



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 15, 2017 – 05:33 am GMT

PDB ID : 3RVD
Title : Crystal structure of the binary complex, obtained by soaking, of photosynthetic a4 glyceraldehyde 3-phosphate dehydrogenase (gapdh) with cp12-2, both from arabidopsis thaliana.
Authors : Fermani, S.; Thumiger, A.; Falini, G.; Marri, L.; Sparla, F.; Trost, P.
Deposited on : 2011-05-06
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	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28683
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

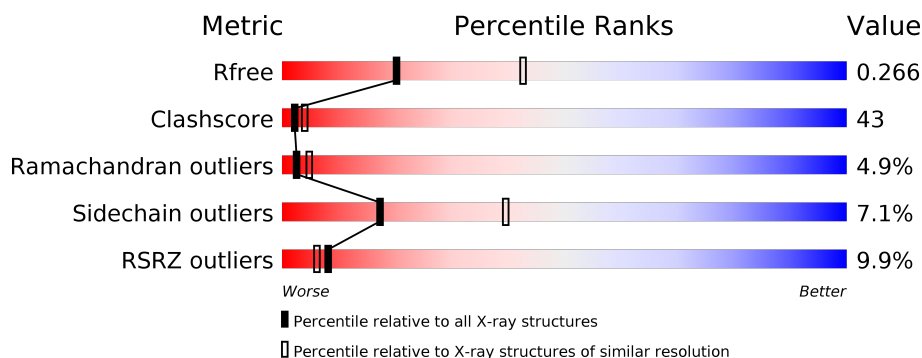
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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}	100719	2259 (2.70-2.70)
Clashscore	112137	2590 (2.70-2.70)
Ramachandran outliers	110173	2550 (2.70-2.70)
Sidechain outliers	110143	2550 (2.70-2.70)
RSRZ outliers	101464	2275 (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	337	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, green 51%, yellow 44%, orange 5%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> % 51% 44% 5% </div> </div>
1	B	337	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 3%, green 46%, yellow 47%, orange 7%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 3% 46% 47% 7% </div> </div>
1	C	337	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 4%, green 51%, yellow 42%, orange 7%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 4% 51% 42% 7% </div> </div>
1	D	337	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 7%, green 30%, yellow 58%, orange 11%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 7% 30% 58% 11% </div> </div>
1	E	337	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 36%, green 25%, yellow 64%, orange 10%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 36% 25% 64% 10% </div> </div>
1	F	337	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 18%, green 28%, yellow 62%, orange 9%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 18% 28% 62% 9% </div> </div>

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Mol	Chain	Length	Quality of chain
1	G	337	
1	H	337	
1	O	337	
1	Q	337	
2	I	82	
2	J	82	
2	K	82	
2	L	82	
2	M	82	
2	N	82	

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
4	SO4	A	407	-	-	-	X
4	SO4	B	403	-	-	-	X
4	SO4	C	406	-	-	-	X
4	SO4	O	402	-	-	-	X
4	SO4	O	403	-	-	-	X
4	SO4	Q	403	-	-	-	X
4	SO4	Q	404	-	-	-	X
4	SO4	Q	405	-	-	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 27674 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 Glyceraldehyde-3-phosphate dehydrogenase A, chloroplastic.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	336	Total	C	N	O	S	0	0	0
			2552	1612	444	487	9			
1	B	336	Total	C	N	O	S	0	0	0
			2552	1612	444	487	9			
1	C	336	Total	C	N	O	S	0	0	0
			2552	1612	444	487	9			
1	D	336	Total	C	N	O	S	0	0	0
			2552	1612	444	487	9			
1	E	336	Total	C	N	O	S	0	0	0
			2547	1609	443	486	9			
1	F	336	Total	C	N	O	S	0	0	0
			2552	1612	444	487	9			
1	G	337	Total	C	N	O	S	0	0	0
			2556	1615	445	487	9			
1	H	335	Total	C	N	O	S	0	0	0
			2542	1606	442	485	9			
1	O	337	Total	C	N	O	S	0	0	0
			2557	1615	445	488	9			
1	Q	336	Total	C	N	O	S	0	0	0
			2552	1612	444	487	9			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	ALA	-	EXPRESSION TAG	UNP P25856
B	-1	ALA	-	EXPRESSION TAG	UNP P25856
C	-1	ALA	-	EXPRESSION TAG	UNP P25856
D	-1	ALA	-	EXPRESSION TAG	UNP P25856
E	-1	ALA	-	EXPRESSION TAG	UNP P25856
F	-1	ALA	-	EXPRESSION TAG	UNP P25856
G	-1	ALA	-	EXPRESSION TAG	UNP P25856
H	-1	ALA	-	EXPRESSION TAG	UNP P25856
O	-1	ALA	-	EXPRESSION TAG	UNP P25856

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Chain	Residue	Modelled	Actual	Comment	Reference
Q	-1	ALA	-	EXPRESSION TAG	UNP P25856

- Molecule 2 is a protein called Photosynthetic glyceraldehyde-3-phosphate dehydrogenase (a4 isoform).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	I	22	Total	C	N	O	S	0	0	0
			182	107	29	44	2			
2	J	21	Total	C	N	O	S	0	0	0
			176	104	28	42	2			
2	K	21	Total	C	N	O	S	0	0	0
			176	104	28	42	2			
2	L	19	Total	C	N	O	S	0	0	0
			148	86	22	38	2			
2	M	22	Total	C	N	O	S	0	0	0
			182	107	29	44	2			
2	N	19	Total	C	N	O	S	0	0	0
			160	96	25	37	2			

There are 24 discrepancies between the modelled and reference sequences:

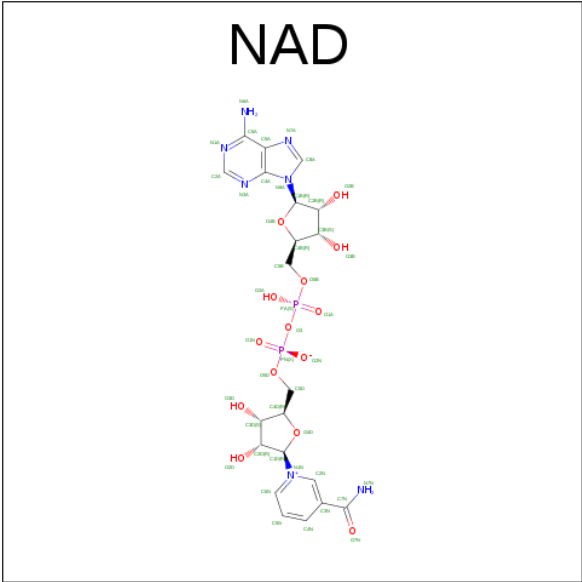
Chain	Residue	Modelled	Actual	Comment	Reference
I	-3	GLY	-	EXPRESSION TAG	UNP Q9LZP9
I	-2	SER	-	EXPRESSION TAG	UNP Q9LZP9
I	-1	HIS	-	EXPRESSION TAG	UNP Q9LZP9
I	0	MET	-	EXPRESSION TAG	UNP Q9LZP9
J	-3	GLY	-	EXPRESSION TAG	UNP Q9LZP9
J	-2	SER	-	EXPRESSION TAG	UNP Q9LZP9
J	-1	HIS	-	EXPRESSION TAG	UNP Q9LZP9
J	0	MET	-	EXPRESSION TAG	UNP Q9LZP9
K	-3	GLY	-	EXPRESSION TAG	UNP Q9LZP9
K	-2	SER	-	EXPRESSION TAG	UNP Q9LZP9
K	-1	HIS	-	EXPRESSION TAG	UNP Q9LZP9
K	0	MET	-	EXPRESSION TAG	UNP Q9LZP9
L	-3	GLY	-	EXPRESSION TAG	UNP Q9LZP9
L	-2	SER	-	EXPRESSION TAG	UNP Q9LZP9
L	-1	HIS	-	EXPRESSION TAG	UNP Q9LZP9
L	0	MET	-	EXPRESSION TAG	UNP Q9LZP9
M	-3	GLY	-	EXPRESSION TAG	UNP Q9LZP9
M	-2	SER	-	EXPRESSION TAG	UNP Q9LZP9
M	-1	HIS	-	EXPRESSION TAG	UNP Q9LZP9
M	0	MET	-	EXPRESSION TAG	UNP Q9LZP9

