



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 12:53 AM GMT

PDB ID : 2C2B
Title : Crystallographic structure of Arabidopsis thaliana Threonine synthase complexed with pyridoxal phosphate and S-adenosylmethionine
Authors : Mas-Droux, C.; Biou, V.; Dumas, R.
Deposited on : 2005-09-27
Resolution : 2.60 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

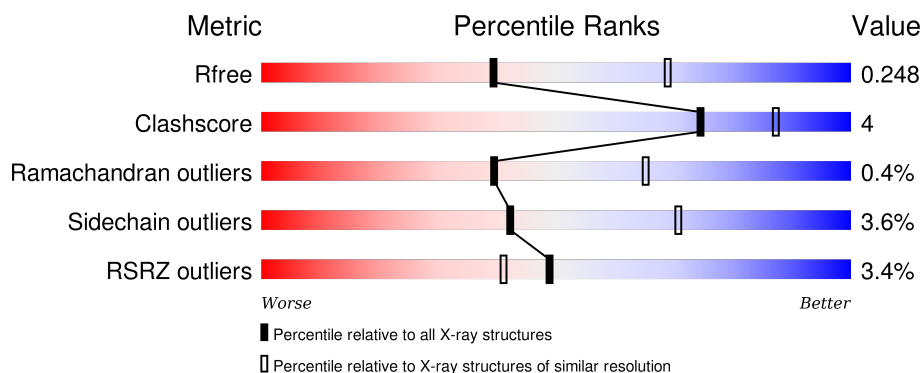
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	2328 (2.60-2.60)
Clashscore	102246	2679 (2.60-2.60)
Ramachandran outliers	100387	2635 (2.60-2.60)
Sidechain outliers	100360	2635 (2.60-2.60)
RSRZ outliers	91569	2334 (2.60-2.60)

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	486	<div> <div>4%</div> <div>81% 9% 8%</div> </div>
1	B	486	<div> <div>3%</div> <div>81% 7% 12%</div> </div>
1	C	486	<div> <div>3%</div> <div>79% 11% 9%</div> </div>
1	D	486	<div> <div>3%</div> <div>79% 9% 12%</div> </div>
1	E	486	<div> <div>3%</div> <div>78% 10% 11%</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	486	 2% 77% 13% 8%

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	PLP	B	1163	-	-	-	X
4	PLP	E	1163	-	-	-	X

2 Entry composition [i](#)

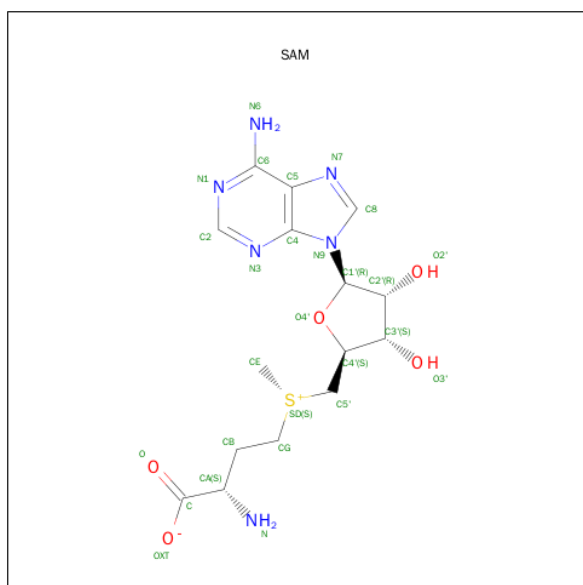
There are 5 unique types of molecules in this entry. The entry contains 20958 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 THREONINE SYNTHASE 1, CHLOROPLASTIC.

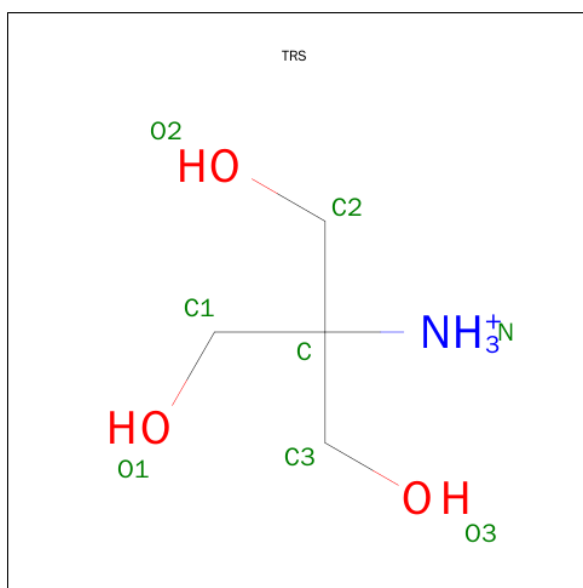
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	445	Total	C	N	O	S	0	0	1
			3428	2189	576	640	23			
1	B	429	Total	C	N	O	S	0	0	1
			3305	2108	558	617	22			
1	C	444	Total	C	N	O	S	0	0	1
			3421	2184	575	639	23			
1	D	429	Total	C	N	O	S	0	0	1
			3305	2108	558	617	22			
1	E	431	Total	C	N	O	S	0	0	1
			3320	2116	561	621	22			
1	F	445	Total	C	N	O	S	0	0	1
			3428	2189	576	640	23			

- Molecule 2 is S-ADENOSYLMETHIONINE (three-letter code: SAM) (formula: $C_{15}H_{22}N_6O_5S$).



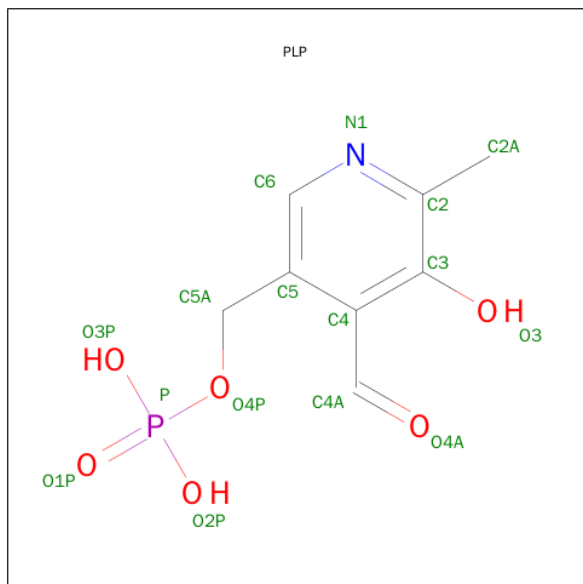
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			27	15	6	5	1		
2	A	1	Total	C	N	O	S	0	0
			27	15	6	5	1		
2	B	1	Total	C	N	O	S	0	0
			27	15	6	5	1		
2	B	1	Total	C	N	O	S	0	0
			27	15	6	5	1		
2	C	1	Total	C	N	O	S	0	0
			27	15	6	5	1		
2	C	1	Total	C	N	O	S	0	0
			27	15	6	5	1		
2	D	1	Total	C	N	O	S	0	0
			27	15	6	5	1		
2	D	1	Total	C	N	O	S	0	0
			27	15	6	5	1		
2	E	1	Total	C	N	O	S	0	0
			27	15	6	5	1		
2	E	1	Total	C	N	O	S	0	0
			27	15	6	5	1		
2	F	1	Total	C	N	O	S	0	0
			27	15	6	5	1		
2	F	1	Total	C	N	O	S	0	0
			27	15	6	5	1		

