Full wwPDB X-ray Structure Validation Report (i)

Sep 16, 2023 – 11:22 PM EDT

PDB ID	:	4WYA
Title	:	Crystal structure of 7,8-diaminopelargonic acid synthase (BioA) from Mycobacterium tuberculosis, complexed with a fragment hit
Authors	:	Finzel, B.C.; Dai, D.; Geders, T.W.
Deposited on	:	2014-11-17
Resolution	:	2.50 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 (i) 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 (i)) were used in the production of this report:

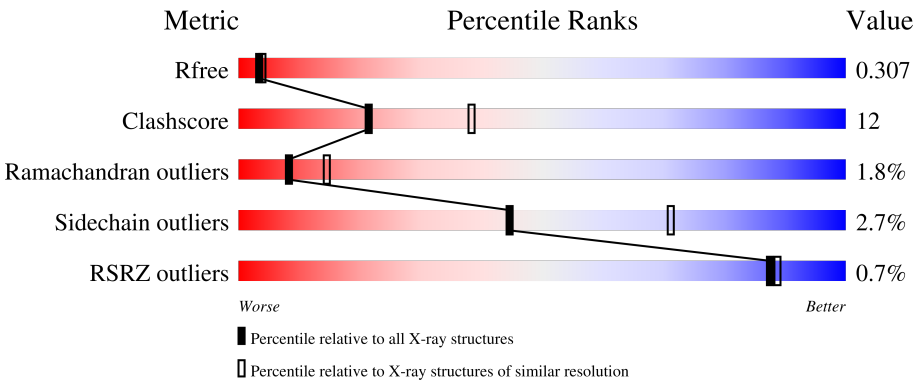
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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}	130704	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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 <=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	457	62% 29% • 8%
1	B	457	% 64% 26% • 8%
1	C	457	% 67% 23% • 8%
1	D	457	% 69% 20% • 9%

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
3	3VQ	D	501	-	-	X	-

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 12702 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 Adenosylmethionine-8-amino-7-oxononanoate aminotransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	420	3129	1989	554	567	19	1	0	0
1	B	422	3147	2001	555	571	20	0	1	0
1	C	419	3124	1987	551	566	20	0	0	0
1	D	414	3100	1973	549	559	19	0	1	0

There are 80 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	initiating methionine	UNP P9WQ81
A	-18	GLY	-	expression tag	UNP P9WQ81
A	-17	SER	-	expression tag	UNP P9WQ81
A	-16	SER	-	expression tag	UNP P9WQ81
A	-15	HIS	-	expression tag	UNP P9WQ81
A	-14	HIS	-	expression tag	UNP P9WQ81
A	-13	HIS	-	expression tag	UNP P9WQ81
A	-12	HIS	-	expression tag	UNP P9WQ81
A	-11	HIS	-	expression tag	UNP P9WQ81
A	-10	HIS	-	expression tag	UNP P9WQ81
A	-9	SER	-	expression tag	UNP P9WQ81
A	-8	SER	-	expression tag	UNP P9WQ81
A	-7	GLY	-	expression tag	UNP P9WQ81
A	-6	LEU	-	expression tag	UNP P9WQ81
A	-5	VAL	-	expression tag	UNP P9WQ81
A	-4	PRO	-	expression tag	UNP P9WQ81
A	-3	ARG	-	expression tag	UNP P9WQ81
A	-2	GLY	-	expression tag	UNP P9WQ81
A	-1	SER	-	expression tag	UNP P9WQ81
A	0	HIS	-	expression tag	UNP P9WQ81

