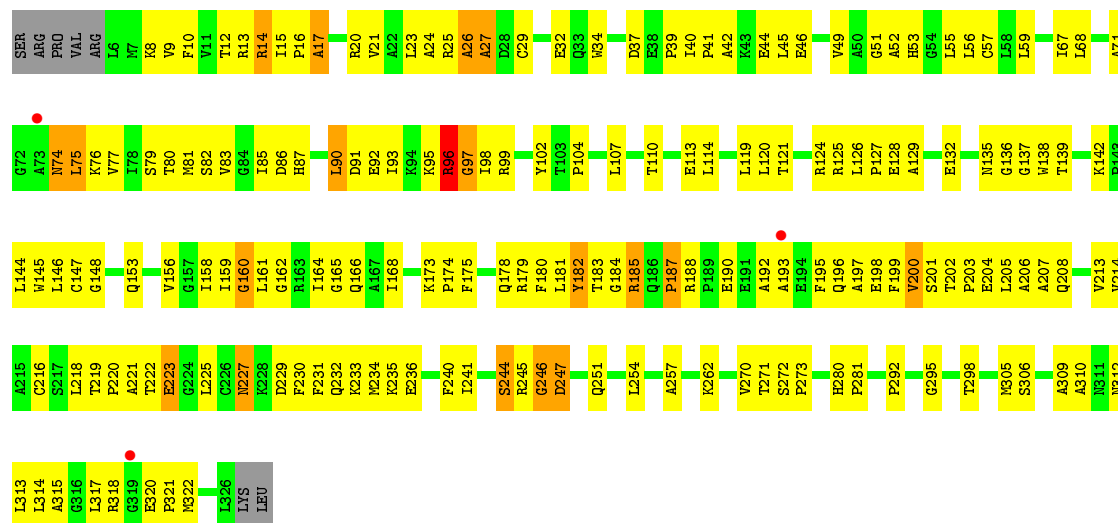
• Molecule 1: Glyoxylate reductase/hydroxypyruvate reductase

Chain 6-D: 




• Molecule 1: Glyoxylate reductase/hydroxypyruvate reductase

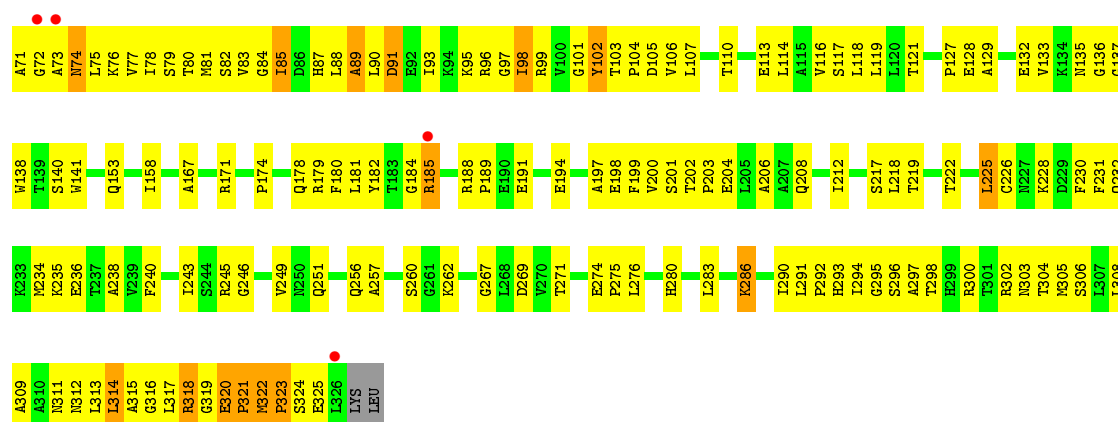
Chain 7-A: 



