



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 06:20 AM UTC

PDB ID : 3A9X / pdb_00003a9x
Title : Crystal structure of rat selenocysteine lyase
Authors : Omi, R.; Hirotsu, K.
Deposited on : 2009-11-08
Resolution : 2.00 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

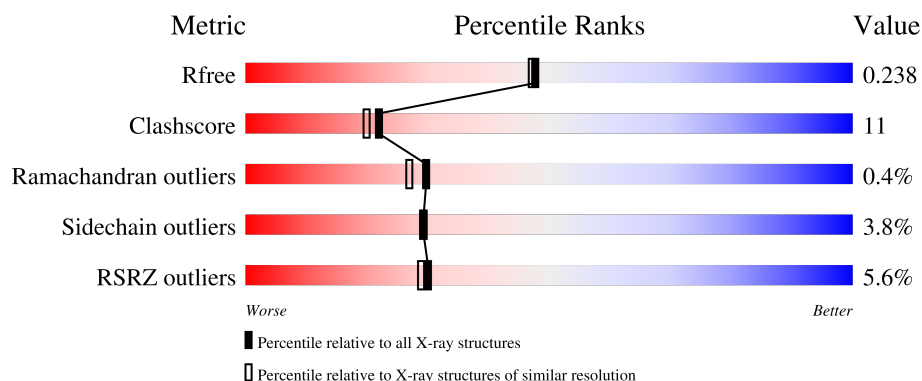
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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}	180053	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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	432	
1	B	432	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 6463 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 Selenocysteine lyase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	388	Total	C	N	O	S	0	0	0
			2965	1853	534	563	15			
1	B	400	Total	C	N	O	S	0	0	0
			3056	1910	550	579	17			

- Molecule 2 is PYRIDOXAL-5'-PHOSPHATE (CCD ID: PLP) (formula: C₈H₁₀NO₆P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
2	B	1	Total	C	N	O	P	0	0
			15	8	1	5	1		

- Molecule 3 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	O	P	0	0
			5	4	1		
3	B	1	Total	O	P	0	0
			5	4	1		
3	B	1	Total	O	P	0	0
			5	4	1		

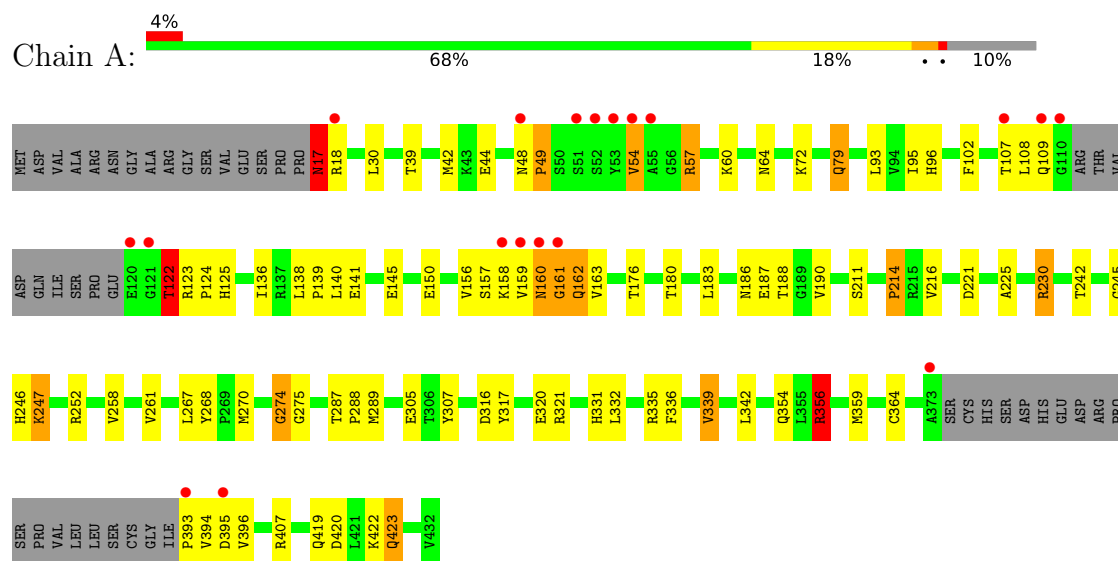
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	198	Total	O	0	0
			198	198		
4	B	199	Total	O	0	0
			199	199		