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-19	MET	-	initiating methionine	UNP P9WQ81
B	-18	GLY	-	expression tag	UNP P9WQ81
B	-17	SER	-	expression tag	UNP P9WQ81
B	-16	SER	-	expression tag	UNP P9WQ81
B	-15	HIS	-	expression tag	UNP P9WQ81
B	-14	HIS	-	expression tag	UNP P9WQ81
B	-13	HIS	-	expression tag	UNP P9WQ81
B	-12	HIS	-	expression tag	UNP P9WQ81
B	-11	HIS	-	expression tag	UNP P9WQ81
B	-10	HIS	-	expression tag	UNP P9WQ81
B	-9	SER	-	expression tag	UNP P9WQ81
B	-8	SER	-	expression tag	UNP P9WQ81
B	-7	GLY	-	expression tag	UNP P9WQ81
B	-6	LEU	-	expression tag	UNP P9WQ81
B	-5	VAL	-	expression tag	UNP P9WQ81
B	-4	PRO	-	expression tag	UNP P9WQ81
B	-3	ARG	-	expression tag	UNP P9WQ81
B	-2	GLY	-	expression tag	UNP P9WQ81
B	-1	SER	-	expression tag	UNP P9WQ81
B	0	HIS	-	expression tag	UNP P9WQ81
C	-19	MET	-	initiating methionine	UNP P9WQ81
C	-18	GLY	-	expression tag	UNP P9WQ81
C	-17	SER	-	expression tag	UNP P9WQ81
C	-16	SER	-	expression tag	UNP P9WQ81
C	-15	HIS	-	expression tag	UNP P9WQ81
C	-14	HIS	-	expression tag	UNP P9WQ81
C	-13	HIS	-	expression tag	UNP P9WQ81
C	-12	HIS	-	expression tag	UNP P9WQ81
C	-11	HIS	-	expression tag	UNP P9WQ81
C	-10	HIS	-	expression tag	UNP P9WQ81
C	-9	SER	-	expression tag	UNP P9WQ81
C	-8	SER	-	expression tag	UNP P9WQ81
C	-7	GLY	-	expression tag	UNP P9WQ81
C	-6	LEU	-	expression tag	UNP P9WQ81
C	-5	VAL	-	expression tag	UNP P9WQ81
C	-4	PRO	-	expression tag	UNP P9WQ81
C	-3	ARG	-	expression tag	UNP P9WQ81
C	-2	GLY	-	expression tag	UNP P9WQ81
C	-1	SER	-	expression tag	UNP P9WQ81
C	0	HIS	-	expression tag	UNP P9WQ81
D	-19	MET	-	initiating methionine	UNP P9WQ81
D	-18	GLY	-	expression tag	UNP P9WQ81

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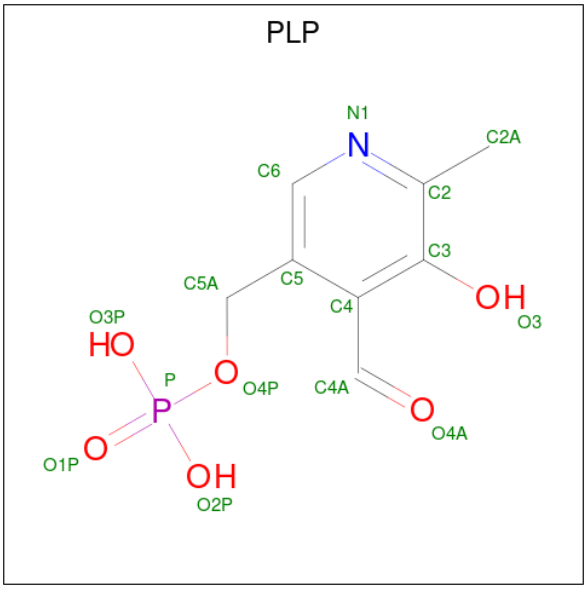
Chain	Residue	Modelled	Actual	Comment	Reference
D	-17	SER	-	expression tag	UNP P9WQ81
D	-16	SER	-	expression tag	UNP P9WQ81
D	-15	HIS	-	expression tag	UNP P9WQ81
D	-14	HIS	-	expression tag	UNP P9WQ81
D	-13	HIS	-	expression tag	UNP P9WQ81
D	-12	HIS	-	expression tag	UNP P9WQ81
D	-11	HIS	-	expression tag	UNP P9WQ81
D	-10	HIS	-	expression tag	UNP P9WQ81
D	-9	SER	-	expression tag	UNP P9WQ81
D	-8	SER	-	expression tag	UNP P9WQ81
D	-7	GLY	-	expression tag	UNP P9WQ81
D	-6	LEU	-	expression tag	UNP P9WQ81
D	-5	VAL	-	expression tag	UNP P9WQ81
D	-4	PRO	-	expression tag	UNP P9WQ81
D	-3	ARG	-	expression tag	UNP P9WQ81
D	-2	GLY	-	expression tag	UNP P9WQ81
D	-1	SER	-	expression tag	UNP P9WQ81
D	0	HIS	-	expression tag	UNP P9WQ81

- Molecule 2 is PYRIDOXAL-5'-PHOSPHATE (three-letter code: PLP) (formula: $C_8H_{10}NO_6P$).