- Molecule 3 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (three-letter code: TRS) (formula: $C_4H_{12}NO_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			8	4	1	3		
3	C	1	Total	C	N	O	0	0
			8	4	1	3		
3	F	1	Total	C	N	O	0	0
			8	4	1	3		

- Molecule 4 is PYRIDOXAL-5'-PHOSPHATE (three-letter code: PLP) (formula: C₈H₁₀NO₆P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
4	B	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
4	C	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
4	D	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
4	E	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
4	F	1	Total	C	N	O	P	0	0
			15	8	1	5	1		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	51	Total	O	0	0
			51	51		

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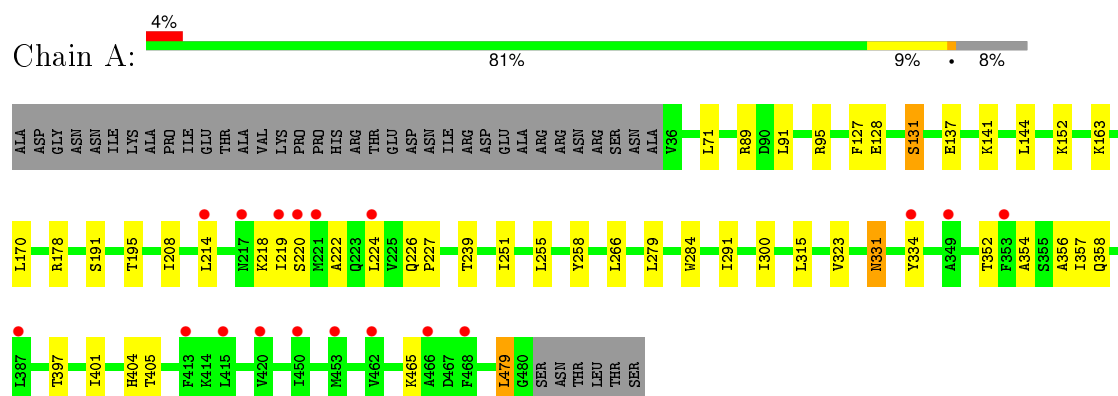
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	55	Total 55	O 55	0	0
5	C	52	Total 52	O 52	0	0
5	D	55	Total 55	O 55	0	0
5	E	44	Total 44	O 44	0	0
5	F	56	Total 56	O 56	0	0

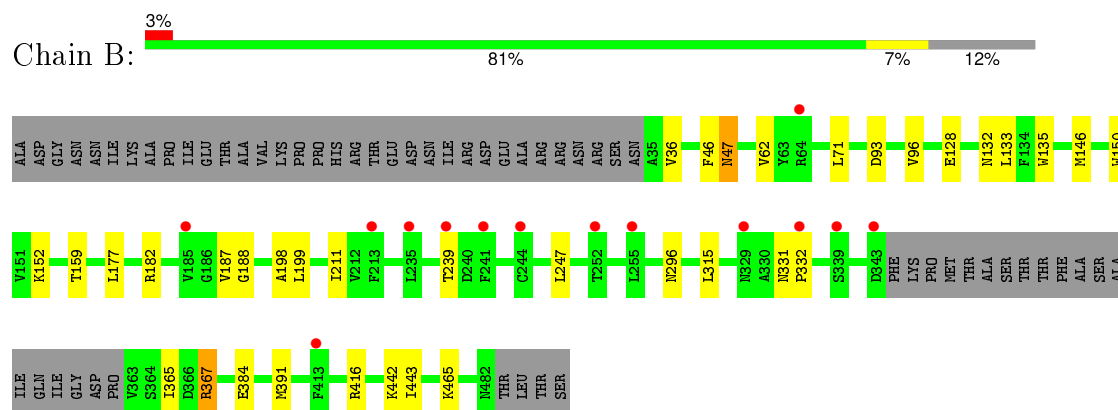
3 Residue-property plots

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.

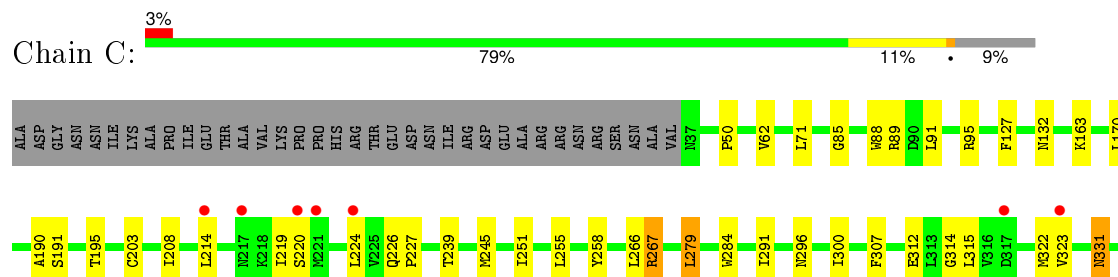
• Molecule 1: THREONINE SYNTHASE 1, CHLOROPLASTIC

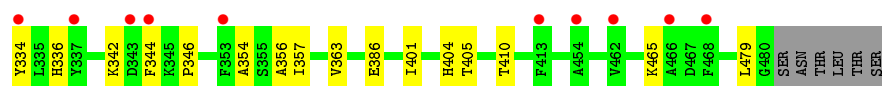


• Molecule 1: THREONINE SYNTHASE 1, CHLOROPLASTIC

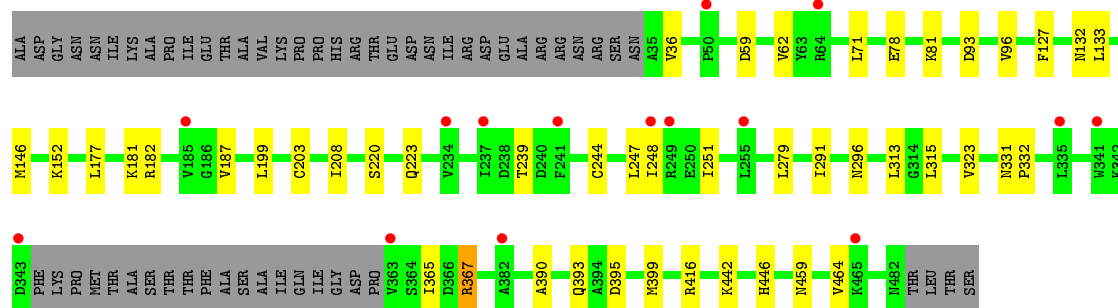
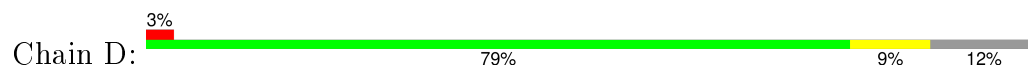