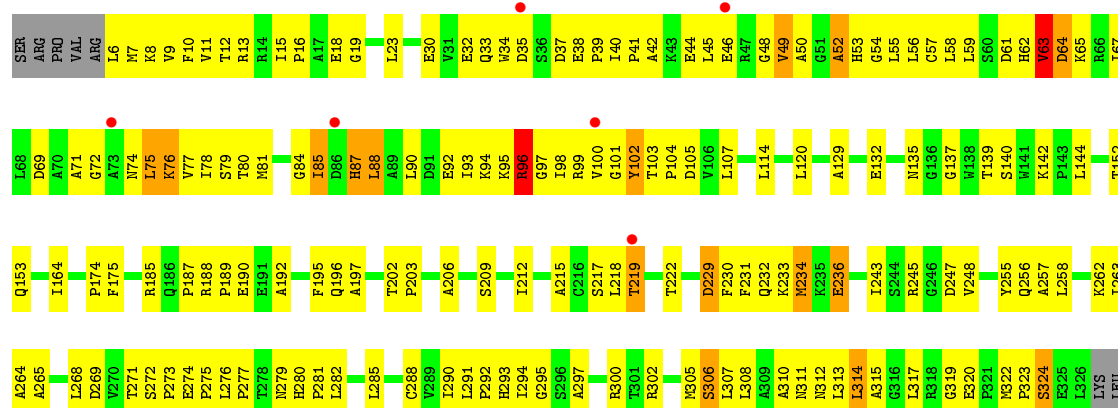
• Molecule 1: Glyoxylate reductase/hydroxypyruvate reductase

Chain 7-B: 

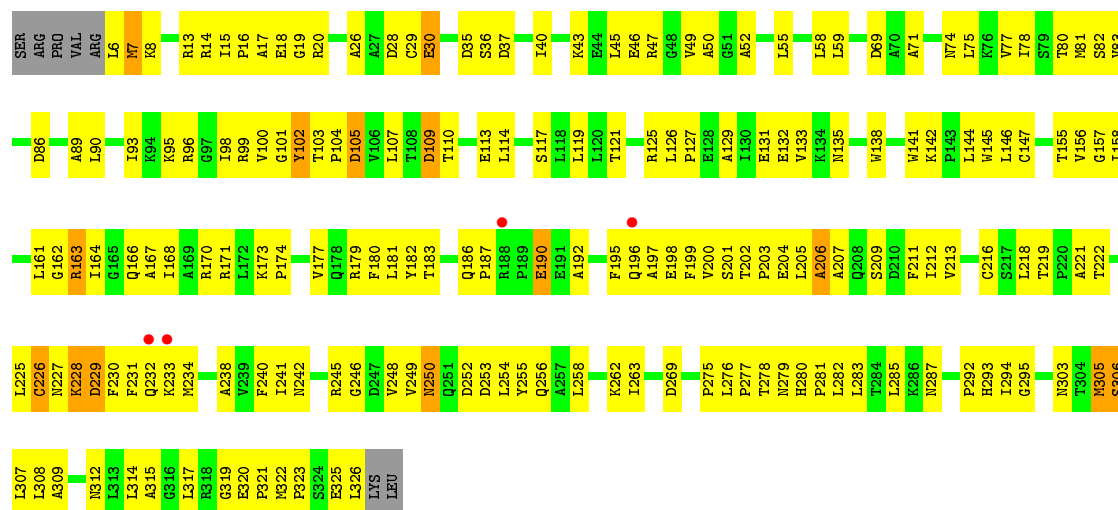
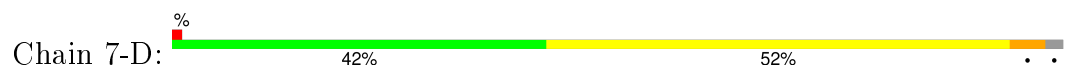