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

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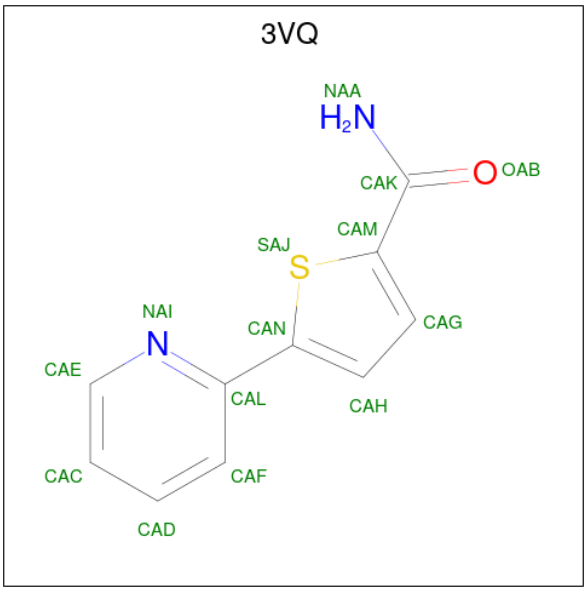
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	C	1	15	8	1	5	1	0	0
2	D	1	15	8	1	5	1	0	0

- Molecule 3 is 5-(pyridin-2-yl)thiophene-2-carboxamide (three-letter code: 3VQ) (formula: $C_{10}H_8N_2OS$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
3	B	1	14	10	2	1	1	0	0
3	D	1	14	10	2	1	1	0	0

- Molecule 4 is water.

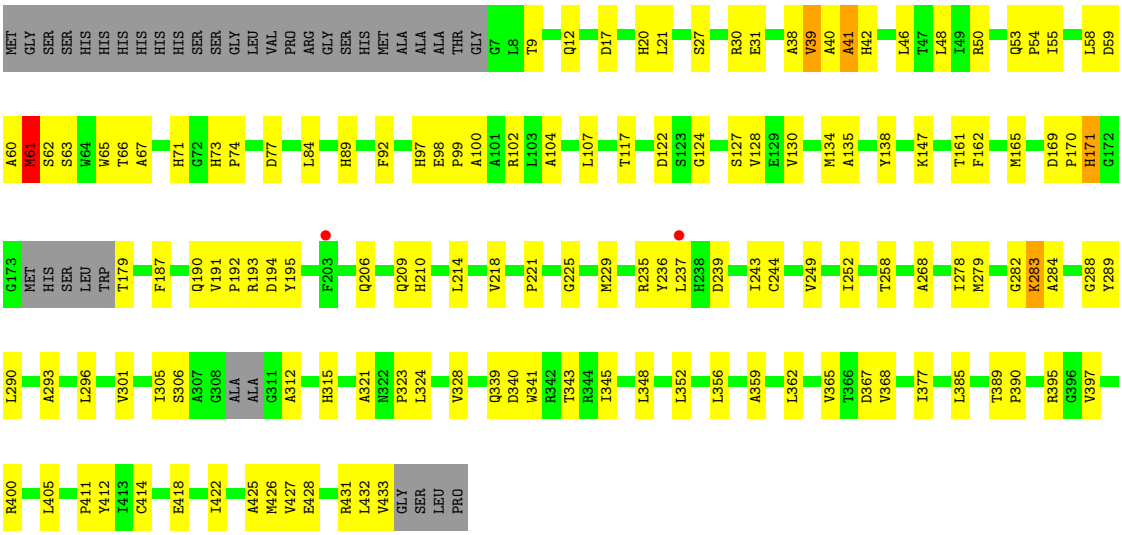
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	34	34	34	0	0
4	B	25	25	25	0	0
4	C	24	24	24	0	0
4	D	31	31	31	0	0

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.