• Molecule 1: THREONINE SYNTHASE 1, CHLOROPLASTIC

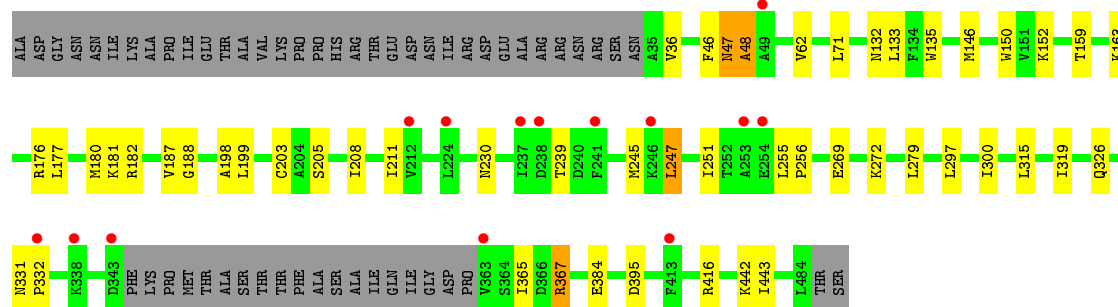
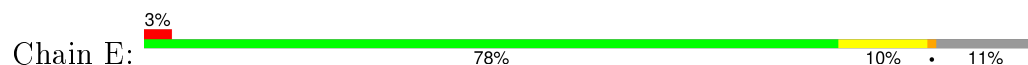




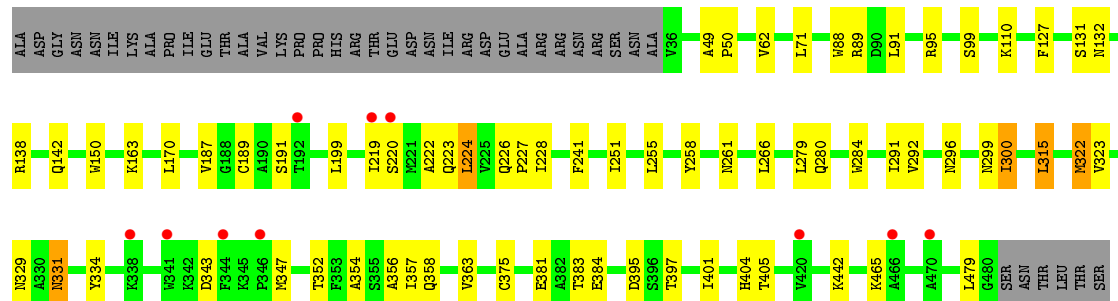
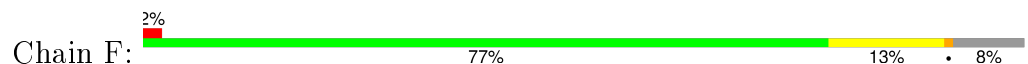
• Molecule 1: THREONINE SYNTHASE 1, CHLOROPLASTIC



• Molecule 1: THREONINE SYNTHASE 1, CHLOROPLASTIC



• Molecule 1: THREONINE SYNTHASE 1, CHLOROPLASTIC



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	191.92Å 110.85Å 152.78Å 90.00° 89.98° 90.00°	Depositor
Resolution (Å)	29.89 – 2.60 29.89 – 2.60	Depositor EDS
% Data completeness (in resolution range)	100.0 (29.89-2.60) 99.6 (29.89-2.60)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.73 (at 2.61Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.206 , 0.248 0.206 , 0.248	Depositor DCC
R_{free} test set	4904 reflections (5.26%)	DCC
Wilson B-factor (Å ²)	53.8	Xtriage
Anisotropy	0.086	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 53.2	EDS
Estimated twinning fraction	0.027 for -1/2*h+3/2*k,1/2*h+1/2*k,-l 0.027 for -1/2*h-3/2*k,-1/2*h+1/2*k,-l 0.459 for 1/2*h+3/2*k,1/2*h-1/2*k,-l 0.467 for 1/2*h-3/2*k,-1/2*h-1/2*k,-l 0.027 for -h,-k,l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 98158 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	20958	wwPDB-VP
Average B, all atoms (Å ²)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.18% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: TRS, SAM, PLP

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	0.34	1/3509 (0.0%)	0.48	0/4763
1	B	0.34	0/3381	0.47	0/4586
1	C	0.35	1/3502 (0.0%)	0.47	0/4753
1	D	0.34	0/3381	0.47	0/4586
1	E	0.34	0/3396	0.48	0/4607
1	F	0.34	1/3509 (0.0%)	0.48	0/4763
All	All	0.34	3/20678 (0.0%)	0.47	0/28058

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	479	LEU	C-N	-5.26	1.23	1.33
1	A	479	LEU	C-N	-5.24	1.23	1.33
1	C	479	LEU	C-N	-5.16	1.23	1.33

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	3428	0	3382	23	0
1	B	3305	0	3257	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	3421	0	3373	27	0
1	D	3305	0	3257	26	0
1	E	3320	0	3270	32	0
1	F	3428	0	3382	38	0
2	A	54	0	44	1	0
2	B	54	0	44	0	0
2	C	54	0	44	2	0
2	D	54	0	44	1	0
2	E	54	0	44	5	0
2	F	54	0	44	7	0
3	A	8	0	12	0	0
3	C	8	0	12	0	0
3	F	8	0	12	0	0
4	A	15	0	6	1	0
4	B	15	0	6	0	0
4	C	15	0	6	1	0
4	D	15	0	6	0	0
4	E	15	0	6	1	0
4	F	15	0	6	1	0
5	A	51	0	0	0	0
5	B	55	0	0	1	0
5	C	52	0	0	0	0
5	D	55	0	0	1	0
5	E	44	0	0	0	0
5	F	56	0	0	0	0
All	All	20958	0	20257	164	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 4.