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Chain	Residue	Modelled	Actual	Comment	Reference
N	-3	GLY	-	EXPRESSION TAG	UNP Q9LZP9
N	-2	SER	-	EXPRESSION TAG	UNP Q9LZP9
N	-1	HIS	-	EXPRESSION TAG	UNP Q9LZP9
N	0	MET	-	EXPRESSION TAG	UNP Q9LZP9

- Molecule 3 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (three-letter code: NAD) (formula: C₂₁H₂₇N₇O₁₄P₂).



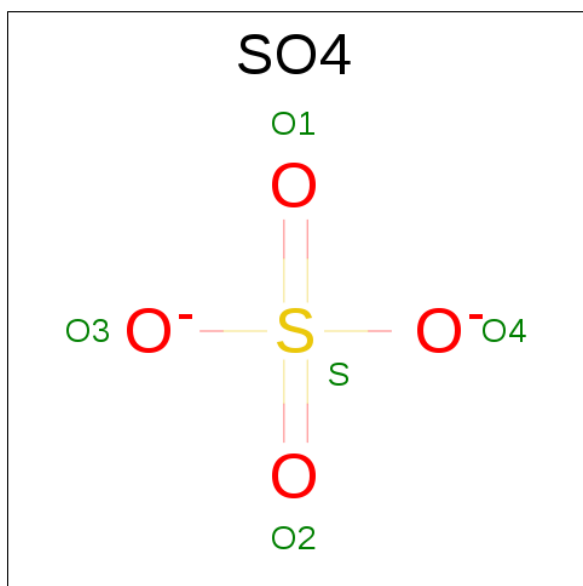
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
3	B	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
3	C	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
3	D	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
3	E	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
3	F	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
3	G	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
3	H	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
3	O	1	Total	C	N	O	P	0	0
			44	21	7	14	2		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	Q	1	Total	C	N	O	P	0	0
			44	21	7	14	2		

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	C	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	C	1	Total	O	S	0	0
			5	4	1		
4	C	1	Total	O	S	0	0
			5	4	1		
4	C	1	Total	O	S	0	0
			5	4	1		
4	C	1	Total	O	S	0	0
			5	4	1		
4	D	1	Total	O	S	0	0
			5	4	1		
4	E	1	Total	O	S	0	0
			5	4	1		
4	E	1	Total	O	S	0	0
			5	4	1		
4	E	1	Total	O	S	0	0
			5	4	1		
4	F	1	Total	O	S	0	0
			5	4	1		
4	F	1	Total	O	S	0	0
			5	4	1		
4	G	1	Total	O	S	0	0
			5	4	1		
4	H	1	Total	O	S	0	0
			5	4	1		
4	O	1	Total	O	S	0	0
			5	4	1		
4	O	1	Total	O	S	0	0
			5	4	1		
4	Q	1	Total	O	S	0	0
			5	4	1		
4	Q	1	Total	O	S	0	0
			5	4	1		
4	Q	1	Total	O	S	0	0
			5	4	1		
4	Q	1	Total	O	S	0	0
			5	4	1		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	72	Total	O	0	0
			72	72		

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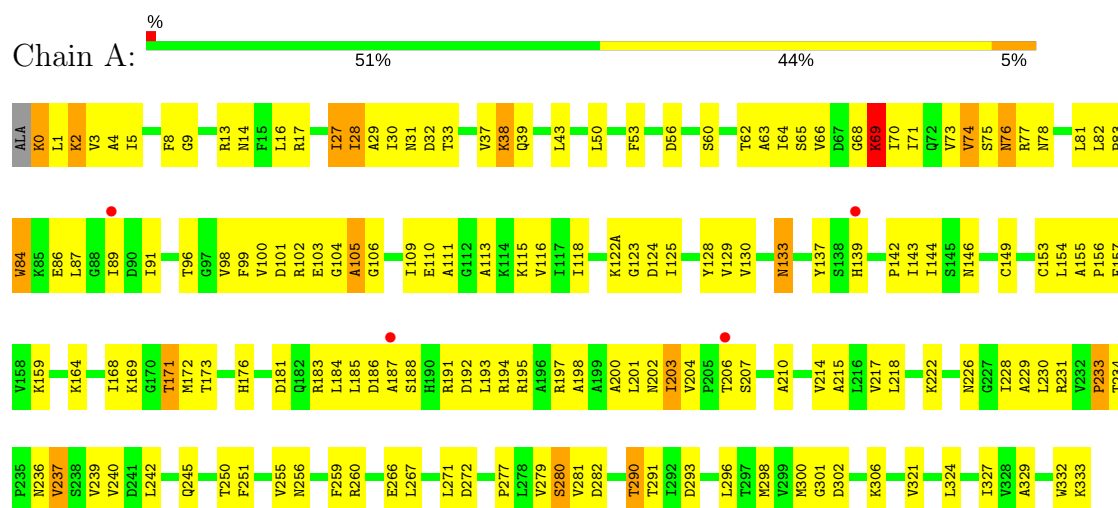
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	35	Total 35	O 35	0	0
5	C	55	Total 55	O 55	0	0
5	D	52	Total 52	O 52	0	0
5	E	42	Total 42	O 42	0	0
5	F	36	Total 36	O 36	0	0
5	G	38	Total 38	O 38	0	0
5	H	31	Total 31	O 31	0	0
5	I	3	Total 3	O 3	0	0
5	J	1	Total 1	O 1	0	0
5	K	20	Total 20	O 20	0	0
5	L	4	Total 4	O 4	0	0
5	M	6	Total 6	O 6	0	0
5	N	10	Total 10	O 10	0	0
5	O	82	Total 82	O 82	0	0
5	Q	69	Total 69	O 69	0	0

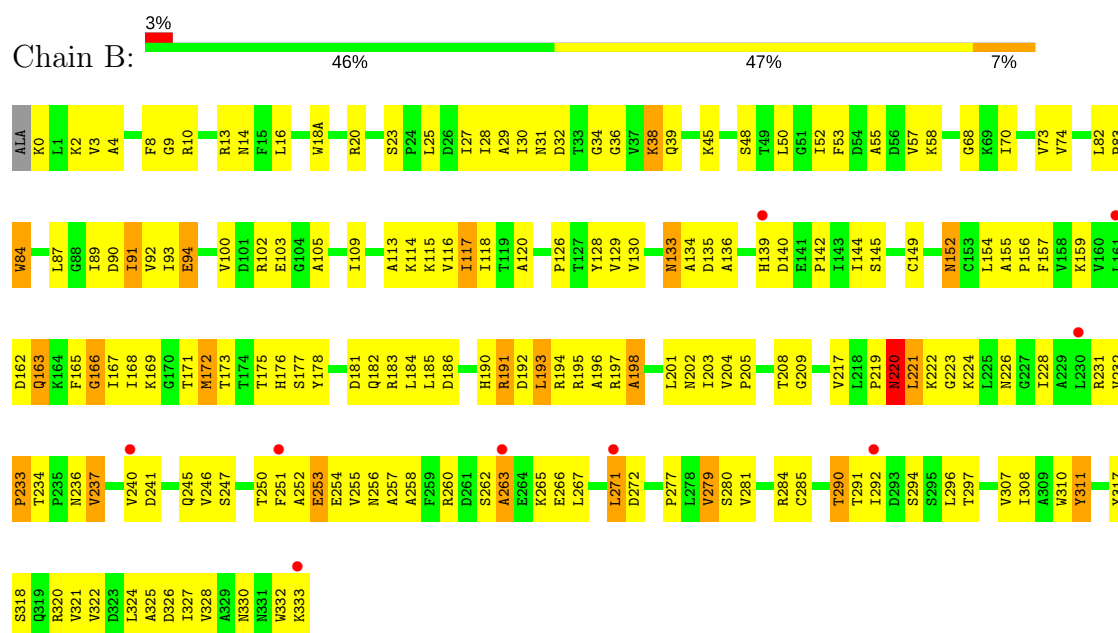
3 Residue-property plots

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.