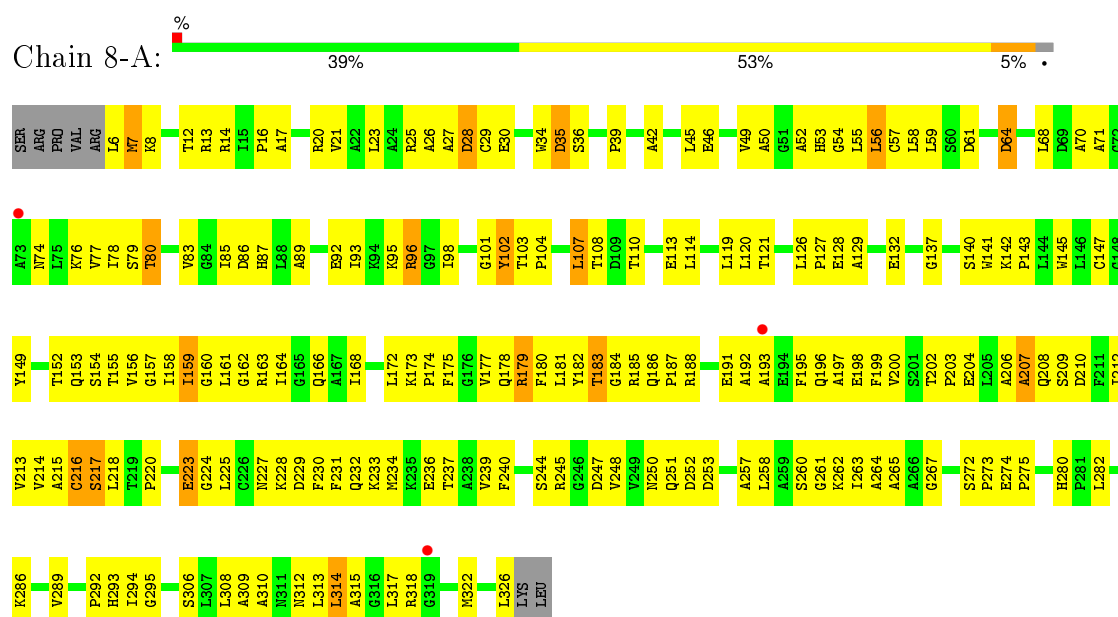
• Molecule 1: Glyoxylate reductase/hydroxypyruvate reductase



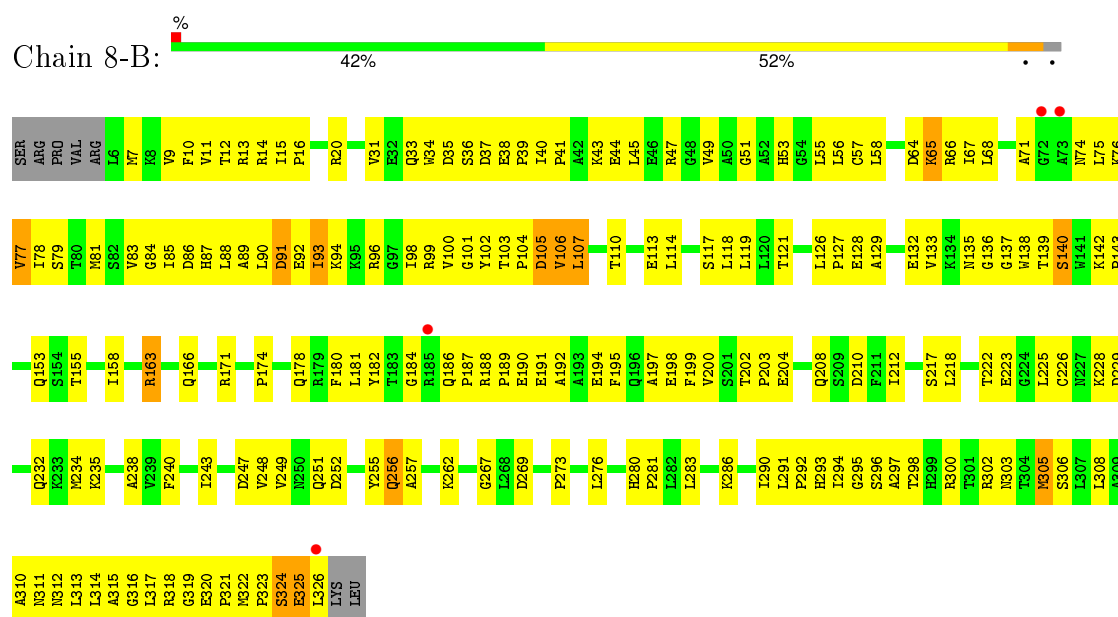
• Molecule 1: Glyoxylate reductase/hydroxypyruvate reductase