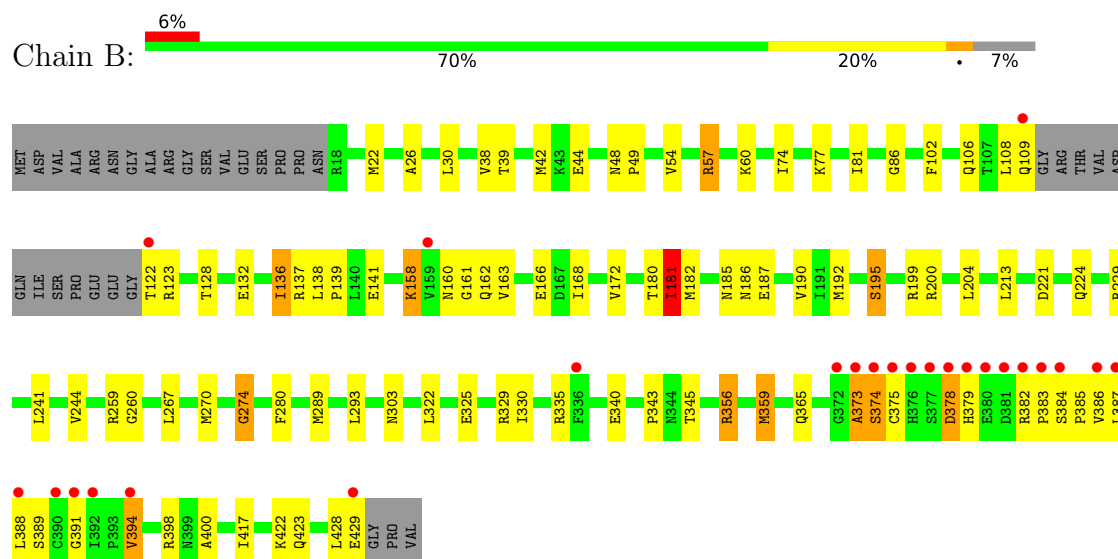
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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: Selenocysteine lyase



• Molecule 1: Selenocysteine lyase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	54.45Å 102.77Å 197.75Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.00 20.00 – 2.00	Depositor EDS
% Data completeness (in resolution range)	(Not available) (20.00-2.00) 91.7 (20.00-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.44 (at 2.00Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.197 , 0.236 0.198 , 0.238	Depositor DCC
R_{free} test set	7053 reflections (10.11%)	wwPDB-VP
Wilson B-factor (Å ²)	31.4	Xtriage
Anisotropy	0.086	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 39.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6463	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.77% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PO4, 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	1.21	5/3012 (0.2%)	1.28	23/4083 (0.6%)
1	B	1.24	5/3107 (0.2%)	1.35	31/4217 (0.7%)
All	All	1.23	10/6119 (0.2%)	1.32	54/8300 (0.7%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	57	ARG	CA-CB	8.65	1.66	1.53
1	B	359	MET	SD-CE	8.40	2.00	1.79
1	A	180	THR	CA-CB	6.04	1.62	1.53
1	A	331	HIS	CA-C	5.88	1.59	1.52
1	B	192	MET	SD-CE	-5.73	1.65	1.79
1	A	395	ASP	CA-CB	5.52	1.62	1.53
1	B	373	ALA	CA-CB	5.47	1.61	1.53
1	A	122	THR	CA-CB	5.33	1.61	1.53
1	B	378	ASP	C-O	5.10	1.30	1.24
1	B	181	ILE	CG1-CD1	-5.07	1.31	1.51