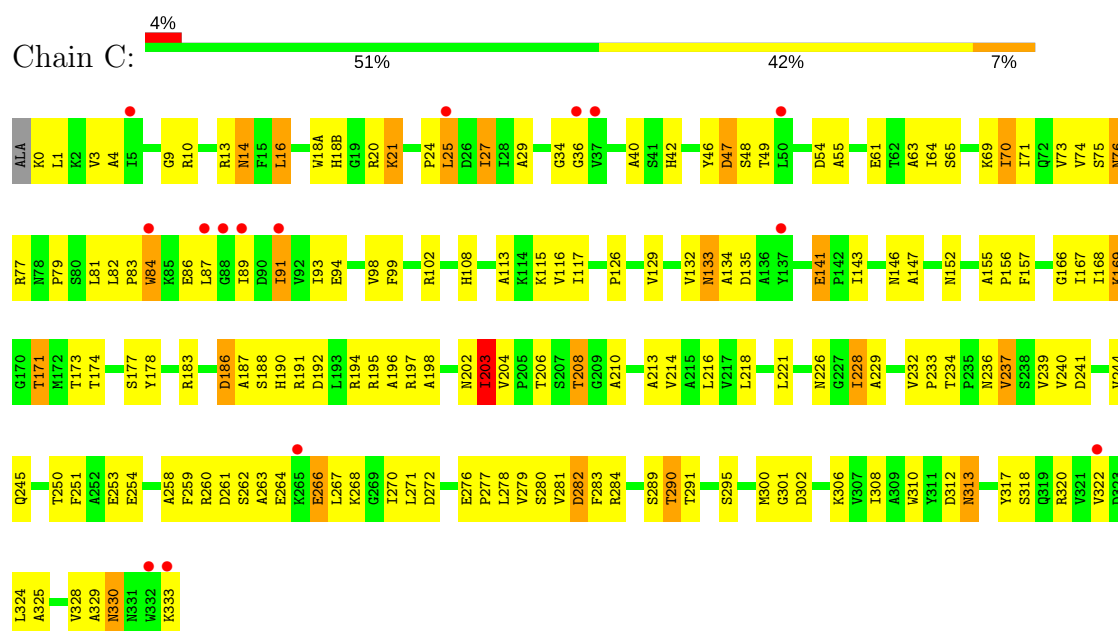
- Molecule 1: Glyceraldehyde-3-phosphate dehydrogenase A, chloroplastic



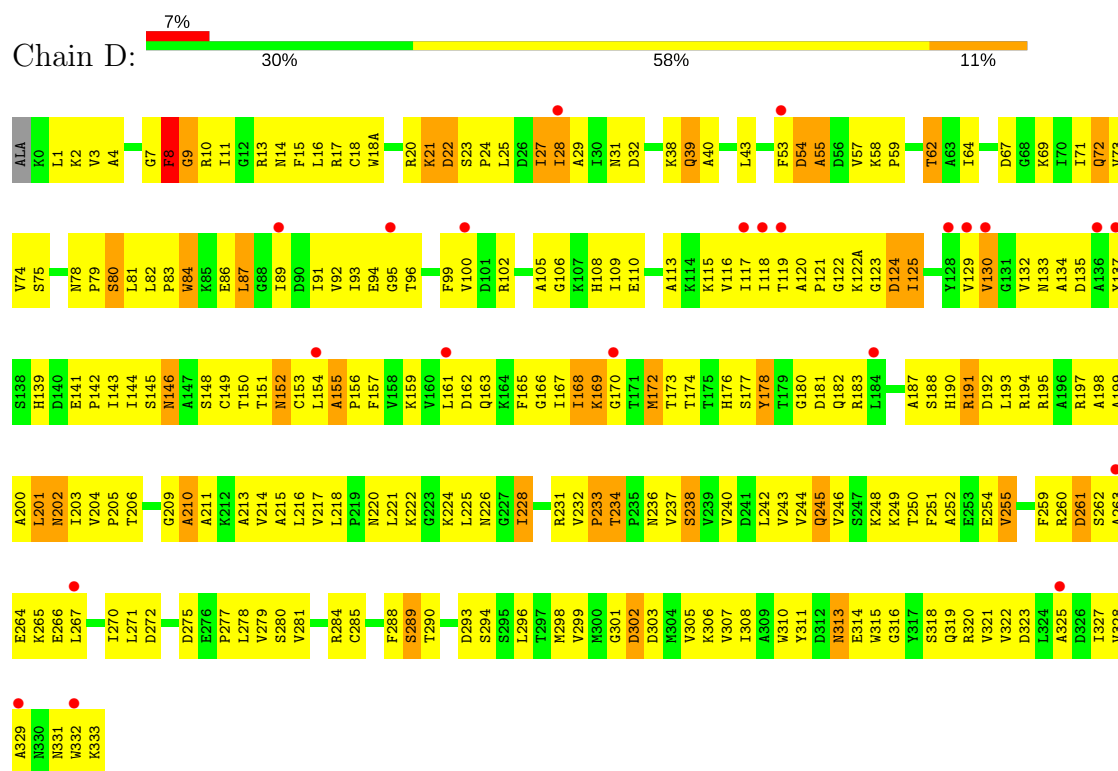
- Molecule 1: Glyceraldehyde-3-phosphate dehydrogenase A, chloroplastic



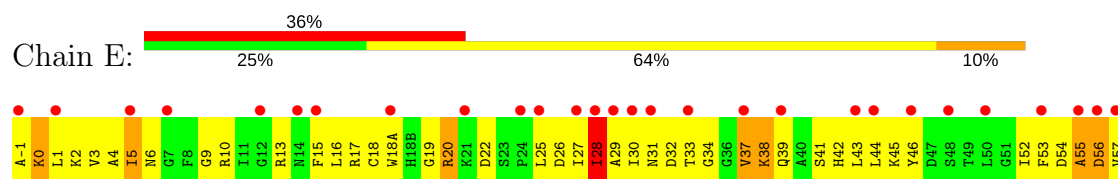
- Molecule 1: Glyceraldehyde-3-phosphate dehydrogenase A, chloroplastic