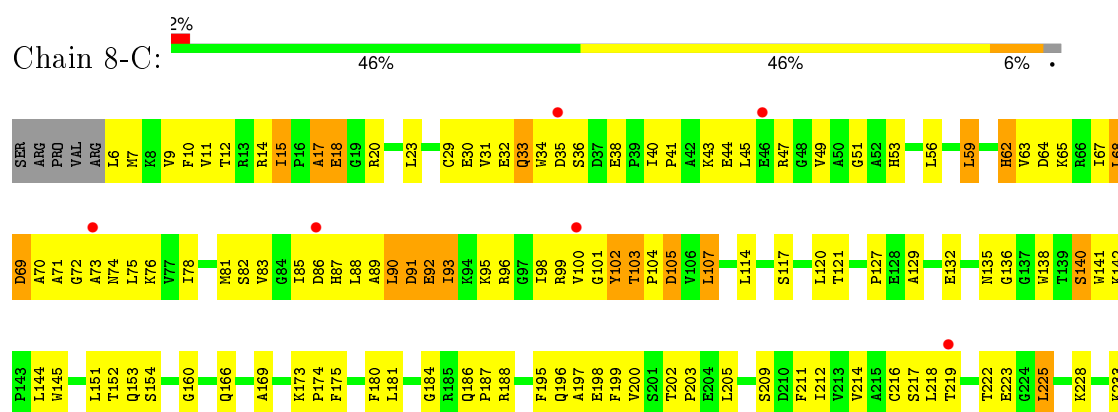
• Molecule 1: Glyoxylate reductase/hydroxypyruvate reductase

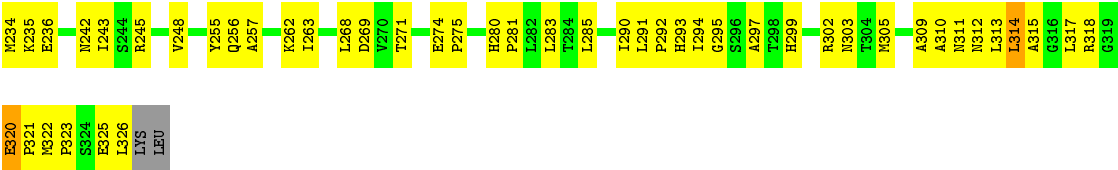


- Molecule 1: Glyoxylate reductase/hydroxypyruvate reductase

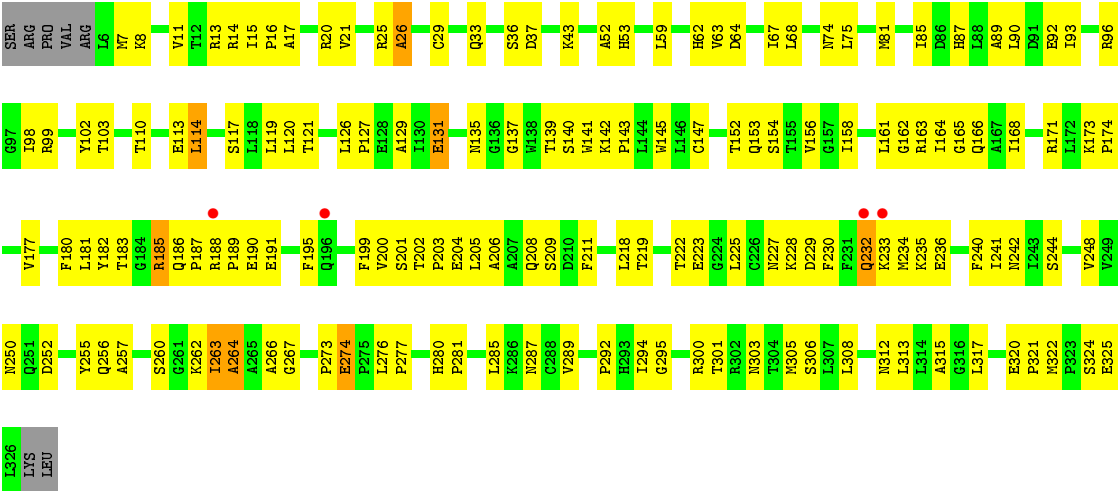


- Molecule 1: Glyoxylate reductase/hydroxypyruvate reductase





● Molecule 1: Glyoxylate reductase/hydroxypyruvate reductase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	76.00Å 66.44Å 148.77Å 90.00° 98.59° 90.00°	Depositor
Resolution (Å)	49.33 – 2.45 49.30 – 2.46	Depositor EDS
% Data completeness (in resolution range)	93.0 (49.33-2.45) 93.1 (49.30-2.46)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.19 (at 2.45Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.200 , 0.286 0.206 , 0.286	Depositor DCC
$R_{free}$ test set	2551 reflections (5.36%)	DCC
Wilson B-factor (Å <sup>2</sup> )	31.6	Xtriage
Anisotropy	0.210	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	(Not available) , (Not available)	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	2 of 50129 reflections (0.004%)	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	81744	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 18.90% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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