All (54) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	394	VAL	N-CA-C	11.64	122.33	110.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	158	LYS	N-CA-C	-9.13	102.06	113.01
1	B	213	LEU	CA-C-N	-8.13	111.98	120.03
1	B	213	LEU	C-N-CA	-8.13	111.98	120.03
1	A	54	VAL	N-CA-C	8.11	118.66	110.23
1	A	275	GLY	N-CA-C	7.23	123.68	115.08
1	B	383	PRO	N-CA-C	-7.17	100.65	111.41
1	B	136	ILE	N-CA-C	-7.12	105.44	111.56
1	B	382	ARG	CA-C-N	-7.11	112.99	120.03
1	B	382	ARG	C-N-CA	-7.11	112.99	120.03
1	A	245	GLY	N-CA-C	7.02	121.13	112.64
1	B	48	ASN	CA-C-N	6.88	127.45	119.47
1	B	48	ASN	C-N-CA	6.88	127.45	119.47
1	A	17	ASN	CA-C-N	6.87	131.12	120.75
1	A	17	ASN	C-N-CA	6.87	131.12	120.75
1	B	303	ASN	N-CA-C	6.79	121.64	112.88
1	B	374	SER	N-CA-C	6.49	119.35	111.82
1	A	188	THR	N-CA-C	6.38	121.34	113.50
1	B	382	ARG	N-CA-C	-6.28	102.22	110.39
1	B	335	ARG	N-CA-C	6.22	118.91	108.02
1	A	109	GLN	N-CA-C	-6.19	104.61	111.36
1	B	394	VAL	N-CA-C	-6.11	103.26	111.44
1	B	375	CYS	N-CA-C	-6.06	105.98	113.19
1	B	44	GLU	N-CA-C	6.01	120.89	113.50
1	B	345	THR	N-CA-C	5.93	118.61	109.07
1	A	122	THR	N-CA-C	-5.86	100.45	109.76
1	A	163	VAL	N-CA-C	-5.84	103.61	110.21
1	A	162	GLN	N-CA-C	-5.74	99.31	109.06
1	B	270	MET	N-CA-C	-5.73	106.45	113.50
1	B	274	GLY	N-CA-C	5.72	126.74	113.18
1	B	81	ILE	N-CA-C	5.69	116.50	108.36
1	A	49	PRO	N-CA-C	5.65	124.11	112.47
1	A	339	VAL	N-CA-C	5.61	115.87	107.51
1	B	244	VAL	N-CA-C	5.60	116.18	107.28
1	A	274	GLY	N-CA-C	5.58	126.41	113.18
1	B	77	LYS	CA-C-N	5.45	125.53	119.32
1	B	77	LYS	C-N-CA	5.45	125.53	119.32
1	B	74	ILE	N-CA-C	5.45	117.34	112.17
1	A	356	ARG	N-CA-C	-5.30	102.54	110.23
1	A	247	LYS	N-CA-C	-5.26	106.70	113.23
1	A	156	VAL	N-CA-C	-5.26	102.14	109.45
1	A	216	VAL	N-CA-C	-5.25	101.02	108.58
1	A	136	ILE	N-CA-C	-5.21	107.08	111.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	102	PHE	N-CA-C	-5.20	105.50	111.07
1	A	161	GLY	N-CA-C	-5.17	100.92	113.18
1	B	163	VAL	N-CA-C	-5.14	102.46	109.55
1	A	214	PRO	CA-C-N	5.11	128.02	120.82
1	A	214	PRO	C-N-CA	5.11	128.02	120.82
1	B	400	ALA	N-CA-C	5.07	117.79	110.28
1	A	44	GLU	N-CA-C	5.07	120.46	113.97
1	B	54	VAL	N-CA-C	5.05	115.48	110.23
1	B	195	SER	N-CA-C	5.04	117.16	111.11
1	B	86	GLY	N-CA-C	5.03	117.40	110.56
1	B	57	ARG	CB-CG-CD	-5.02	99.75	111.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	268	TYR	Sidechain

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	2965	0	2966	63	0
1	B	3056	0	3055	69	0
2	A	15	0	7	1	0
2	B	15	0	7	1	0
3	B	15	0	0	1	0
4	A	198	0	0	2	0
4	B	199	0	0	4	0
All	All	6463	0	6035	130	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 11.