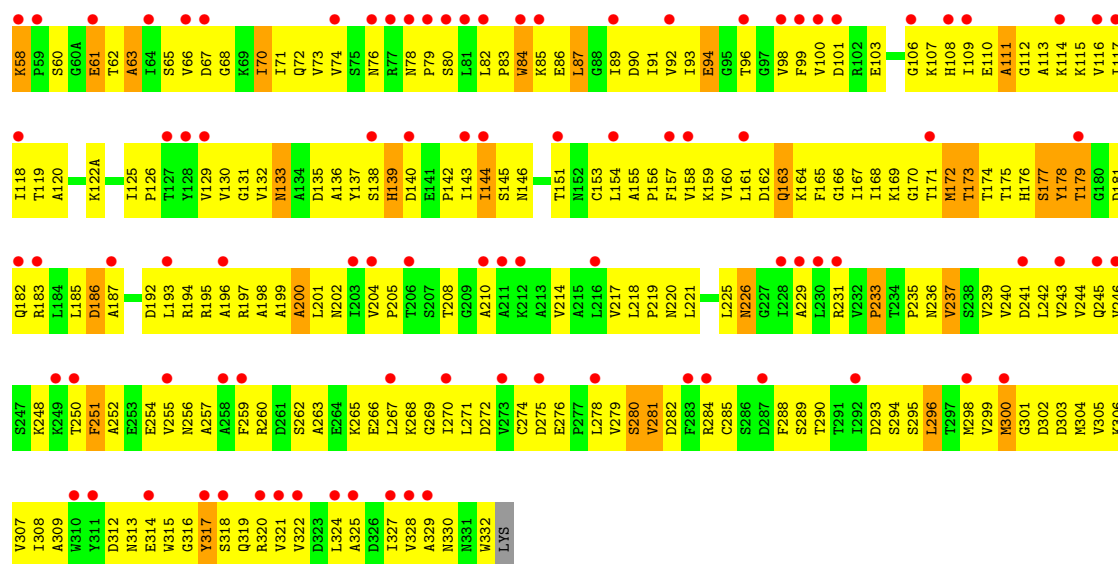


- Molecule 1: Glyceraldehyde-3-phosphate dehydrogenase A, chloroplastic

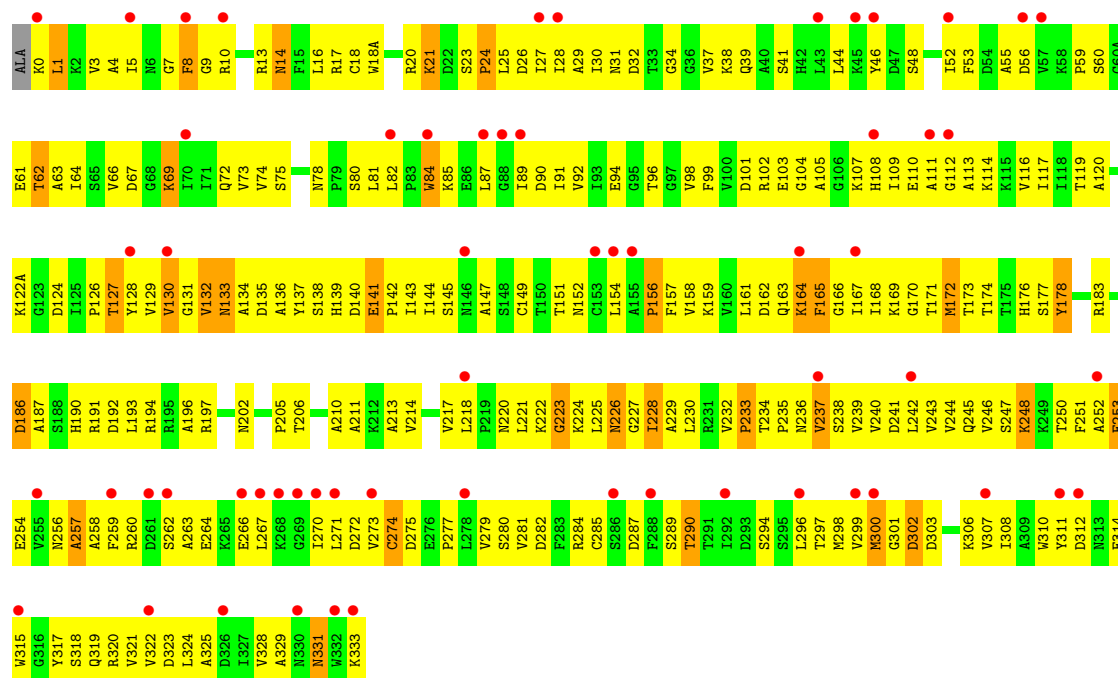


- Molecule 1: Glyceraldehyde-3-phosphate dehydrogenase A, chloroplastic

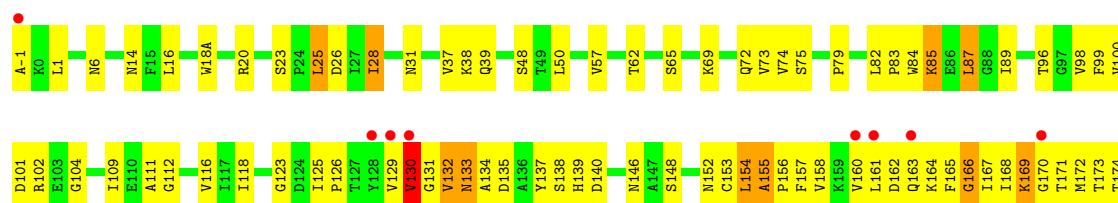
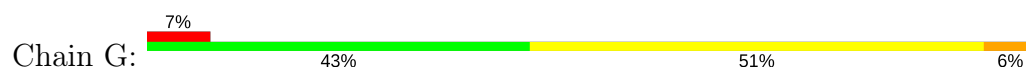