All (164) 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:B:367:ARG:HH11	1:B:367:ARG:HG2	1.05	1.16
1:E:367:ARG:HH11	1:E:367:ARG:HG2	1.08	1.09
1:C:291:ILE:HG13	1:C:323:VAL:HB	1.57	0.85
1:B:367:ARG:HG2	1:B:367:ARG:NH1	1.85	0.84
1:E:367:ARG:HG2	1:E:367:ARG:NH1	1.88	0.83
2:F:500:SAM:H5'2	2:F:501:SAM:H2	1.61	0.82
1:E:150:TRP:CH2	2:F:500:SAM:HG2	2.14	0.81
1:B:367:ARG:HH11	1:B:367:ARG:CG	1.94	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:500:SAM:HG2	1:F:150:TRP:CH2	2.21	0.75
1:F:251:ILE:HG23	1:F:255:LEU:HD12	1.68	0.74
1:E:367:ARG:HH11	1:E:367:ARG:CG	1.96	0.73
1:F:219:ILE:HD11	1:F:223:GLN:HB2	1.70	0.72
1:B:46:PHE:O	1:B:47:ASN:HB2	1.90	0.72
1:F:331:ASN:HD22	1:F:331:ASN:H	1.38	0.72
1:C:331:ASN:H	1:C:331:ASN:HD22	1.37	0.72
1:C:195:THR:HG23	1:C:267:ARG:HH21	1.54	0.71
1:E:331:ASN:HB2	1:E:332:PRO:CD	2.20	0.71
1:D:331:ASN:HB2	1:D:332:PRO:CD	2.22	0.70
1:F:291:ILE:HG13	1:F:323:VAL:HB	1.73	0.70
1:A:331:ASN:H	1:A:331:ASN:HD22	1.38	0.70
1:C:251:ILE:HG23	1:C:255:LEU:HD12	1.75	0.68
1:D:446:HIS:HD2	1:D:459:ASN:H	1.38	0.68
1:D:367:ARG:HG2	1:D:367:ARG:HH11	1.57	0.68
1:E:46:PHE:O	1:E:47:ASN:HB2	1.92	0.68
1:A:251:ILE:HG23	1:A:255:LEU:HD12	1.75	0.68
1:A:131:SER:HB3	1:A:152:LYS:HE2	1.78	0.66
1:B:331:ASN:HB2	1:B:332:PRO:CD	2.25	0.66
1:A:291:ILE:HG13	1:A:323:VAL:HB	1.78	0.66
1:E:331:ASN:HB2	1:E:332:PRO:HD2	1.78	0.66
1:D:331:ASN:HB2	1:D:332:PRO:HD2	1.79	0.63
1:A:170:LEU:HD11	1:A:258:TYR:CE2	2.34	0.62
1:C:170:LEU:HD11	1:C:258:TYR:CE2	2.35	0.61
1:D:367:ARG:NH1	1:D:367:ARG:HG2	2.13	0.61
1:F:99:SER:HB2	2:F:500:SAM:HE3	1.82	0.61
1:B:331:ASN:HB2	1:B:332:PRO:HD2	1.86	0.58
1:E:443:ILE:HD11	1:F:222:ALA:HA	1.84	0.58
2:C:500:SAM:H8	1:D:132:ASN:HD21	1.71	0.56
1:C:386:GLU:HB3	1:C:410:THR:HG21	1.89	0.55
1:E:187:VAL:HG11	1:E:199:LEU:HD11	1.88	0.55
1:E:133:LEU:HD13	1:E:152:LYS:HD3	1.88	0.55
1:C:296:ASN:O	1:C:363:VAL:O	2.24	0.55
2:E:500:SAM:HG2	1:F:150:TRP:HH2	1.71	0.55
1:D:187:VAL:HG11	1:D:199:LEU:HD11	1.89	0.54
1:B:177:LEU:O	1:B:182:ARG:HB2	2.07	0.54
1:F:226:GLN:HB2	1:F:227:PRO:HD3	1.91	0.53
1:F:110:LYS:NZ	1:F:280:GLN:OE1	2.42	0.53
1:D:367:ARG:CG	1:D:367:ARG:HH11	2.21	0.53
2:E:500:SAM:H5'2	2:E:501:SAM:H2	1.92	0.52
1:F:356:ALA:H	1:F:404:HIS:HE1	1.58	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:187:VAL:HG11	1:B:199:LEU:HD11	1.92	0.52
1:E:135:TRP:CH2	2:F:501:SAM:HG2	2.45	0.51
1:E:163:LYS:NZ	4:E:1163:PLP:O3	2.44	0.51
1:F:296:ASN:O	1:F:363:VAL:O	2.29	0.50
1:D:446:HIS:CD2	1:D:459:ASN:H	2.25	0.50
1:B:133:LEU:HD13	1:B:152:LYS:HD3	1.93	0.50
1:E:150:TRP:HH2	2:F:500:SAM:HG2	1.73	0.50
1:F:354:ALA:O	1:F:357:ILE:HG22	2.11	0.49
1:A:163:LYS:NZ	4:A:1163:PLP:O3	2.44	0.49
1:A:214:LEU:HD22	1:A:219:ILE:HD11	1.94	0.49
1:C:356:ALA:H	1:C:404:HIS:HE1	1.60	0.49
1:A:397:THR:HG22	1:A:397:THR:O	2.13	0.49
1:E:132:ASN:ND2	2:F:500:SAM:H1'	2.27	0.49
1:A:356:ALA:H	1:A:404:HIS:HE1	1.60	0.49
1:D:244:CYS:O	1:D:248:ILE:HG12	2.13	0.49
1:F:49:ALA:HB1	1:F:50:PRO:HD2	1.96	0.48
1:D:177:LEU:O	1:D:182:ARG:HB2	2.14	0.48
1:C:163:LYS:NZ	4:C:1163:PLP:O3	2.45	0.48
1:C:336:HIS:CD2	1:C:344:PHE:HB3	2.49	0.48
1:F:91:LEU:O	1:F:95:ARG:HG3	2.14	0.48
1:C:354:ALA:O	1:C:357:ILE:HG22	2.14	0.48
1:C:85:GLY:HA2	1:C:315:LEU:HD23	1.96	0.48
1:F:88:TRP:CB	1:F:315:LEU:HD11	2.44	0.48
1:C:88:TRP:HB2	1:C:315:LEU:CD2	2.44	0.48
1:F:331:ASN:HB2	1:F:334:TYR:HB3	1.95	0.47
1:C:88:TRP:HB2	1:C:315:LEU:HD21	1.97	0.47
1:C:190:ALA:HB3	1:C:245:MET:HE2	1.97	0.47
1:B:159:THR:HG21	1:B:198:ALA:HA	1.97	0.47
1:E:395:ASP:OD2	1:E:442:LYS:NZ	2.46	0.47
1:C:331:ASN:HB2	1:C:334:TYR:HB3	1.96	0.47
1:A:222:ALA:HA	1:B:443:ILE:HD11	1.97	0.47