### 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	1-A	0.32	0/2481	0.58	0/3363
1	1-B	0.32	0/2481	0.58	0/3363
1	1-C	0.33	0/2481	0.61	0/3363
1	1-D	0.33	0/2481	0.59	0/3363
1	2-A	0.33	0/2481	0.60	0/3363
1	2-B	0.32	0/2481	0.59	0/3363
1	2-C	0.33	0/2481	0.62	0/3363
1	2-D	0.33	0/2481	0.58	0/3363
1	3-A	0.32	0/2481	0.59	0/3363
1	3-B	0.32	0/2481	0.58	0/3363
1	3-C	0.33	0/2481	0.60	0/3363
1	3-D	0.33	0/2481	0.60	0/3363
1	4-A	0.32	0/2481	0.59	0/3363
1	4-B	0.32	0/2481	0.58	0/3363
1	4-C	0.32	0/2481	0.60	0/3363
1	4-D	0.33	0/2481	0.58	0/3363
1	5-A	0.34	0/2481	0.60	0/3363
1	5-B	0.33	0/2481	0.63	0/3363
1	5-C	0.35	0/2481	0.64	0/3363
1	5-D	0.33	0/2481	0.61	0/3363
1	6-A	0.34	0/2481	0.61	0/3363
1	6-B	0.33	0/2481	0.61	0/3363
1	6-C	0.34	0/2481	0.64	0/3363
1	6-D	0.34	0/2481	0.61	0/3363
1	7-A	0.34	0/2481	0.62	0/3363
1	7-B	0.35	0/2481	0.63	0/3363
1	7-C	0.34	0/2481	0.65	0/3363
1	7-D	0.34	0/2481	0.60	0/3363
1	8-A	0.34	0/2481	0.62	0/3363
1	8-B	0.33	0/2481	0.61	0/3363
1	8-C	0.34	0/2481	0.64	0/3363
1	8-D	0.34	0/2481	0.61	0/3363
All	All	0.33	0/79392	0.61	0/107616

There are no bond length outliers.

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	1-A	2442	0	2491	176	0
1	1-B	2442	0	2491	134	0
1	1-C	2442	0	2491	170	0
1	1-D	2442	0	2491	226	0
1	2-A	2442	0	2491	213	0
1	2-B	2442	0	2491	201	0
1	2-C	2442	0	2491	167	0
1	2-D	2442	0	2491	189	0
1	3-A	2442	0	2491	178	0
1	3-B	2442	0	2491	205	0
1	3-C	2442	0	2491	163	0
1	3-D	2442	0	2491	140	0
1	4-A	2442	0	2491	250	0
1	4-B	2442	0	2491	200	0
1	4-C	2442	0	2491	178	0
1	4-D	2442	0	2491	165	0
1	5-A	2442	0	2491	207	0
1	5-B	2442	0	2491	197	0
1	5-C	2442	0	2491	188	0
1	5-D	2442	0	2491	148	0
1	6-A	2442	0	2491	270	0
1	6-B	2442	0	2491	217	0
1	6-C	2442	0	2491	215	0
1	6-D	2442	0	2491	201	0
1	7-A	2442	0	2491	205	0
1	7-B	2442	0	2491	249	0
1	7-C	2442	0	2491	200	0
1	7-D	2442	0	2491	220	0
1	8-A	2442	0	2491	232	0
1	8-B	2442	0	2491	209	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	8-C	2442	0	2491	191	0
1	8-D	2442	0	2491	147	0
2	1-A	103	0	0	9	0
2	1-B	130	0	0	12	0
2	1-C	122	0	0	11	0
2	1-D	95	0	0	15	0
2	2-A	104	0	0	19	0
2	2-B	128	0	0	18	0
2	2-C	122	0	0	13	0
2	2-D	96	0	0	8	0
2	3-A	104	0	0	11	0
2	3-B	128	0	0	15	0
2	3-C	121	0	0	12	0
2	3-D	97	0	0	9	0
2	4-A	104	0	0	15	0
2	4-B	128	0	0	18	0
2	4-C	122	0	0	7	0
2	4-D	96	0	0	7	0
2	5-A	111	0	0	10	0
2	5-B	121	0	0	12	0
2	5-C	121	0	0	11	0
2	5-D	97	0	0	10	0
2	6-A	107	0	0	24	0
2	6-B	125	0	0	15	0
2	6-C	120	0	0	11	0
2	6-D	98	0	0	10	0
2	7-A	106	0	0	6	0
2	7-B	126	0	0	11	0
2	7-C	119	0	0	8	0
2	7-D	99	0	0	10	0
2	8-A	108	0	0	14	0
2	8-B	124	0	0	19	0
2	8-C	119	0	0	11	0
2	8-D	99	0	0	2	0
All	All	81744	0	79712	5967	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 38.