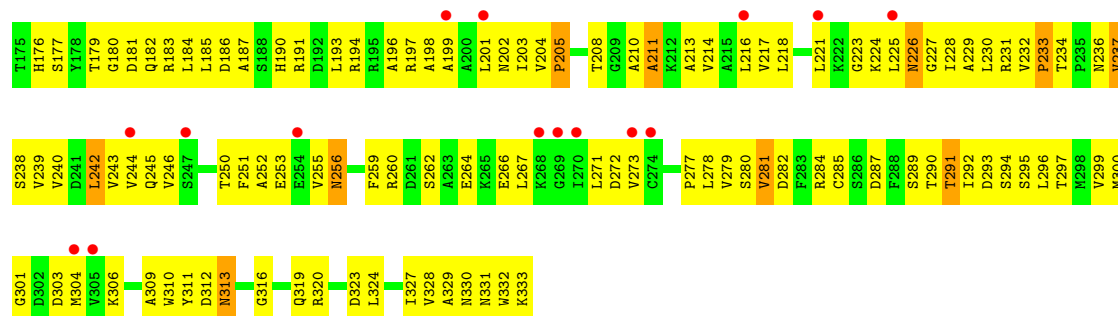


• Molecule 1: Glyceraldehyde-3-phosphate dehydrogenase A, chloroplatic

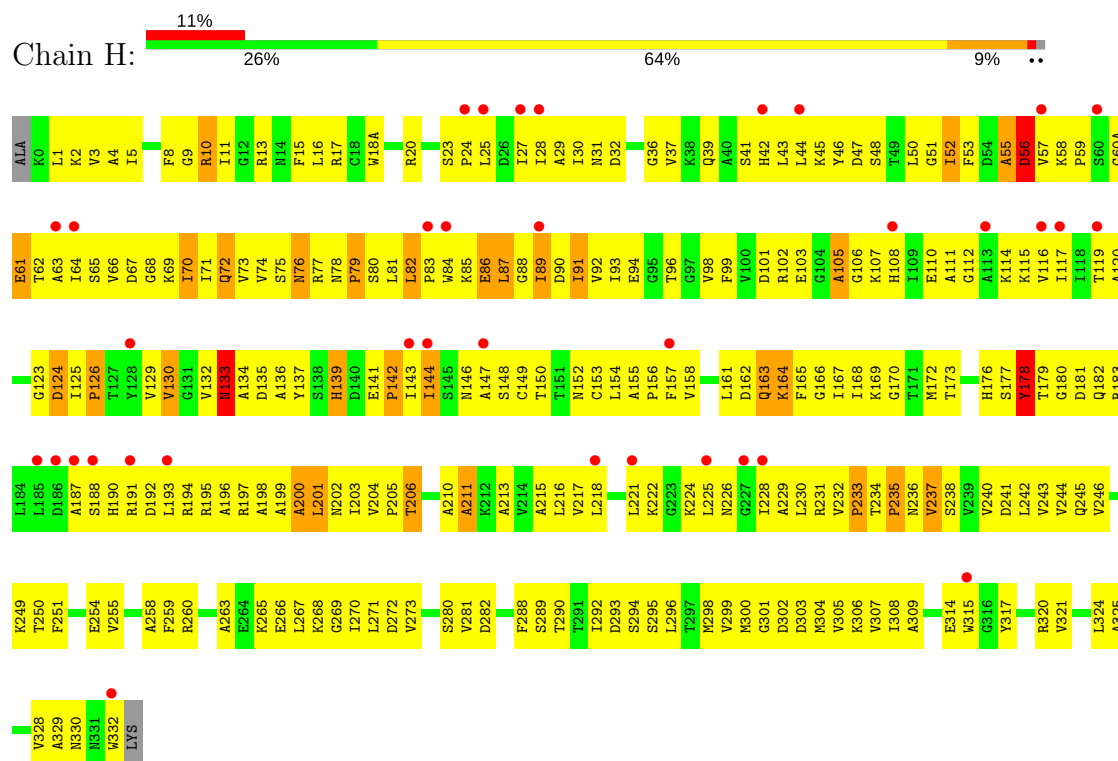


• Molecule 1: Glyceraldehyde-3-phosphate dehydrogenase A, chloroplatic

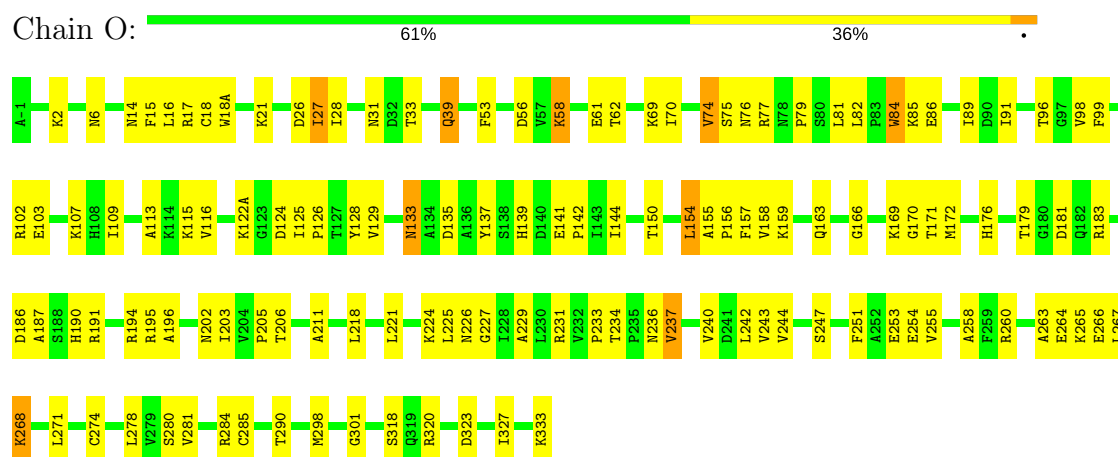




- Molecule 1: Glyceraldehyde-3-phosphate dehydrogenase A, chloroplactic

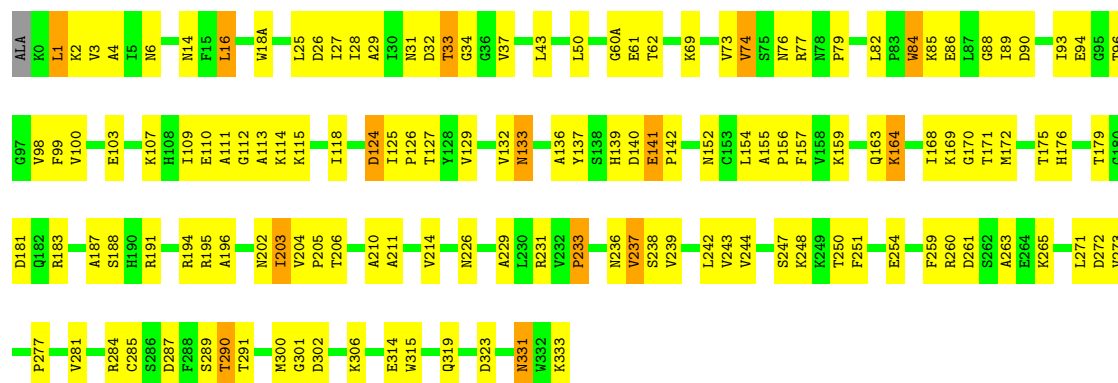


- Molecule 1: Glyceraldehyde-3-phosphate dehydrogenase A, chloroplactic



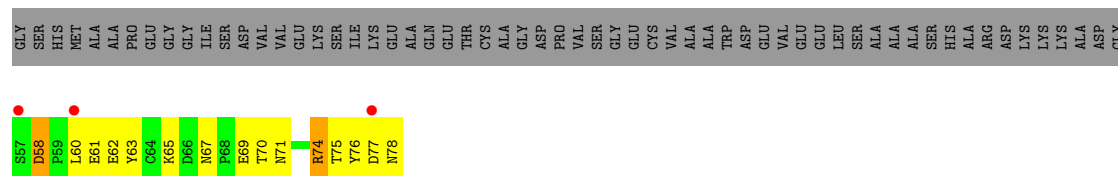
- Molecule 1: Glyceraldehyde-3-phosphate dehydrogenase A, chloroplactic

Chain Q:  58% 37% .



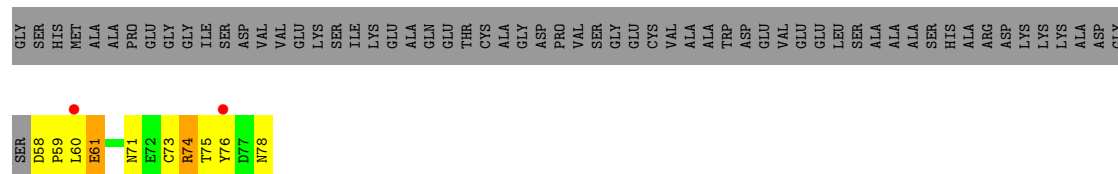
- Molecule 2: Photosynthetic glyceraldehyde-3-phosphate dehydrogenase (a4 isoform)

Chain I:  4% 9% 16% 73% .



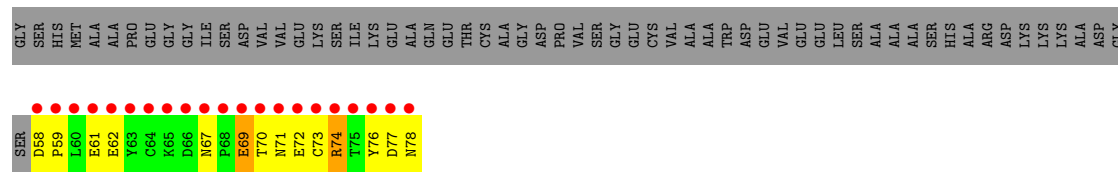
- Molecule 2: Photosynthetic glyceraldehyde-3-phosphate dehydrogenase (a4 isoform)

Chain J:  29% 13% 10% 74% .