1:E:205:SER:HA	1:F:397:THR:O	2.15	0.46
2:A:500:SAM:H8	1:B:132:ASN:HD21	1.80	0.46
1:F:163:LYS:NZ	4:F:1163:PLP:O3	2.48	0.46
1:B:46:PHE:O	1:B:47:ASN:CB	2.62	0.46
1:F:170:LEU:HD11	1:F:258:TYR:CE2	2.51	0.46
1:C:91:LEU:O	1:C:95:ARG:HG3	2.15	0.46
1:A:331:ASN:HB2	1:A:334:TYR:HB3	1.97	0.46
1:E:247:LEU:O	1:E:251:ILE:HD12	2.15	0.45
1:E:132:ASN:HD21	2:F:500:SAM:H8	1.82	0.45
1:F:187:VAL:HG11	1:F:199:LEU:HD11	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:220:SER:HB3	1:D:223:GLN:HB2	1.98	0.45
1:F:138:ARG:O	1:F:142:GLN:HB2	2.17	0.45
1:F:401:ILE:HD13	1:F:405:THR:HB	1.99	0.45
1:D:247:LEU:O	1:D:251:ILE:HG12	2.17	0.45
1:C:132:ASN:HD21	2:D:500:SAM:H8	1.82	0.45
1:E:230:ASN:HA	1:F:395:ASP:O	2.16	0.45
1:A:226:GLN:HB2	1:A:227:PRO:HD3	1.98	0.45
1:A:352:THR:HG22	1:A:354:ALA:H	1.81	0.45
1:A:91:LEU:O	1:A:95:ARG:HG3	2.17	0.44
1:A:358:GLN:O	1:A:358:GLN:HG3	2.17	0.44
1:A:397:THR:CG2	1:A:397:THR:O	2.66	0.44
1:F:88:TRP:HB2	1:F:315:LEU:HD11	2.00	0.44
1:C:214:LEU:HD22	1:C:219:ILE:HD11	2.00	0.44
1:C:50:PRO:HG3	1:E:319:ILE:O	2.18	0.44
1:F:352:THR:HG22	1:F:354:ALA:H	1.82	0.44
1:E:188:GLY:HA2	1:E:211:ILE:O	2.18	0.44
1:F:322:MET:HB2	1:F:375:CYS:SG	2.58	0.44
1:E:177:LEU:O	1:E:182:ARG:HB2	2.17	0.44
1:D:395:ASP:OD2	1:D:442:LYS:NZ	2.49	0.43
1:E:297:LEU:HD21	1:E:326:GLN:NE2	2.33	0.43
1:A:137:GLU:HG3	1:A:141:LYS:HE2	1.99	0.43
1:E:269:GLU:O	1:E:272:LYS:HG2	2.18	0.43
1:D:203:CYS:HB3	1:D:208:ILE:O	2.18	0.43
1:B:391:MET:SD	1:B:442:LYS:NZ	2.86	0.43
1:D:291:ILE:HG12	1:D:323:VAL:HB	2.01	0.43
1:A:191:SER:HB3	1:A:195:THR:HB	2.00	0.43
1:E:159:THR:HG21	1:E:198:ALA:HA	2.00	0.43
1:F:261:ASN:HD22	1:F:261:ASN:HA	1.65	0.43
1:B:93:ASP:O	1:B:96:VAL:HG12	2.18	0.43
1:D:93:ASP:O	1:D:96:VAL:HG12	2.19	0.43
1:C:401:ILE:HD13	1:C:405:THR:HB	2.01	0.43
2:E:500:SAM:H8	1:F:132:ASN:HD21	1.84	0.42
2:E:500:SAM:HN1	2:E:501:SAM:H5'1	1.83	0.42
1:A:128:GLU:CD	1:A:128:GLU:H	2.23	0.42
1:B:296:ASN:ND2	5:B:2035:HOH:O	2.51	0.42
1:D:296:ASN:ND2	5:D:2038:HOH:O	2.52	0.42
1:C:85:GLY:HA3	1:C:314:GLY:O	2.19	0.42
1:D:395:ASP:HA	1:D:399:MET:O	2.19	0.42
1:F:191:SER:HA	1:F:241:PHE:HE1	1.85	0.42
1:F:138:ARG:HB3	1:F:397:THR:HG23	2.01	0.42
1:F:358:GLN:O	1:F:358:GLN:HG3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:292:VAL:HB	1:F:300:ILE:HG12	2.01	0.42
1:E:255:LEU:HA	1:E:256:PRO:HD3	1.93	0.42
1:D:390:ALA:HA	1:D:393:GLN:HE21	1.85	0.42
1:F:331:ASN:N	1:F:331:ASN:HD22	2.08	0.41
1:E:176:ARG:O	1:E:180:MET:HG2	2.19	0.41
1:B:146:MET:SD	1:B:416:ARG:HD2	2.60	0.41
1:A:89:ARG:HD2	1:A:284:TRP:CD1	2.55	0.41
1:C:279:LEU:HD13	1:C:307:PHE:HE1	1.85	0.41
1:E:146:MET:SD	1:E:416:ARG:HD2	2.60	0.41
1:C:191:SER:HB3	1:C:195:THR:HB	2.02	0.41
1:D:59:ASP:HA	1:D:177:LEU:HD21	2.01	0.41
2:C:500:SAM:H8	1:D:132:ASN:ND2	2.35	0.41
1:D:81:LYS:HG3	1:D:313:LEU:HD23	2.01	0.41
1:E:47:ASN:HB3	1:E:48:ALA:H	1.58	0.41
1:B:135:TRP:HB2	1:B:150:TRP:CZ3	2.56	0.41
1:D:446:HIS:HD2	1:D:459:ASN:N	2.12	0.41
1:A:354:ALA:O	1:A:357:ILE:HG22	2.20	0.41
1:C:226:GLN:HB2	1:C:227:PRO:HD3	2.03	0.41
1:D:133:LEU:HD13	1:D:152:LYS:HD3	2.03	0.41
1:A:401:ILE:HD13	1:A:405:THR:HB	2.03	0.41
1:E:203:CYS:HB3	1:E:208:ILE:O	2.20	0.41
1:B:128:GLU:CD	1:B:128:GLU:H	2.24	0.41
1:F:89:ARG:HD2	1:F:284:TRP:CD1	2.56	0.41
1:C:203:CYS:HB3	1:C:208:ILE:O	2.21	0.41
1:F:329:ASN:HD21	1:F:384:GLU:HG3	1.86	0.41
1:E:135:TRP:HB2	1:E:150:TRP:CZ3	2.55	0.40
1:F:395:ASP:OD2	1:F:442:LYS:NZ	2.53	0.40
1:C:89:ARG:HD2	1:C:284:TRP:CD1	2.55	0.40
1:D:146:MET:SD	1:D:416:ARG:HD2	2.61	0.40
1:E:46:PHE:O	1:E:47:ASN:CB	2.67	0.40
1:F:224:LEU:O	1:F:228:ILE:HG12	2.21	0.40
1:A:178:ARG:HH11	1:A:208:ILE:HG12	1.86	0.40
1:B:188:GLY:HA2	1:B:211:ILE:O	2.22	0.40