The worst 5 of 5967 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:A:99:ARG:HH21	1:A:316:GLY:HA2	1.07	1.16
1:A:8:LYS:HA	1:A:30:GLU:HB3	1.27	1.15
1:C:46:GLU:HG3	1:C:67:ILE:HD13	1.22	1.14
1:B:167:ALA:HA	1:B:170:ARG:HH12	1.16	1.09
1:A:174:PRO:HG2	1:B:174:PRO:HG3	1.33	1.09

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	1-A	319/328 (97%)	263 (82%)	48 (15%)	8 (2%)	7	4
1	1-B	319/328 (97%)	276 (86%)	42 (13%)	1 (0%)	46	57
1	1-C	319/328 (97%)	269 (84%)	41 (13%)	9 (3%)	6	3
1	1-D	319/328 (97%)	258 (81%)	44 (14%)	17 (5%)	2	1
1	2-A	319/328 (97%)	253 (79%)	53 (17%)	13 (4%)	3	1
1	2-B	319/328 (97%)	269 (84%)	40 (12%)	10 (3%)	5	2
1	2-C	319/328 (97%)	272 (85%)	41 (13%)	6 (2%)	10	8
1	2-D	319/328 (97%)	276 (86%)	33 (10%)	10 (3%)	5	2
1	3-A	319/328 (97%)	263 (82%)	48 (15%)	8 (2%)	7	4
1	3-B	319/328 (97%)	275 (86%)	31 (10%)	13 (4%)	3	1
1	3-C	319/328 (97%)	276 (86%)	35 (11%)	8 (2%)	7	4
1	3-D	319/328 (97%)	266 (83%)	47 (15%)	6 (2%)	10	8
1	4-A	319/328 (97%)	253 (79%)	55 (17%)	11 (3%)	5	2
1	4-B	319/328 (97%)	267 (84%)	44 (14%)	8 (2%)	7	4
1	4-C	319/328 (97%)	266 (83%)	39 (12%)	14 (4%)	3	1
1	4-D	319/328 (97%)	275 (86%)	35 (11%)	9 (3%)	6	3

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	5-A	319/328 (97%)	276 (86%)	39 (12%)	4 (1%)	15	15
1	5-B	319/328 (97%)	272 (85%)	38 (12%)	9 (3%)	6	3
1	5-C	319/328 (97%)	274 (86%)	37 (12%)	8 (2%)	7	4
1	5-D	319/328 (97%)	278 (87%)	34 (11%)	7 (2%)	8	6
1	6-A	319/328 (97%)	247 (77%)	51 (16%)	21 (7%)	1	0
1	6-B	319/328 (97%)	268 (84%)	37 (12%)	14 (4%)	3	1
1	6-C	319/328 (97%)	263 (82%)	42 (13%)	14 (4%)	3	1
1	6-D	319/328 (97%)	268 (84%)	40 (12%)	11 (3%)	5	2
1	7-A	319/328 (97%)	255 (80%)	45 (14%)	19 (6%)	2	0
1	7-B	319/328 (97%)	239 (75%)	59 (18%)	21 (7%)	1	0
1	7-C	319/328 (97%)	273 (86%)	35 (11%)	11 (3%)	5	2
1	7-D	319/328 (97%)	270 (85%)	41 (13%)	8 (2%)	7	4
1	8-A	319/328 (97%)	264 (83%)	45 (14%)	10 (3%)	5	2
1	8-B	319/328 (97%)	275 (86%)	35 (11%)	9 (3%)	6	3
1	8-C	319/328 (97%)	271 (85%)	39 (12%)	9 (3%)	6	3
1	8-D	319/328 (97%)	277 (87%)	36 (11%)	6 (2%)	10	8
All	All	10208/10496 (97%)	8547 (84%)	1329 (13%)	332 (3%)	5	2