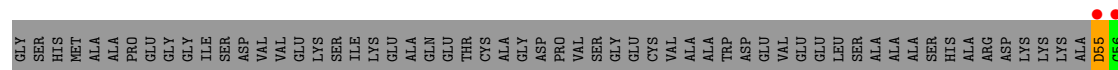
- Molecule 2: Photosynthetic glyceraldehyde-3-phosphate dehydrogenase (a4 isoform)

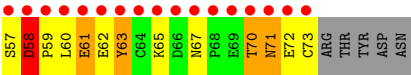
Chain K:  26% 9% 15% 74% .



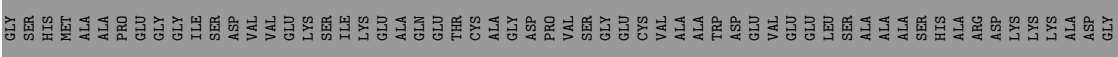
- Molecule 2: Photosynthetic glyceraldehyde-3-phosphate dehydrogenase (a4 isoform)

Chain L:  23% 6% 10% 77% .

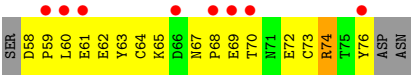
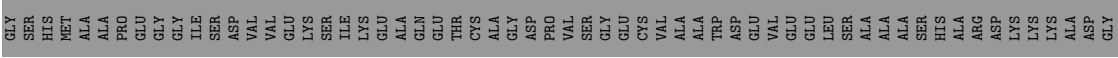




● Molecule 2: Photosyntetic glyceraldehyde-3-phosphate dehydrogenase (a4 isoform)



● Molecule 2: Photosyntetic glyceraldehyde-3-phosphate dehydrogenase (a4 isoform)



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	153.18Å 188.75Å 312.17Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	94.61 – 2.70 94.60 – 2.70	Depositor EDS
% Data completeness (in resolution range)	95.7 (94.61-2.70) 95.8 (94.60-2.70)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.76 (at 2.69Å)	Xtriage
Refinement program	CNS 1.3	Depositor
R, R_{free}	0.247 , 0.318 0.243 , 0.266	Depositor DCC
R_{free} test set	11850 reflections (10.00%)	DCC
Wilson B-factor (Å ²)	47.8	Xtriage
Anisotropy	0.841	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 86.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.36$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	27674	wwPDB-VP
Average B, all atoms (Å ²)	63.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 11.18% 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 [i](#)

5.1 Standard geometry [i](#)

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

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	0.45	0/2596	0.69	1/3523 (0.0%)
1	B	0.44	0/2596	0.73	2/3523 (0.1%)
1	C	0.44	0/2596	0.70	1/3523 (0.0%)
1	D	0.40	0/2596	0.66	0/3523
1	E	0.44	0/2591	0.68	0/3519
1	F	0.40	0/2596	0.64	0/3523
1	G	0.42	0/2600	0.68	0/3530
1	H	0.40	0/2586	0.65	0/3512
1	O	0.55	0/2601	0.77	1/3530 (0.0%)
1	Q	0.51	0/2596	0.77	2/3523 (0.1%)
2	I	0.75	0/185	0.64	0/251
2	J	0.84	1/179 (0.6%)	0.64	0/243
2	K	0.46	0/179	0.65	0/243
2	L	0.64	0/150	0.86	0/203
2	M	0.66	0/185	0.70	0/251
2	N	0.55	0/163	0.56	0/221
All	All	0.46	1/26995 (0.0%)	0.70	7/36641 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	J	61	GLU	CG-CD	5.06	1.59	1.51

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Q	203	ILE	N-CA-C	-6.16	94.37	111.00
1	O	203	ILE	N-CA-C	-5.87	95.16	111.00
1	B	203	ILE	N-CA-C	-5.82	95.30	111.00
1	A	203	ILE	N-CA-C	-5.62	95.83	111.00
1	Q	60(A)	GLY	N-CA-C	-5.54	99.24	113.10

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	2552	0	2593	200	0
1	B	2552	0	2593	218	0
1	C	2552	0	2593	198	0
1	D	2552	0	2593	318	0
1	E	2547	0	2585	369	0
1	F	2552	0	2593	312	0
1	G	2556	0	2598	264	0
1	H	2542	0	2580	338	0
1	O	2557	0	2598	135	0
1	Q	2552	0	2593	129	0
2	I	182	0	149	25	0
2	J	176	0	144	14	0
2	K	176	0	144	25	0
2	L	148	0	117	23	0
2	M	182	0	149	23	0
2	N	160	0	134	31	0
3	A	44	0	26	3	0
3	B	44	0	26	1	0
3	C	44	0	26	2	0
3	D	44	0	26	6	0
3	E	44	0	26	5	0
3	F	44	0	26	6	0
3	G	44	0	26	1	0
3	H	44	0	26	13	0
3	O	44	0	26	0	0
3	Q	44	0	26	1	0
4	A	35	0	0	1	0
4	B	10	0	0	1	0
4	C	25	0	0	1	0
4	D	5	0	0	1	0
4	E	15	0	0	2	0
4	F	10	0	0	0	0
4	G	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	H	5	0	0	0	0
4	O	10	0	0	0	0
4	Q	20	0	0	1	0
5	A	72	0	0	3	0
5	B	35	0	0	2	0
5	C	55	0	0	1	0
5	D	52	0	0	4	0
5	E	42	0	0	6	0
5	F	36	0	0	5	0
5	G	38	0	0	3	0
5	H	31	0	0	1	0
5	I	3	0	0	0	0
5	J	1	0	0	0	0
5	K	20	0	0	1	0
5	L	4	0	0	2	0
5	M	6	0	0	1	0
5	N	10	0	0	2	0
5	O	82	0	0	3	0
5	Q	69	0	0	3	1
All	All	27674	0	27016	2311	1

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 43.

The worst 5 of 2311 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:D:117:ILE:HG23	1:D:144:ILE:HD11	1.23	1.17
1:D:78:ASN:HD22	1:D:81:LEU:HG	1.11	1.13
1:G:161:LEU:HB3	1:G:167:ILE:HD11	1.19	1.12
1:A:202:ASN:HD21	1:C:281:VAL:HG12	1.06	1.11
1:C:183:ARG:HE	1:C:187:ALA:HB3	1.12	1.11

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:Q:541:HOH:O	5:Q:541:HOH:O[2_665]	2.11	0.09

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	334/337 (99%)	272 (81%)	54 (16%)	8 (2%)	7	17
1	B	334/337 (99%)	267 (80%)	55 (16%)	12 (4%)	4	9
1	C	334/337 (99%)	281 (84%)	44 (13%)	9 (3%)	6	15
1	D	334/337 (99%)	247 (74%)	63 (19%)	24 (7%)	1	1
1	E	334/337 (99%)	248 (74%)	58 (17%)	28 (8%)	1	1
1	F	334/337 (99%)	250 (75%)	64 (19%)	20 (6%)	2	3
1	G	335/337 (99%)	270 (81%)	47 (14%)	18 (5%)	2	4
1	H	333/337 (99%)	250 (75%)	51 (15%)	32 (10%)	1	0
1	O	335/337 (99%)	303 (90%)	29 (9%)	3 (1%)	20	46
1	Q	334/337 (99%)	294 (88%)	32 (10%)	8 (2%)	7	17
2	I	20/82 (24%)	19 (95%)	1 (5%)	0	100	100
2	J	19/82 (23%)	15 (79%)	3 (16%)	1 (5%)	2	4
2	K	19/82 (23%)	16 (84%)	1 (5%)	2 (10%)	0	0
2	L	17/82 (21%)	12 (71%)	4 (24%)	1 (6%)	2	3
2	M	20/82 (24%)	16 (80%)	3 (15%)	1 (5%)	2	4
2	N	17/82 (21%)	9 (53%)	7 (41%)	1 (6%)	2	3
All	All	3453/3862 (89%)	2769 (80%)	516 (15%)	168 (5%)	2	5