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	443/486 (91%)	424 (96%)	18 (4%)	1 (0%)	52	77
1	B	425/486 (87%)	406 (96%)	17 (4%)	2 (0%)	34	60
1	C	442/486 (91%)	422 (96%)	18 (4%)	2 (0%)	34	60
1	D	425/486 (87%)	399 (94%)	25 (6%)	1 (0%)	52	77
1	E	427/486 (88%)	400 (94%)	24 (6%)	3 (1%)	26	51
1	F	443/486 (91%)	420 (95%)	21 (5%)	2 (0%)	34	60
All	All	2605/2916 (89%)	2471 (95%)	123 (5%)	11 (0%)	39	65

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	47	ASN
1	E	47	ASN
1	A	220	SER
1	C	220	SER
1	F	220	SER
1	E	48	ALA
1	B	36	VAL
1	C	346	PRO
1	E	36	VAL
1	F	343	ASP
1	D	36	VAL

5.3.2 Protein sidechains [i](#)

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	368/403 (91%)	354 (96%)	14 (4%)	40	68
1	B	354/403 (88%)	345 (98%)	9 (2%)	55	81
1	C	367/403 (91%)	353 (96%)	14 (4%)	40	68
1	D	354/403 (88%)	343 (97%)	11 (3%)	47	76
1	E	356/403 (88%)	344 (97%)	12 (3%)	44	72
1	F	368/403 (91%)	351 (95%)	17 (5%)	33	61
All	All	2167/2418 (90%)	2090 (96%)	77 (4%)	42	71

All (77) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	71	LEU
1	A	127	PHE
1	A	131	SER
1	A	144	LEU
1	A	218	LYS
1	A	224	LEU
1	A	239	THR
1	A	266	LEU
1	A	279	LEU
1	A	300	ILE
1	A	315	LEU
1	A	331	ASN
1	A	465	LYS
1	A	479	LEU
1	B	62	VAL
1	B	71	LEU
1	B	239	THR
1	B	247	LEU
1	B	315	LEU
1	B	365	ILE
1	B	367	ARG
1	B	384	GLU
1	B	465	LYS
1	C	62	VAL
1	C	71	LEU
1	C	127	PHE
1	C	224	LEU
1	C	239	THR
1	C	266	LEU
1	C	267	ARG

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Mol	Chain	Res	Type
1	C	279	LEU
1	C	300	ILE
1	C	312	GLU
1	C	322	MET
1	C	331	ASN
1	C	342	LYS
1	C	465	LYS
1	D	62	VAL
1	D	71	LEU
1	D	78	GLU
1	D	127	PHE
1	D	181	LYS
1	D	239	THR
1	D	279	LEU
1	D	315	LEU
1	D	365	ILE
1	D	367	ARG
1	D	464	VAL
1	E	62	VAL
1	E	71	LEU
1	E	181	LYS
1	E	239	THR
1	E	245	MET
1	E	247	LEU
1	E	279	LEU
1	E	300	ILE
1	E	315	LEU
1	E	365	ILE
1	E	367	ARG
1	E	384	GLU
1	F	62	VAL
1	F	71	LEU
1	F	127	PHE
1	F	131	SER
1	F	189	CYS
1	F	224	LEU
1	F	266	LEU
1	F	279	LEU
1	F	299	ASN
1	F	300	ILE
1	F	315	LEU
1	F	322	MET

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Mol	Chain	Res	Type
1	F	331	ASN
1	F	347	MET
1	F	381	GLU
1	F	383	THR
1	F	465	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (46) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	132	ASN
1	A	226	GLN
1	A	230	ASN
1	A	261	ASN
1	A	280	GLN
1	A	299	ASN
1	A	326	GLN
1	A	331	ASN
1	A	404	HIS
1	B	47	ASN
1	B	132	ASN
1	B	230	ASN
1	B	336	HIS
1	B	393	GLN
1	C	132	ASN
1	C	226	GLN
1	C	230	ASN
1	C	261	ASN
1	C	280	GLN
1	C	299	ASN
1	C	326	GLN
1	C	331	ASN
1	C	358	GLN
1	C	404	HIS
1	D	132	ASN
1	D	226	GLN
1	D	230	ASN
1	D	326	GLN
1	D	336	HIS
1	D	393	GLN
1	D	404	HIS
1	D	434	HIS
1	D	446	HIS

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Mol	Chain	Res	Type
1	D	448	ASN
1	E	132	ASN
1	E	226	GLN
1	E	329	ASN
1	E	336	HIS
1	F	132	ASN
1	F	230	ASN
1	F	261	ASN
1	F	299	ASN
1	F	326	GLN
1	F	329	ASN
1	F	331	ASN
1	F	404	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](#)

21 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	$\# Z > 2$
4	PLP	A	1163	1	15,15,16	1.83	1 (6%)	21,22,23	1.75	3 (14%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	SAM	A	500	-	21,29,29	1.14	2 (9%)	17,42,42	3.13	3 (17%)
2	SAM	A	501	-	21,29,29	1.13	2 (9%)	17,42,42	2.97	2 (11%)
3	TRS	A	800	-	7,7,7	0.93	1 (14%)	9,9,9	0.27	0
4	PLP	B	1163	1	15,15,16	1.85	3 (20%)	21,22,23	1.61	2 (9%)
2	SAM	B	500	-	21,29,29	1.13	2 (9%)	17,42,42	3.11	2 (11%)
2	SAM	B	501	-	21,29,29	1.15	2 (9%)	17,42,42	2.95	1 (5%)
4	PLP	C	1163	1	15,15,16	1.82	2 (13%)	21,22,23	1.86	2 (9%)
2	SAM	C	500	-	21,29,29	1.14	2 (9%)	17,42,42	3.13	3 (17%)
2	SAM	C	501	-	21,29,29	1.14	2 (9%)	17,42,42	2.88	2 (11%)
3	TRS	C	800	-	7,7,7	0.91	1 (14%)	9,9,9	0.47	0
4	PLP	D	1163	1	15,15,16	1.84	3 (20%)	21,22,23	1.70	2 (9%)
2	SAM	D	500	-	21,29,29	1.15	2 (9%)	17,42,42	3.19	2 (11%)
2	SAM	D	501	-	21,29,29	1.16	2 (9%)	17,42,42	2.92	1 (5%)
4	PLP	E	1163	1	15,15,16	1.84	3 (20%)	21,22,23	1.82	3 (14%)
2	SAM	E	500	-	21,29,29	1.12	2 (9%)	17,42,42	3.21	3 (17%)
2	SAM	E	501	-	21,29,29	1.15	2 (9%)	17,42,42	2.95	2 (11%)
4	PLP	F	1163	1	15,15,16	1.80	1 (6%)	21,22,23	1.86	4 (19%)
2	SAM	F	500	-	21,29,29	1.13	2 (9%)	17,42,42	3.11	3 (17%)
2	SAM	F	501	-	21,29,29	1.12	2 (9%)	17,42,42	2.89	1 (5%)
3	TRS	F	800	-	7,7,7	0.88	1 (14%)	9,9,9	0.45	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
4	PLP	A	1163	1	-	0/6/6/8	0/1/1/1
2	SAM	A	500	-	-	0/8/33/33	0/3/3/3
2	SAM	A	501	-	-	0/8/33/33	0/3/3/3
3	TRS	A	800	-	-	0/9/9/9	0/0/0/0
4	PLP	B	1163	1	-	0/6/6/8	0/1/1/1
2	SAM	B	500	-	-	0/8/33/33	0/3/3/3
2	SAM	B	501	-	-	0/8/33/33	0/3/3/3
4	PLP	C	1163	1	-	0/6/6/8	0/1/1/1
2	SAM	C	500	-	-	0/8/33/33	0/3/3/3
2	SAM	C	501	-	-	0/8/33/33	0/3/3/3
3	TRS	C	800	-	-	0/9/9/9	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	PLP	D	1163	1	-	0/6/6/8	0/1/1/1
2	SAM	D	500	-	-	0/8/33/33	0/3/3/3
2	SAM	D	501	-	-	0/8/33/33	0/3/3/3
4	PLP	E	1163	1	-	0/6/6/8	0/1/1/1
2	SAM	E	500	-	-	0/8/33/33	0/3/3/3
2	SAM	E	501	-	-	0/8/33/33	0/3/3/3
4	PLP	F	1163	1	-	0/6/6/8	0/1/1/1
2	SAM	F	500	-	-	0/8/33/33	0/3/3/3
2	SAM	F	501	-	-	0/8/33/33	0/3/3/3
3	TRS	F	800	-	-	0/9/9/9	0/0/0/0