All (130) 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:356:ARG:HG3	1:B:356:ARG:HH11	1.12	1.13
1:A:230:ARG:HH11	1:A:230:ARG:HG3	1.03	1.11
1:B:385:PRO:HA	1:B:388:LEU:HD12	1.34	1.08
1:B:384:SER:O	1:B:388:LEU:HG	1.68	0.93
1:A:356:ARG:HB2	1:A:359:MET:HE2	1.52	0.91
1:B:356:ARG:HD2	1:B:398:ARG:HG2	1.54	0.89
1:B:162:GLN:HG2	1:B:190:VAL:HG11	1.54	0.88
1:A:230:ARG:HG3	1:A:230:ARG:NH1	1.75	0.87
1:B:356:ARG:HD3	4:B:633:HOH:O	1.75	0.86
1:B:356:ARG:NE	1:B:398:ARG:HD3	1.94	0.81
1:B:356:ARG:HG3	1:B:356:ARG:NH1	1.86	0.79
1:A:159:VAL:HG12	1:A:160:ASN:N	1.99	0.76
1:A:356:ARG:CB	1:A:359:MET:HE2	2.18	0.73
1:A:356:ARG:H	1:A:359:MET:HE2	1.53	0.73
1:B:365:GLN:HA	1:B:365:GLN:OE1	1.89	0.72
1:B:162:GLN:HG2	1:B:190:VAL:CG1	2.20	0.71
1:A:356:ARG:H	1:A:359:MET:CE	2.03	0.71
1:B:373:ALA:HB1	3:B:503:PO4:O3	1.92	0.70
1:A:336:PHE:HB2	1:A:339:VAL:CG2	2.24	0.68
1:A:354:GLN:O	1:A:359:MET:HE3	1.91	0.68
1:A:230:ARG:HH11	1:A:230:ARG:CG	1.90	0.67
1:A:157:SER:O	1:A:159:VAL:N	2.27	0.67
1:B:385:PRO:CA	1:B:388:LEU:HD12	2.20	0.66
1:A:246:HIS:HB3	1:A:252:ARG:HD3	1.77	0.66
1:B:378:ASP:OD2	1:B:379:HIS:ND1	2.28	0.66
1:B:356:ARG:HE	1:B:398:ARG:HD3	1.59	0.64
1:A:221:ASP:OD2	2:A:501:PLP:N1	2.32	0.62
1:B:106:GLN:NE2	1:B:106:GLN:HA	2.14	0.61
1:A:183:LEU:HD22	1:A:225:ALA:HB2	1.83	0.61
1:B:38:VAL:HG12	1:B:42:MET:HE2	1.83	0.60
1:A:157:SER:C	1:A:159:VAL:H	2.09	0.60
1:B:325:GLU:OE2	1:B:422:LYS:HD2	2.01	0.60
1:A:123:ARG:HH21	1:A:150:GLU:CD	2.10	0.59
1:A:270:MET:HE3	4:A:605:HOH:O	2.03	0.59
1:A:102:PHE:CD2	1:A:124:PRO:HD3	2.38	0.59
1:A:102:PHE:HZ	1:A:122:THR:HG23	1.68	0.58
1:B:384:SER:O	1:B:388:LEU:CG	2.47	0.58
1:A:289:MET:HE3	1:B:289:MET:HE3	1.86	0.57
1:A:157:SER:C	1:A:159:VAL:N	2.62	0.56
1:A:252:ARG:HG3	1:A:252:ARG:HH11	1.70	0.56
1:A:230:ARG:NH1	1:A:230:ARG:CG	2.55	0.56
1:B:137:ARG:O	1:B:141:GLU:HG3	2.05	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:325:GLU:CD	1:B:422:LYS:HD2	2.31	0.55
1:B:356:ARG:CD	1:B:398:ARG:HG2	2.31	0.55
1:B:322:LEU:HB3	1:B:330:ILE:HD13	1.88	0.54
1:B:356:ARG:NH1	1:B:356:ARG:CG	2.67	0.54
1:B:106:GLN:HA	1:B:106:GLN:HE21	1.72	0.53
1:B:387:LEU:HD11	4:B:537:HOH:O	2.09	0.53
1:A:57:ARG:HA	4:A:556:HOH:O	2.08	0.52
1:B:182:MET:HE2	1:B:185:ASN:HA	1.92	0.52
1:B:221:ASP:OD2	2:B:501:PLP:N1	2.43	0.51
1:A:79:GLN:NE2	1:A:79:GLN:H	2.07	0.51
1:B:172:VAL:HG11	1:B:204:LEU:HD21	1.92	0.51
1:B:229:ARG:NH2	1:B:340:GLU:OE1	2.42	0.51
1:B:329:ARG:HH22	1:B:429:GLU:HG3	1.76	0.51
1:A:39:THR:HA	1:A:42:MET:HE3	1.92	0.50
1:B:160:ASN:OD1	1:B:162:GLN:HG3	2.11	0.50
1:B:359:MET:HE2	1:B:428:LEU:HD22	1.94	0.50
1:B:423:GLN:OE1	1:B:423:GLN:C	2.55	0.49
1:A:419:GLN:O	1:A:423:GLN:HG2	2.11	0.49
1:B:166:GLU:CD	1:B:200:ARG:HH22	2.20	0.49
1:B:160:ASN:OD1	1:B:161:GLY:N	2.45	0.49
1:A:356:ARG:N	1:A:359:MET:HE2	2.24	0.49
1:A:96:HIS:CG	1:A:270:MET:HG2	2.49	0.48
1:B:106:GLN:NE2	1:B:106:GLN:CA	2.75	0.48
1:B:136:ILE:C	1:B:139:PRO:HD2	2.39	0.48
1:A:258:VAL:HG11	1:A:261:VAL:HG23	1.96	0.48