5 of 168 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	186	ASP
1	B	221	LEU
1	D	22	ASP
1	D	199	ALA
1	D	210	ALA

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	279/279 (100%)	260 (93%)	19 (7%)	18	41
1	B	279/279 (100%)	259 (93%)	20 (7%)	17	39
1	C	279/279 (100%)	255 (91%)	24 (9%)	12	28
1	D	279/279 (100%)	255 (91%)	24 (9%)	12	28
1	E	278/279 (100%)	255 (92%)	23 (8%)	13	30
1	F	279/279 (100%)	259 (93%)	20 (7%)	17	39
1	G	279/279 (100%)	261 (94%)	18 (6%)	20	44
1	H	278/279 (100%)	265 (95%)	13 (5%)	30	60
1	O	279/279 (100%)	260 (93%)	19 (7%)	18	41
1	Q	279/279 (100%)	266 (95%)	13 (5%)	30	60
2	I	22/65 (34%)	19 (86%)	3 (14%)	4	10
2	J	21/65 (32%)	21 (100%)	0	100	100
2	K	21/65 (32%)	19 (90%)	2 (10%)	10	23
2	L	18/65 (28%)	10 (56%)	8 (44%)	0	0
2	M	22/65 (34%)	22 (100%)	0	100	100
2	N	19/65 (29%)	19 (100%)	0	100	100
All	All	2911/3180 (92%)	2705 (93%)	206 (7%)	17	39

5 of 206 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	61	GLU
1	F	84	TRP
1	O	247	SER
1	E	70	ILE
1	E	179	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 92 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	330	ASN
1	F	256	ASN
1	Q	152	ASN
1	F	14	ASN
1	F	139	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](#)

38 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	NAD	A	401	-	41,48,48	1.43	7 (17%)	43,73,73	1.87	13 (30%)
4	SO4	A	402	-	4,4,4	0.34	0	6,6,6	0.17	0
4	SO4	A	403	-	4,4,4	0.36	0	6,6,6	0.10	0
4	SO4	A	404	-	4,4,4	0.34	0	6,6,6	0.18	0
4	SO4	A	405	-	4,4,4	0.39	0	6,6,6	0.08	0
4	SO4	A	406	-	4,4,4	0.31	0	6,6,6	0.11	0
4	SO4	A	407	-	4,4,4	0.29	0	6,6,6	0.13	0
4	SO4	A	408	-	4,4,4	0.31	0	6,6,6	0.06	0
3	NAD	B	401	-	41,48,48	1.57	8 (19%)	43,73,73	1.82	11 (25%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	SO4	B	402	-	4,4,4	0.32	0	6,6,6	0.14	0
4	SO4	B	403	-	4,4,4	0.35	0	6,6,6	0.15	0
3	NAD	C	401	-	41,48,48	1.54	6 (14%)	43,73,73	1.79	11 (25%)
4	SO4	C	402	-	4,4,4	0.35	0	6,6,6	0.12	0
4	SO4	C	403	-	4,4,4	0.36	0	6,6,6	0.17	0
4	SO4	C	404	-	4,4,4	0.34	0	6,6,6	0.15	0
4	SO4	C	405	-	4,4,4	0.33	0	6,6,6	0.08	0
4	SO4	C	406	-	4,4,4	0.32	0	6,6,6	0.21	0
3	NAD	D	401	-	41,48,48	1.41	7 (17%)	43,73,73	1.98	12 (27%)
4	SO4	D	402	-	4,4,4	0.33	0	6,6,6	0.14	0
3	NAD	E	401	-	41,48,48	1.38	7 (17%)	43,73,73	1.95	12 (27%)
4	SO4	E	402	-	4,4,4	0.30	0	6,6,6	0.05	0
4	SO4	E	403	-	4,4,4	0.27	0	6,6,6	0.09	0
4	SO4	E	404	-	4,4,4	0.36	0	6,6,6	0.09	0
3	NAD	F	401	-	41,48,48	1.55	6 (14%)	43,73,73	1.92	12 (27%)
4	SO4	F	402	-	4,4,4	0.29	0	6,6,6	0.18	0
4	SO4	F	403	-	4,4,4	0.29	0	6,6,6	0.12	0
3	NAD	G	401	-	41,48,48	1.55	8 (19%)	43,73,73	1.87	11 (25%)
4	SO4	G	402	-	4,4,4	0.30	0	6,6,6	0.12	0
3	NAD	H	401	-	41,48,48	1.42	5 (12%)	43,73,73	1.91	12 (27%)
4	SO4	H	402	-	4,4,4	0.42	0	6,6,6	0.09	0
3	NAD	O	401	-	41,48,48	1.37	6 (14%)	43,73,73	1.86	12 (27%)
4	SO4	O	402	-	4,4,4	0.30	0	6,6,6	0.13	0
4	SO4	O	403	-	4,4,4	0.30	0	6,6,6	0.12	0
3	NAD	Q	401	-	41,48,48	1.62	7 (17%)	43,73,73	1.79	10 (23%)
4	SO4	Q	402	-	4,4,4	0.39	0	6,6,6	0.14	0
4	SO4	Q	403	-	4,4,4	0.27	0	6,6,6	0.07	0
4	SO4	Q	404	-	4,4,4	0.41	0	6,6,6	0.13	0
4	SO4	Q	405	-	4,4,4	0.40	0	6,6,6	0.13	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	NAD	A	401	-	-	0/22/62/62	0/5/5/5
4	SO4	A	402	-	-	0/0/0/0	0/0/0/0
4	SO4	A	403	-	-	0/0/0/0	0/0/0/0
4	SO4	A	404	-	-	0/0/0/0	0/0/0/0
4	SO4	A	405	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	SO4	A	406	-	-	0/0/0/0	0/0/0/0
4	SO4	A	407	-	-	0/0/0/0	0/0/0/0
4	SO4	A	408	-	-	0/0/0/0	0/0/0/0
3	NAD	B	401	-	-	0/22/62/62	0/5/5/5
4	SO4	B	402	-	-	0/0/0/0	0/0/0/0
4	SO4	B	403	-	-	0/0/0/0	0/0/0/0
3	NAD	C	401	-	-	0/22/62/62	0/5/5/5
4	SO4	C	402	-	-	0/0/0/0	0/0/0/0
4	SO4	C	403	-	-	0/0/0/0	0/0/0/0
4	SO4	C	404	-	-	0/0/0/0	0/0/0/0
4	SO4	C	405	-	-	0/0/0/0	0/0/0/0
4	SO4	C	406	-	-	0/0/0/0	0/0/0/0
3	NAD	D	401	-	-	0/22/62/62	0/5/5/5
4	SO4	D	402	-	-	0/0/0/0	0/0/0/0
3	NAD	E	401	-	-	0/22/62/62	0/5/5/5
4	SO4	E	402	-	-	0/0/0/0	0/0/0/0
4	SO4	E	403	-	-	0/0/0/0	0/0/0/0
4	SO4	E	404	-	-	0/0/0/0	0/0/0/0
3	NAD	F	401	-	-	0/22/62/62	0/5/5/5
4	SO4	F	402	-	-	0/0/0/0	0/0/0/0
4	SO4	F	403	-	-	0/0/0/0	0/0/0/0
3	NAD	G	401	-	-	0/22/62/62	0/5/5/5
4	SO4	G	402	-	-	0/0/0/0	0/0/0/0
3	NAD	H	401	-	-	0/22/62/62	0/5/5/5
4	SO4	H	402	-	-	0/0/0/0	0/0/0/0
3	NAD	O	401	-	-	0/22/62/62	0/5/5/5
4	SO4	O	402	-	-	0/0/0/0	0/0/0/0
4	SO4	O	403	-	-	0/0/0/0	0/0/0/0
3	NAD	Q	401	-	-	0/22/62/62	0/5/5/5
4	SO4	Q	402	-	-	0/0/0/0	0/0/0/0
4	SO4	Q	403	-	-	0/0/0/0	0/0/0/0
4	SO4	Q	404	-	-	0/0/0/0	0/0/0/0
4	SO4	Q	405	-	-	0/0/0/0	0/0/0/0