All (40) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1163	PLP	O3-C3	-5.76	1.23	1.37
4	E	1163	PLP	O3-C3	-5.73	1.23	1.37
4	C	1163	PLP	O3-C3	-5.71	1.23	1.37
4	B	1163	PLP	O3-C3	-5.70	1.23	1.37
4	D	1163	PLP	O3-C3	-5.67	1.23	1.37
4	F	1163	PLP	O3-C3	-5.62	1.23	1.37
3	A	800	TRS	C-N	-2.38	1.47	1.50
3	C	800	TRS	C-N	-2.33	1.47	1.50
3	F	800	TRS	C-N	-2.24	1.47	1.50
4	E	1163	PLP	C6-N1	2.01	1.38	1.34
4	B	1163	PLP	C6-N1	2.02	1.38	1.34
4	C	1163	PLP	C2-N1	2.02	1.38	1.34
4	D	1163	PLP	C6-N1	2.06	1.38	1.34
4	B	1163	PLP	C2-N1	2.15	1.38	1.34
4	E	1163	PLP	C2-N1	2.17	1.38	1.34
4	D	1163	PLP	C2-N1	2.20	1.38	1.34
2	D	500	SAM	C2-N1	2.37	1.38	1.33
2	F	500	SAM	C2-N1	2.43	1.38	1.33
2	E	500	SAM	C2-N1	2.44	1.38	1.33
2	C	500	SAM	C2-N1	2.45	1.38	1.33
2	A	500	SAM	C2-N1	2.45	1.38	1.33
2	B	500	SAM	C2-N1	2.48	1.38	1.33
2	F	501	SAM	C2-N1	2.50	1.38	1.33
2	B	501	SAM	C2-N1	2.58	1.38	1.33
2	D	501	SAM	C2-N1	2.62	1.38	1.33
2	A	501	SAM	C2-N1	2.63	1.38	1.33
2	E	501	SAM	C2-N1	2.64	1.38	1.33
2	C	501	SAM	C2-N1	2.70	1.39	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	501	SAM	C2-N3	3.59	1.38	1.32
2	E	500	SAM	C2-N3	3.59	1.38	1.32
2	C	501	SAM	C2-N3	3.64	1.38	1.32
2	A	501	SAM	C2-N3	3.64	1.38	1.32
2	B	500	SAM	C2-N3	3.71	1.38	1.32
2	E	501	SAM	C2-N3	3.72	1.38	1.32
2	F	500	SAM	C2-N3	3.76	1.38	1.32
2	D	500	SAM	C2-N3	3.76	1.38	1.32
2	D	501	SAM	C2-N3	3.76	1.38	1.32
2	B	501	SAM	C2-N3	3.77	1.38	1.32
2	C	500	SAM	C2-N3	3.85	1.39	1.32
2	A	500	SAM	C2-N3	3.86	1.39	1.32

All (41) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	500	SAM	N3-C2-N1	-12.21	119.54	128.89
2	E	500	SAM	N3-C2-N1	-12.21	119.54	128.89
2	F	500	SAM	N3-C2-N1	-12.04	119.67	128.89
2	C	500	SAM	N3-C2-N1	-11.96	119.74	128.89
2	B	500	SAM	N3-C2-N1	-11.89	119.79	128.89
2	A	500	SAM	N3-C2-N1	-11.86	119.81	128.89
2	A	501	SAM	N3-C2-N1	-11.62	120.00	128.89
2	E	501	SAM	N3-C2-N1	-11.58	120.03	128.89
2	B	501	SAM	N3-C2-N1	-11.52	120.08	128.89
2	D	501	SAM	N3-C2-N1	-11.50	120.09	128.89
2	F	501	SAM	N3-C2-N1	-11.36	120.19	128.89
2	C	501	SAM	N3-C2-N1	-11.29	120.25	128.89
2	A	500	SAM	C2'-C1'-N9	-4.07	108.08	114.29
2	D	500	SAM	C2'-C1'-N9	-3.90	108.34	114.29
2	B	500	SAM	C2'-C1'-N9	-3.72	108.61	114.29
2	C	500	SAM	C2'-C1'-N9	-3.65	108.71	114.29
2	E	500	SAM	C2'-C1'-N9	-3.34	109.19	114.29
4	E	1163	PLP	C4A-C4-C5	-2.74	118.03	120.88
2	F	500	SAM	C2'-C1'-N9	-2.71	110.14	114.29
4	B	1163	PLP	C5-C6-N1	-2.28	119.90	123.86
2	A	501	SAM	C2'-C1'-N9	-2.27	110.83	114.29
4	D	1163	PLP	C5-C6-N1	-2.23	119.99	123.86
4	F	1163	PLP	C4A-C4-C5	-2.18	118.61	120.88
4	F	1163	PLP	C5-C6-N1	-2.18	120.08	123.86
2	C	501	SAM	C2'-C1'-N9	-2.13	111.03	114.29
4	E	1163	PLP	C5-C6-N1	-2.10	120.21	123.86