1:A:419:GLN:HE22	1:A:422:LYS:HD3	1.79	0.47
1:A:159:VAL:HG12	1:A:160:ASN:OD1	2.14	0.47
1:B:106:GLN:O	1:B:109:GLN:N	2.34	0.47
1:B:187:GLU:HG3	1:B:386:VAL:HG11	1.95	0.47
1:A:423:GLN:HG2	1:A:423:GLN:H	1.56	0.47
1:A:60:LYS:NZ	1:A:64:ASN:HD21	2.12	0.47
1:A:354:GLN:C	1:A:359:MET:HE3	2.40	0.47
1:B:195:SER:HB3	1:B:199:ARG:HH22	1.80	0.46
1:A:287:THR:HB	1:A:288:PRO:HD3	1.97	0.46
1:B:39:THR:HA	1:B:42:MET:HE3	1.96	0.46
1:B:128:THR:OG1	1:B:132:GLU:HG3	2.16	0.46
1:B:356:ARG:CZ	1:B:398:ARG:HD3	2.44	0.46
1:B:241:LEU:C	1:B:241:LEU:HD23	2.39	0.46
1:B:49:PRO:O	1:B:60:LYS:HB2	2.16	0.45
1:B:138:LEU:HD23	1:B:138:LEU:HA	1.82	0.45
1:A:125:HIS:HB3	1:A:176:THR:HA	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:389:SER:HB3	4:B:613:HOH:O	2.15	0.45
1:A:17:ASN:OD1	1:A:17:ASN:N	2.49	0.45
1:A:336:PHE:HB2	1:A:339:VAL:HG23	1.98	0.45
1:B:378:ASP:OD2	1:B:379:HIS:CE1	2.69	0.45
1:B:158:LYS:O	1:B:391:GLY:HA3	2.16	0.45
1:B:166:GLU:OE1	1:B:166:GLU:HA	2.16	0.45
1:B:267:LEU:HD23	1:B:280:PHE:HB3	1.99	0.45
1:A:246:HIS:CE1	1:A:247:LYS:HE3	2.52	0.45
1:B:384:SER:O	1:B:388:LEU:CD1	2.66	0.44
1:A:18:ARG:O	1:A:18:ARG:HG3	2.18	0.44
1:A:96:HIS:CD2	1:A:270:MET:HG2	2.53	0.44
1:B:106:GLN:HE21	1:B:106:GLN:CA	2.30	0.44
1:A:93:LEU:HB2	1:A:270:MET:HE2	2.00	0.44
1:A:160:ASN:N	1:A:160:ASN:OD1	2.50	0.43
1:B:259:ARG:O	1:B:260:GLY:C	2.60	0.43
1:B:160:ASN:OD1	1:B:160:ASN:C	2.62	0.43
1:A:183:LEU:C	1:A:183:LEU:HD23	2.43	0.43
1:A:332:LEU:HD12	1:A:335:ARG:CZ	2.49	0.42
1:A:95:ILE:HD12	1:A:140:LEU:HD21	2.00	0.42
1:A:221:ASP:HA	1:A:242:THR:HB	2.02	0.42
1:B:168:ILE:HD12	1:B:181:ILE:HD11	2.02	0.42
1:A:187:GLU:N	1:A:187:GLU:CD	2.77	0.42
1:A:307:TYR:CD1	1:A:407:ARG:HG2	2.55	0.42
1:B:356:ARG:CZ	1:B:398:ARG:HH11	2.33	0.42
1:B:394:VAL:O	1:B:398:ARG:HB2	2.19	0.42
1:A:42:MET:HB3	1:B:30:LEU:HD12	2.02	0.42
1:A:258:VAL:HG21	1:A:267:LEU:HD22	2.02	0.42
1:A:316:ASP:O	1:A:320:GLU:HG3	2.20	0.41
1:A:317:TYR:O	1:A:321:ARG:HG2	2.20	0.41
1:A:157:SER:O	1:A:161:GLY:N	2.47	0.41
1:B:136:ILE:O	1:B:139:PRO:HD2	2.19	0.41
1:B:186:ASN:HB3	1:B:224:GLN:HG3	2.03	0.41
1:B:22:MET:CE	1:B:417:ILE:HG12	2.50	0.41
1:B:123:ARG:HE	1:B:123:ARG:HB2	1.61	0.41
1:A:364:CYS:HB3	1:A:420:ASP:OD2	2.20	0.41
1:A:141:GLU:O	1:A:145:GLU:HG3	2.21	0.41
1:A:162:GLN:HG2	1:A:190:VAL:CG1	2.50	0.41
1:B:384:SER:HB3	1:B:387:LEU:HD12	2.03	0.41
1:A:138:LEU:HD23	1:A:138:LEU:HA	1.93	0.40
1:A:138:LEU:N	1:A:139:PRO:HD2	2.37	0.40
1:B:180:THR:O	1:B:181:ILE:HG13	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:30:LEU:HD12	1:A:30:LEU:N	2.37	0.40
1:A:342:LEU:HD23	1:A:342:LEU:HA	1.75	0.40
1:A:317:TYR:CE1	1:A:321:ARG:HD3	2.57	0.40
1:B:26:ALA:HB1	1:B:374:SER:OG	2.21	0.40
1:B:356:ARG:CD	4:B:633:HOH:O	2.51	0.40
1:B:293:LEU:HA	1:B:293:LEU:HD12	1.86	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	382/432 (88%)	362 (95%)	18 (5%)	2 (0%)	24	21
1	B	396/432 (92%)	379 (96%)	16 (4%)	1 (0%)	36	35
All	All	778/864 (90%)	741 (95%)	34 (4%)	3 (0%)	30	27