The worst 5 of 67 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	F	401	NAD	C2B-C1B	-2.48	1.49	1.53
3	O	401	NAD	C2A-N1A	2.01	1.37	1.33
3	B	401	NAD	C2A-N3A	2.01	1.35	1.32
3	E	401	NAD	C2A-N1A	2.01	1.37	1.33
3	E	401	NAD	O3D-C3D	2.05	1.47	1.43

The worst 5 of 116 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	401	NAD	C5N-C6N-N1N	-5.38	112.13	120.40
3	D	401	NAD	C5N-C6N-N1N	-5.34	112.19	120.40
3	O	401	NAD	C5N-C6N-N1N	-5.34	112.20	120.40
3	C	401	NAD	C5N-C6N-N1N	-5.25	112.34	120.40
3	B	401	NAD	C5N-C6N-N1N	-5.23	112.37	120.40

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

16 monomers are involved in 45 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	401	NAD	3	0
4	A	406	SO4	1	0
3	B	401	NAD	1	0
4	B	402	SO4	1	0
3	C	401	NAD	2	0
4	C	404	SO4	1	0
3	D	401	NAD	6	0
4	D	402	SO4	1	0
3	E	401	NAD	5	0
4	E	402	SO4	1	0
4	E	403	SO4	1	0
3	F	401	NAD	6	0
3	G	401	NAD	1	0
3	H	401	NAD	13	0
3	Q	401	NAD	1	0
4	Q	404	SO4	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	336/337 (99%)	0.24	4 (1%) 79 80	32, 50, 71, 80	0
1	B	336/337 (99%)	0.46	9 (2%) 55 55	37, 58, 81, 95	0
1	C	336/337 (99%)	0.53	15 (4%) 34 32	39, 57, 76, 95	0
1	D	336/337 (99%)	0.70	22 (6%) 20 17	50, 80, 97, 116	0
1	E	336/337 (99%)	1.73	121 (36%) 0 0	62, 87, 108, 113	0
1	F	336/337 (99%)	1.07	60 (17%) 2 1	46, 83, 102, 118	0
1	G	337/337 (100%)	0.70	23 (6%) 18 16	38, 66, 89, 98	0
1	H	335/337 (99%)	0.88	36 (10%) 7 5	51, 83, 109, 115	0
1	O	337/337 (100%)	0.31	0 100 100	17, 31, 47, 54	0
1	Q	336/337 (99%)	0.19	0 100 100	20, 37, 54, 74	0
2	I	22/82 (26%)	0.96	3 (13%) 3 2	76, 81, 88, 93	0
2	J	21/82 (25%)	0.69	2 (9%) 9 7	66, 75, 86, 91	0
2	K	21/82 (25%)	4.37	21 (100%) 0 0	9, 24, 31, 31	21 (100%)
2	L	19/82 (23%)	4.71	19 (100%) 0 0	38, 51, 70, 76	19 (100%)
2	M	22/82 (26%)	1.30	3 (13%) 3 2	64, 76, 98, 107	0
2	N	19/82 (23%)	2.25	8 (42%) 0 0	67, 81, 85, 86	19 (100%)
All	All	3485/3862 (90%)	0.74	346 (9%) 8 6	9, 64, 99, 118	59 (1%)

The worst 5 of 346 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	25	LEU	9.1
2	L	55	ASP	7.7
1	E	129	VAL	7.6
2	K	58	ASP	6.8
2	L	58	ASP	6.5

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
4	SO4	O	403	5/5	0.88	0.41	15.99	48,48,49,49	5
4	SO4	B	403	5/5	0.80	0.49	10.31	61,62,63,64	5
4	SO4	O	402	5/5	0.92	0.29	6.06	38,38,40,41	5
4	SO4	Q	404	5/5	0.79	0.33	5.15	50,51,52,52	5
4	SO4	Q	403	5/5	0.90	0.25	5.03	50,50,50,52	5
4	SO4	Q	405	5/5	0.86	0.29	4.71	80,81,81,82	5
4	SO4	A	407	5/5	0.91	0.27	3.46	46,47,48,48	5
4	SO4	C	406	5/5	0.89	0.25	2.17	42,43,44,45	5
4	SO4	G	402	5/5	0.80	0.33	1.64	54,54,55,55	5
4	SO4	H	402	5/5	0.90	0.23	1.07	90,91,91,92	0
4	SO4	C	404	5/5	0.91	0.22	0.92	69,69,70,70	5
4	SO4	D	402	5/5	0.80	0.25	0.74	44,45,46,47	5
4	SO4	A	405	5/5	0.96	0.20	0.62	75,75,76,76	0
3	NAD	B	401	44/44	0.96	0.20	0.11	52,57,59,60	0
3	NAD	D	401	44/44	0.91	0.24	0.05	70,76,81,81	0
4	SO4	A	403	5/5	0.95	0.16	0.05	82,82,83,83	0
3	NAD	Q	401	44/44	0.97	0.21	-0.02	32,39,41,44	0
4	SO4	C	405	5/5	0.92	0.21	-0.18	68,69,70,70	5
3	NAD	H	401	44/44	0.87	0.25	-0.25	100,103,104,104	0
3	NAD	G	401	44/44	0.97	0.20	-0.28	40,47,52,54	0
3	NAD	A	401	44/44	0.95	0.18	-0.42	51,54,57,60	0
3	NAD	O	401	44/44	0.98	0.21	-0.46	20,26,30,33	0
4	SO4	F	403	5/5	0.92	0.16	-0.69	78,79,79,80	5
3	NAD	C	401	44/44	0.96	0.18	-0.80	50,55,58,60	0
3	NAD	E	401	44/44	0.92	0.25	-0.87	87,90,92,94	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	NAD	F	401	44/44	0.94	0.20	-0.89	70,73,76,77	0
4	SO4	C	403	5/5	0.98	0.15	-1.50	70,70,71,71	0
4	SO4	A	404	5/5	0.98	0.18	-1.56	58,60,60,61	0
4	SO4	E	403	5/5	0.84	0.20	-1.83	58,58,59,60	5
4	SO4	E	404	5/5	0.91	0.11	-2.73	72,72,73,74	5
4	SO4	A	406	5/5	0.95	0.15	-	63,64,65,65	5
4	SO4	A	408	5/5	0.84	0.24	-	69,70,70,71	5
4	SO4	F	402	5/5	0.94	0.19	-	89,89,90,90	0
4	SO4	Q	402	5/5	0.96	0.20	-	80,80,80,81	0
4	SO4	A	402	5/5	0.98	0.19	-	74,74,75,76	0
4	SO4	E	402	5/5	0.89	0.27	-	79,80,81,81	5
4	SO4	B	402	5/5	0.86	0.23	-	52,52,53,53	5
4	SO4	C	402	5/5	0.95	0.20	-	85,86,87,87	0

6.5 Other polymers [i](#)

There are no such residues in this entry.