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1163	PLP	C5-C6-N1	-2.09	120.23	123.86
2	F	500	SAM	C4-C5-N7	-2.02	107.62	109.48
2	E	501	SAM	C4'-O4'-C1'	2.03	111.95	109.72
4	C	1163	PLP	C6-C5-C4	2.07	119.90	118.15
2	E	500	SAM	O4'-C1'-N9	2.17	112.64	108.10
2	A	500	SAM	O4'-C1'-N9	2.21	112.72	108.10
2	C	500	SAM	O4'-C1'-N9	2.22	112.75	108.10
4	A	1163	PLP	C6-C5-C4	2.34	120.13	118.15
4	F	1163	PLP	C6-C5-C4	2.55	120.31	118.15
4	B	1163	PLP	O4P-C5A-C5	5.27	117.70	108.99
4	D	1163	PLP	O4P-C5A-C5	5.58	118.22	108.99
4	E	1163	PLP	O4P-C5A-C5	6.12	119.10	108.99
4	A	1163	PLP	O4P-C5A-C5	6.19	119.23	108.99
4	F	1163	PLP	O4P-C5A-C5	6.41	119.59	108.99
4	C	1163	PLP	O4P-C5A-C5	7.00	120.57	108.99

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

11 monomers are involved in 20 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1163	PLP	1	0
2	A	500	SAM	1	0
4	C	1163	PLP	1	0
2	C	500	SAM	2	0
2	D	500	SAM	1	0
4	E	1163	PLP	1	0
2	E	500	SAM	5	0
2	E	501	SAM	2	0
4	F	1163	PLP	1	0
2	F	500	SAM	6	0
2	F	501	SAM	2	0

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	445/486 (91%)	0.21	18 (4%) 42 34	48, 58, 80, 94	0
1	B	429/486 (88%)	0.12	14 (3%) 50 43	51, 59, 77, 89	0
1	C	444/486 (91%)	0.25	17 (3%) 44 36	48, 58, 79, 95	0
1	D	429/486 (88%)	0.10	15 (3%) 48 40	50, 59, 77, 89	0
1	E	431/486 (88%)	0.10	14 (3%) 51 44	51, 59, 77, 91	0
1	F	445/486 (91%)	0.19	10 (2%) 65 59	48, 58, 81, 94	0
All	All	2623/2916 (89%)	0.16	88 (3%) 49 41	48, 59, 79, 95	0

All (88) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	238	ASP	5.5
1	F	344	PHE	4.7
1	C	221	MET	4.7
1	E	237	ILE	4.7
1	A	466	ALA	4.2
1	E	241	PHE	4.2
1	B	241	PHE	4.1
1	C	220	SER	4.0
1	E	343	ASP	4.0
1	A	334	TYR	3.9
1	A	387	LEU	3.8
1	A	220	SER	3.5
1	C	343	ASP	3.5
1	A	214	LEU	3.5
1	D	363	VAL	3.3
1	B	244	CYS	3.3
1	B	329	ASN	3.2
1	E	254	GLU	3.2
1	F	338	LYS	3.2

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Mol	Chain	Res	Type	RSRZ
1	C	466	ALA	3.1
1	A	462	VAL	3.1
1	A	221	MET	3.1
1	A	224	LEU	3.1
1	E	49	ALA	3.0
1	C	468	PHE	3.0
1	B	185	VAL	3.0
1	D	185	VAL	2.9
1	D	50	PRO	2.9
1	D	343	ASP	2.9
1	F	420	VAL	2.9
1	C	323	VAL	2.8
1	D	465	LYS	2.8
1	E	413	PHE	2.8
1	D	248	ILE	2.8
1	D	234	VAL	2.8
1	C	353	PHE	2.8
1	F	220	SER	2.7
1	B	343	ASP	2.7
1	C	214	LEU	2.7
1	A	349	ALA	2.7
1	B	252	THR	2.7
1	D	64	ARG	2.7
1	C	344	PHE	2.6
1	D	237	ILE	2.6
1	C	454	ALA	2.5
1	A	217	ASN	2.5
1	E	212	VAL	2.5
1	B	235	LEU	2.5
1	E	224	LEU	2.5
1	C	224	LEU	2.5
1	A	415	LEU	2.5
1	F	341	TRP	2.5
1	A	420	VAL	2.4
1	A	450	ILE	2.4
1	E	363	VAL	2.4
1	D	255	LEU	2.4
1	F	346	PRO	2.4
1	C	462	VAL	2.3
1	A	413	PHE	2.3
1	B	255	LEU	2.3
1	D	341	TRP	2.3

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Mol	Chain	Res	Type	RSRZ
1	C	413	PHE	2.3
1	D	241	PHE	2.3
1	F	470	ALA	2.3
1	B	64	ARG	2.2
1	E	253	ALA	2.2
1	C	217	ASN	2.2
1	B	332	PRO	2.2
1	E	332	PRO	2.2
1	E	246	LYS	2.2
1	F	219	ILE	2.1
1	F	466	ALA	2.1
1	D	335	LEU	2.1
1	B	213	PHE	2.1
1	F	192	THR	2.1
1	A	453	MET	2.1
1	A	468	PHE	2.1
1	C	317	ASP	2.1
1	C	337	TYR	2.1
1	E	338	LYS	2.1
1	B	339	SER	2.1
1	B	239	THR	2.0
1	A	219	ILE	2.0
1	A	353	PHE	2.0
1	B	413	PHE	2.0
1	C	334	TYR	2.0
1	D	249	ARG	2.0
1	D	382	ALA	2.0

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	PLP	B	1163	15/16	0.90	0.25	2.25	55,57,59,59	15
4	PLP	E	1163	15/16	0.88	0.23	2.03	56,58,60,60	15
4	PLP	D	1163	15/16	0.89	0.21	1.23	57,58,60,60	15
2	SAM	D	500	27/27	0.91	0.21	0.58	42,50,83,83	0
2	SAM	B	500	27/27	0.93	0.17	0.04	47,55,75,76	0
2	SAM	A	501	27/27	0.94	0.14	-0.16	45,56,68,68	0
2	SAM	D	501	27/27	0.93	0.18	-0.31	53,65,82,82	0
2	SAM	C	500	27/27	0.96	0.16	-0.36	31,41,57,58	0
2	SAM	B	501	27/27	0.93	0.18	-0.44	62,70,81,82	0
2	SAM	E	501	27/27	0.95	0.17	-0.46	52,63,81,81	0
2	SAM	E	500	27/27	0.93	0.15	-0.54	46,52,77,78	0
2	SAM	F	501	27/27	0.96	0.14	-0.54	40,55,68,69	0
4	PLP	C	1163	15/16	0.94	0.14	-0.70	49,52,53,55	0
4	PLP	F	1163	15/16	0.94	0.14	-1.02	48,54,56,57	0
2	SAM	C	501	27/27	0.94	0.14	-1.05	49,58,65,65	0
4	PLP	A	1163	15/16	0.95	0.13	-1.26	51,53,57,58	0
2	SAM	A	500	27/27	0.96	0.12	-1.80	32,43,60,62	0
3	TRS	A	800	8/8	0.86	0.13	-1.94	96,96,96,96	0
2	SAM	F	500	27/27	0.96	0.12	-1.99	36,43,64,65	0
3	TRS	C	800	8/8	0.79	0.17	-	96,96,96,97	0
3	TRS	F	800	8/8	0.62	0.18	-	96,96,96,97	0

6.5 Other polymers ⓘ

There are no such residues in this entry.