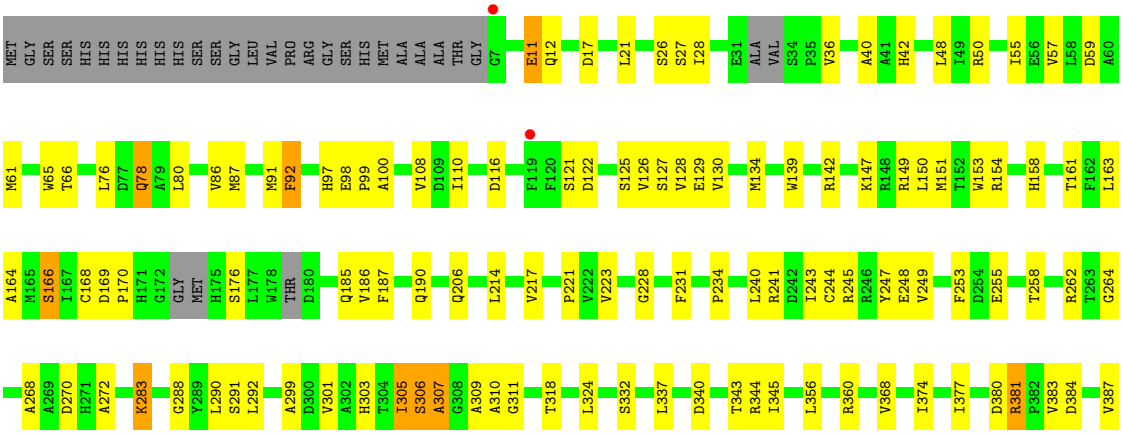
• Molecule 1: Adenosylmethionine-8-amino-7-oxononanoate aminotransferase

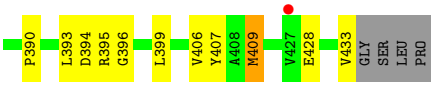
Chain A:



• Molecule 1: Adenosylmethionine-8-amino-7-oxononanoate aminotransferase

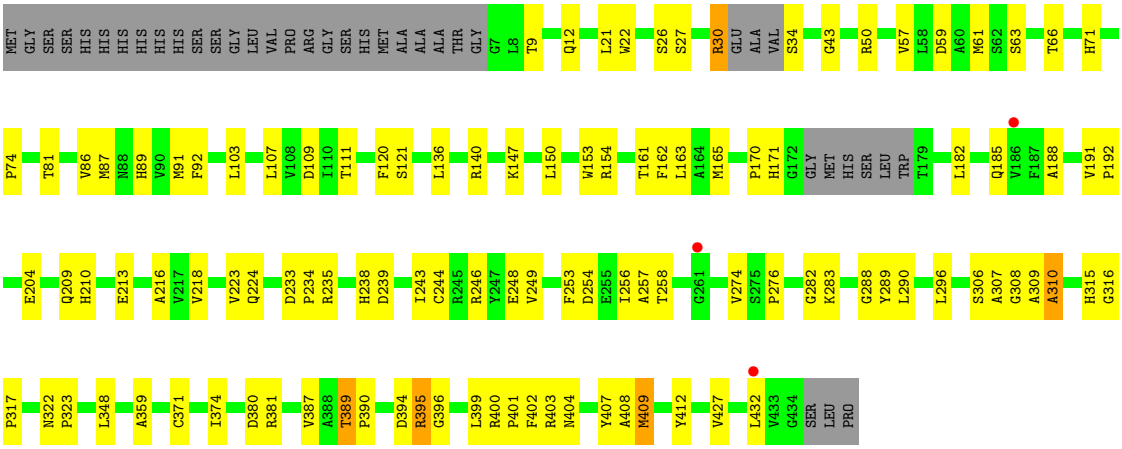
Chain B:





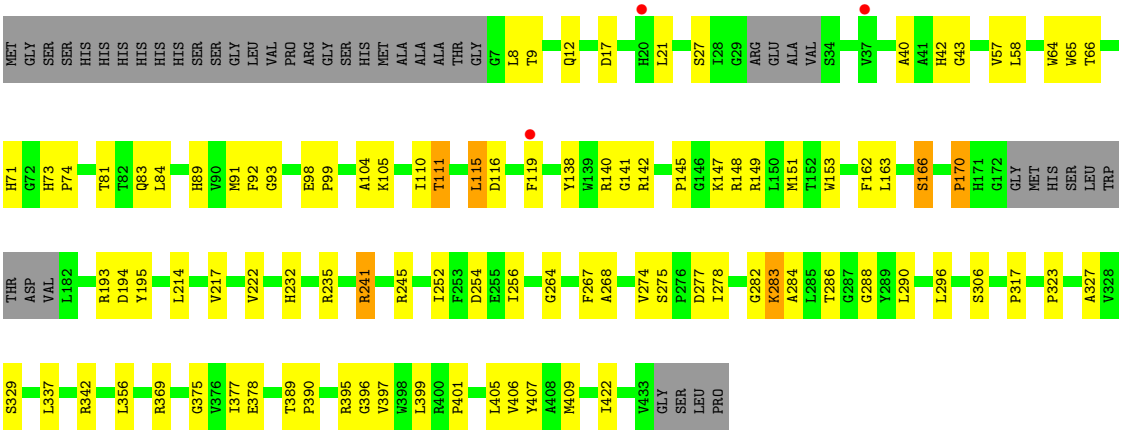
• Molecule 1: Adenosylmethionine-8-amino-7-oxononanoate aminotransferase

Chain C:



• Molecule 1: Adenosylmethionine-8-amino-7-oxononanoate aminotransferase

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	62.65Å 65.67Å 201.34Å 90.00° 90.29° 90.00°	Depositor
Resolution (Å)	29.87 – 2.50 29.95 – 2.50	Depositor EDS
% Data completeness (in resolution range)	87.6 (29.87-2.50) 86.1 (29.95-2.50)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.24 (at 2.51Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.224 , 0.306 0.226 , 0.307	Depositor DCC
R_{free} test set	2568 reflections (5.13%)	wwPDB-VP
Wilson B-factor (Å^2)	40.1	Xtriage
Anisotropy	0.659	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 27.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	0.025 for -k,-h,-l 0.024 for k,h,-l 0.347 for h,-k,-l	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	12702	wwPDB-VP
Average B, all atoms (Å^2)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.71% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: 3VQ, 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	0.42	0/3204	0.64	0/4378
1	B	0.44	0/3220	0.63	0/4398
1	C	0.44	0/3198	0.62	0/4369
1	D	0.45	0/3175	0.64	2/4338 (0.0%)
All	All	0.44	0/12797	0.63	2/17483 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	8	LEU	CA-CB-CG	5.54	128.05	115.30
1	D	399	LEU	CA-CB-CG	5.00	126.80	115.30

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	3129	0	3091	96	0
1	B	3147	0	3105	90	0
1	C	3124	0	3100	71	1
1	D	3100	0	3075	71	1
2	A	15	0	6	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	15	0	6	1	0
2	C	15	0	6	2	0
2	D	15	0	6	1	0
3	B	14	0	8	0	0
3	D	14	0	8	8	0
4	A	34	0	0	2	0
4	B	25	0	0	1	0
4	C	24	0	0	0	1
4	D	31	0	0	0	1
All	All	12702	0	12411	299	2

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 12.