5 of 332 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	1-A	251	GLN
1	1-B	22	ALA
1	1-C	18	GLU
1	1-C	163	ARG
1	1-C	244	SER

### 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	1-A	262/264 (99%)	253 (97%)	9 (3%)	44	61
1	1-B	262/264 (99%)	254 (97%)	8 (3%)	47	64
1	1-C	262/264 (99%)	255 (97%)	7 (3%)	52	69
1	1-D	262/264 (99%)	255 (97%)	7 (3%)	52	69
1	2-A	262/264 (99%)	253 (97%)	9 (3%)	44	61
1	2-B	262/264 (99%)	257 (98%)	5 (2%)	65	79
1	2-C	262/264 (99%)	247 (94%)	15 (6%)	25	35
1	2-D	262/264 (99%)	257 (98%)	5 (2%)	65	79
1	3-A	262/264 (99%)	254 (97%)	8 (3%)	47	64
1	3-B	262/264 (99%)	254 (97%)	8 (3%)	47	64
1	3-C	262/264 (99%)	252 (96%)	10 (4%)	40	55
1	3-D	262/264 (99%)	257 (98%)	5 (2%)	65	79
1	4-A	262/264 (99%)	249 (95%)	13 (5%)	30	42
1	4-B	262/264 (99%)	250 (95%)	12 (5%)	33	46
1	4-C	262/264 (99%)	251 (96%)	11 (4%)	36	51
1	4-D	262/264 (99%)	257 (98%)	5 (2%)	65	79
1	5-A	262/264 (99%)	253 (97%)	9 (3%)	44	61
1	5-B	262/264 (99%)	249 (95%)	13 (5%)	30	42
1	5-C	262/264 (99%)	246 (94%)	16 (6%)	23	32
1	5-D	262/264 (99%)	253 (97%)	9 (3%)	44	61
1	6-A	262/264 (99%)	248 (95%)	14 (5%)	28	39
1	6-B	262/264 (99%)	248 (95%)	14 (5%)	28	39
1	6-C	262/264 (99%)	247 (94%)	15 (6%)	25	35
1	6-D	262/264 (99%)	251 (96%)	11 (4%)	36	51
1	7-A	262/264 (99%)	253 (97%)	9 (3%)	44	61
1	7-B	262/264 (99%)	248 (95%)	14 (5%)	28	39
1	7-C	262/264 (99%)	250 (95%)	12 (5%)	33	46
1	7-D	262/264 (99%)	251 (96%)	11 (4%)	36	51
1	8-A	262/264 (99%)	249 (95%)	13 (5%)	30	42
1	8-B	262/264 (99%)	252 (96%)	10 (4%)	40	55
1	8-C	262/264 (99%)	248 (95%)	14 (5%)	28	39
1	8-D	262/264 (99%)	254 (97%)	8 (3%)	47	64

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	8384/8448 (99%)	8055 (96%)	329 (4%)	39 54

5 of 329 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	5-B	37	ASP
1	6-A	20	ARG
1	8-B	200	VAL
1	5-B	185	ARG
1	5-C	191	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 142 such sidechains are listed below:

Mol	Chain	Res	Type
1	4-B	232	GLN
1	5-B	74	ASN
1	8-A	208	GLN
1	4-B	299	HIS
1	5-A	33	GLN