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	158	LYS
1	B	274	GLY
1	A	274	GLY

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	319/364 (88%)	300 (94%)	19 (6%)	17	14
1	B	332/364 (91%)	326 (98%)	6 (2%)	51	58
All	All	651/728 (89%)	626 (96%)	25 (4%)	29	29

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	17	ASN
1	A	48	ASN
1	A	49	PRO
1	A	54	VAL
1	A	72	LYS
1	A	79	GLN
1	A	107	THR
1	A	108	LEU
1	A	122	THR
1	A	160	ASN
1	A	186	ASN
1	A	211	SER
1	A	214	PRO
1	A	230	ARG
1	A	305	GLU
1	A	356	ARG
1	A	393	PRO
1	A	396	VAL
1	A	423	GLN
1	B	57	ARG
1	B	108	LEU
1	B	122	THR
1	B	181	ILE
1	B	343	PRO
1	B	356	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	64	ASN
1	A	79	GLN
1	A	91	ASN
1	A	96	HIS
1	A	162	GLN

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Mol	Chain	Res	Type
1	A	186	ASN
1	A	303	ASN
1	A	419	GLN
1	A	423	GLN
1	B	36	GLN
1	B	96	HIS
1	B	105	GLN
1	B	106	GLN
1	B	351	GLN
1	B	354	GLN
1	B	399	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

5 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	PO4	B	504	-	4,4,4	0.90	0	6,6,6	0.56	0
3	PO4	B	502	-	4,4,4	1.16	1 (25%)	6,6,6	0.57	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	PLP	B	501	1	15,15,16	2.72	6 (40%)	21,22,23	1.65	5 (23%)
3	PO4	B	503	-	4,4,4	0.93	0	6,6,6	0.64	0
2	PLP	A	501	1	15,15,16	2.65	8 (53%)	21,22,23	1.53	3 (14%)