### 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	1-A	316/328 (96%)	-0.49	3 (0%) 85 87	18, 24, 31, 38	316 (100%)
1	1-B	316/328 (96%)	-0.49	4 (1%) 79 81	18, 24, 31, 39	316 (100%)
1	1-C	316/328 (96%)	-0.42	6 (1%) 70 72	17, 23, 31, 39	316 (100%)
1	1-D	316/328 (96%)	-0.58	4 (1%) 79 81	18, 24, 30, 39	316 (100%)
1	2-A	316/328 (96%)	-0.49	3 (0%) 85 87	18, 24, 31, 38	316 (100%)
1	2-B	316/328 (96%)	-0.49	4 (1%) 79 81	18, 24, 31, 39	316 (100%)
1	2-C	316/328 (96%)	-0.42	6 (1%) 70 72	17, 23, 31, 39	316 (100%)
1	2-D	316/328 (96%)	-0.58	4 (1%) 79 81	18, 24, 30, 39	316 (100%)
1	3-A	316/328 (96%)	-0.49	3 (0%) 85 87	18, 24, 31, 38	316 (100%)
1	3-B	316/328 (96%)	-0.49	4 (1%) 79 81	18, 24, 31, 39	316 (100%)
1	3-C	316/328 (96%)	-0.42	6 (1%) 70 72	17, 23, 31, 39	316 (100%)
1	3-D	316/328 (96%)	-0.58	4 (1%) 79 81	18, 24, 30, 39	316 (100%)
1	4-A	316/328 (96%)	-0.49	3 (0%) 85 87	18, 24, 31, 38	316 (100%)
1	4-B	316/328 (96%)	-0.49	4 (1%) 79 81	18, 24, 31, 39	316 (100%)
1	4-C	316/328 (96%)	-0.42	6 (1%) 70 72	17, 23, 31, 39	316 (100%)
1	4-D	316/328 (96%)	-0.58	4 (1%) 79 81	18, 24, 30, 39	316 (100%)
1	5-A	316/328 (96%)	-0.49	3 (0%) 85 87	18, 24, 31, 38	316 (100%)
1	5-B	316/328 (96%)	-0.49	4 (1%) 79 81	18, 24, 31, 39	316 (100%)
1	5-C	316/328 (96%)	-0.42	6 (1%) 70 72	17, 23, 31, 39	316 (100%)
1	5-D	316/328 (96%)	-0.58	4 (1%) 79 81	18, 24, 30, 39	316 (100%)
1	6-A	316/328 (96%)	-0.49	3 (0%) 85 87	18, 24, 31, 38	316 (100%)
1	6-B	316/328 (96%)	-0.49	4 (1%) 79 81	18, 24, 31, 39	316 (100%)
1	6-C	316/328 (96%)	-0.42	6 (1%) 70 72	17, 23, 31, 39	316 (100%)
1	6-D	316/328 (96%)	-0.58	4 (1%) 79 81	18, 24, 30, 39	316 (100%)

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	7-A	316/328 (96%)	-0.49	3 (0%) 85 87	18, 24, 31, 38	316 (100%)
1	7-B	316/328 (96%)	-0.49	4 (1%) 79 81	18, 24, 31, 39	316 (100%)
1	7-C	316/328 (96%)	-0.42	6 (1%) 70 72	17, 23, 31, 39	316 (100%)
1	7-D	316/328 (96%)	-0.58	4 (1%) 79 81	18, 24, 30, 39	316 (100%)
1	8-A	316/328 (96%)	-0.49	3 (0%) 85 87	18, 24, 31, 38	316 (100%)
1	8-B	316/328 (96%)	-0.49	4 (1%) 79 81	18, 24, 31, 39	316 (100%)
1	8-C	316/328 (96%)	-0.42	6 (1%) 70 72	17, 23, 31, 39	316 (100%)
1	8-D	316/328 (96%)	-0.58	4 (1%) 79 81	18, 24, 30, 39	316 (100%)
All	All	10112/10496 (96%)	-0.50	136 (1%) 71 81	17, 24, 31, 39	10112 (100%)

The worst 5 of 136 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	1-B	185	ARG	5.8
1	2-B	185	ARG	5.8
1	3-B	185	ARG	5.8
1	4-B	185	ARG	5.8
1	5-B	185	ARG	5.8

## 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.