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
2	PLP	B	501	1	-	0/6/6/8	0/1/1/1
2	PLP	A	501	1	-	0/6/6/8	0/1/1/1

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	PLP	C2A-C2	6.45	1.60	1.50
2	B	501	PLP	C5-C4	6.38	1.47	1.40
2	A	501	PLP	C2-N1	4.52	1.41	1.33
2	B	501	PLP	C2A-C2	3.85	1.56	1.50
2	B	501	PLP	C4A-C4	3.81	1.59	1.51
2	A	501	PLP	C5A-C5	3.13	1.59	1.50
2	A	501	PLP	P-O2P	-2.74	1.44	1.54
2	B	501	PLP	C3-C2	-2.72	1.38	1.41
2	B	501	PLP	P-O4P	2.66	1.68	1.60
2	A	501	PLP	C3-C2	-2.62	1.38	1.41
2	A	501	PLP	P-O3P	-2.17	1.46	1.54
2	B	501	PLP	P-O3P	-2.17	1.46	1.54
3	B	502	PO4	P-O3	-2.08	1.48	1.54
2	A	501	PLP	P-O1P	-2.05	1.44	1.50
2	A	501	PLP	C3-C4	2.01	1.43	1.40

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	PLP	O4P-C5A-C5	5.26	119.22	109.36
2	B	501	PLP	O3P-P-O4P	-3.80	96.75	106.67
2	B	501	PLP	C6-N1-C2	2.34	123.45	119.20
2	A	501	PLP	C3-C2-N1	-2.34	118.01	120.96
2	B	501	PLP	C2A-C2-N1	2.32	122.02	117.64
2	A	501	PLP	C2A-C2-C3	2.14	123.30	120.80
2	B	501	PLP	O2P-P-O1P	2.04	118.80	110.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	501	PLP	C2A-C2-C3	-2.00	118.45	120.80

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	501	PLP	1	0
3	B	503	PO4	1	0
2	A	501	PLP	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	388/432 (89%)	-0.07	19 (4%) 35 34	20, 31, 49, 74	0
1	B	400/432 (92%)	0.03	25 (6%) 26 24	20, 31, 52, 71	0
All	All	788/864 (91%)	-0.02	44 (5%) 30 29	20, 31, 51, 74	0

All (44) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	377	SER	5.4
1	B	375	CYS	5.3
1	B	374	SER	4.9
1	A	159	VAL	4.9
1	B	380	GLU	4.2
1	B	376	HIS	4.2
1	A	121	GLY	3.8
1	B	381	ASP	3.7
1	B	391	GLY	3.6
1	B	390	CYS	3.5
1	B	336	PHE	3.4
1	A	161	GLY	3.4
1	B	384	SER	3.4
1	B	378	ASP	3.1
1	B	387	LEU	3.0
1	A	110	GLY	3.0
1	B	373	ALA	2.9
1	A	160	ASN	2.9
1	B	383	PRO	2.7
1	A	55	ALA	2.7
1	B	372	GLY	2.7
1	A	120	GLU	2.6
1	A	395	ASP	2.6
1	A	158	LYS	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	122	THR	2.6
1	B	386	VAL	2.6
1	B	382	ARG	2.6
1	B	429	GLU	2.5
1	A	53	TYR	2.5
1	B	388	LEU	2.5
1	A	393	PRO	2.5
1	A	54	VAL	2.4
1	B	392	ILE	2.4
1	A	51	SER	2.4
1	A	373	ALA	2.4
1	A	107	THR	2.4
1	B	379	HIS	2.3
1	A	109	GLN	2.3
1	A	48	ASN	2.3
1	A	18	ARG	2.3
1	B	159	VAL	2.2
1	B	109	GLN	2.2
1	A	52	SER	2.1
1	B	394	VAL	2.1

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 oligosaccharides 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. 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	B-factors(Å ²)	Q<0.9
3	PO4	B	502	5/5	0.90	0.19	64,64,66,67	0
3	PO4	B	504	5/5	0.90	0.10	60,60,61,62	0
3	PO4	B	503	5/5	0.92	0.20	54,54,58,59	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	PLP	B	501	15/16	0.97	0.06	25,28,32,34	0
2	PLP	A	501	15/16	0.97	0.07	28,32,35,36	0

6.5 Other polymers [i](#)

There are no such residues in this entry.