All (299) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:278:ILE:O	4:A:601:HOH:O	1.78	1.01
1:C:147:LYS:NZ	1:C:248:GLU:O	2.02	0.91
1:D:92:PHE:H	3:D:501:3VQ:H3	1.37	0.87
1:D:264:GLY:O	1:D:342:ARG:NH1	2.11	0.84
1:A:42:HIS:HA	1:A:71:HIS:HB2	1.63	0.80
1:B:147:LYS:NZ	1:B:248:GLU:O	2.17	0.77
1:A:195:TYR:CE1	1:A:235:ARG:HG2	2.21	0.76
1:D:147:LYS:NZ	1:D:214:LEU:O	2.19	0.75
1:A:315:HIS:O	4:A:602:HOH:O	2.03	0.74
1:D:241[A]:ARG:HE	1:D:274:VAL:HG13	1.51	0.74
1:D:91:MET:HB2	3:D:501:3VQ:H4	1.71	0.71
1:C:91:MET:HE3	1:D:64:TRP:HB2	1.74	0.69
1:B:142:ARG:HH11	1:B:142:ARG:HG2	1.57	0.69
1:D:317:PRO:O	3:D:501:3VQ:H2	1.92	0.69
1:D:140:ARG:HH22	1:D:148:ARG:HB3	1.57	0.69
1:B:163:LEU:O	1:B:166:SER:HB3	1.94	0.68
1:D:241[A]:ARG:HH21	1:D:275:SER:H	1.42	0.66
1:D:65:TRP:HB2	1:D:283:LYS:HD3	1.77	0.65
1:A:283:LYS:HG3	1:B:318:THR:HG21	1.77	0.65
1:A:190:GLN:NE2	1:A:191:VAL:O	2.24	0.65
1:A:98:GLU:HG2	1:A:102:ARG:HH21	1.61	0.65
1:B:299:ALA:HB1	1:B:303:HIS:CE1	2.32	0.64
1:B:78:GLN:HE22	1:D:395:ARG:HA	1.63	0.64
1:D:93:GLY:H	3:D:501:3VQ:H4	1.63	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:256:ILE:HG22	1:C:283:LYS:HG3	1.80	0.63
1:A:63:SER:HB3	1:B:91:MET:H	1.63	0.63
1:C:9:THR:HG23	1:C:12:GLN:H	1.61	0.63
1:C:307:ALA:C	1:C:309:ALA:HB3	2.19	0.62
1:A:397:VAL:HG21	1:A:422:ILE:HA	1.81	0.62
1:A:282:GLY:O	1:A:284:ALA:N	2.32	0.62
1:A:301:VAL:O	1:A:305:ILE:HG12	1.99	0.62
1:A:359:ALA:HA	1:A:362:LEU:HD23	1.82	0.61
1:C:89:HIS:HA	1:C:323:PRO:HG2	1.81	0.61
1:B:168:CYS:SG	1:B:169:ASP:N	2.74	0.61
1:A:359:ALA:HB2	1:A:427:VAL:HG22	1.83	0.60
1:A:356:LEU:HD22	1:A:377:ILE:HD11	1.82	0.60
1:B:76:LEU:HD21	1:B:332:SER:HB2	1.84	0.59
1:D:163:LEU:O	1:D:166:SER:HB3	2.02	0.59
1:A:89:HIS:HA	1:A:323:PRO:HG2	1.85	0.59
1:A:60:ALA:N	1:A:61:MET:O	2.35	0.59
1:D:375:GLY:O	1:D:407:TYR:HB2	2.02	0.59
1:C:26:SER:OG	1:C:27:SER:N	2.33	0.59
1:A:61:MET:HE3	1:A:400:ARG:H	1.68	0.58
1:B:65:TRP:HB2	1:B:283:LYS:HD3	1.84	0.58
1:D:241[A]:ARG:HH11	1:D:245:ARG:HH22	1.52	0.58
1:B:66:THR:HB	1:B:288:GLY:HA2	1.86	0.58
1:C:204:GLU:OE2	1:C:246:ARG:NH1	2.21	0.58
1:B:142:ARG:HG2	1:B:142:ARG:NH1	2.18	0.58
1:C:57:VAL:HG12	1:C:396:GLY:HA2	1.86	0.57
1:B:150:LEU:O	1:B:185:GLN:HB3	2.04	0.57
1:A:59:ASP:HA	1:A:60:ALA:O	2.04	0.57
1:B:27:SER:O	1:B:27:SER:OG	2.16	0.57
1:D:283:LYS:NZ	2:D:502:PLP:O3	2.38	0.57
1:C:387:VAL:HG11	1:C:432:LEU:HD22	1.85	0.56
1:A:46:LEU:HG	1:A:59:ASP:HB2	1.86	0.56
1:D:57:VAL:HG12	1:D:396:GLY:HA2	1.86	0.56
1:C:59:ASP:OD2	1:C:63:SER:OG	2.23	0.56
1:C:307:ALA:O	1:C:309:ALA:HB3	2.05	0.56
1:C:309:ALA:HA	1:C:310:ALA:C	2.26	0.56
1:A:362:LEU:HD11	1:A:431:ARG:HE	1.71	0.55
1:B:270:ASP:OD2	4:B:601:HOH:O	2.18	0.55
1:B:356:LEU:HD22	1:B:377:ILE:HD11	1.89	0.55
1:B:170:PRO:HD3	1:B:187:PHE:CE2	2.41	0.55
1:C:61:MET:HE2	1:C:400:ARG:HB3	1.88	0.55
1:B:17:ASP:HA	1:B:21:LEU:HD12	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:153:TRP:HD1	1:B:154:ARG:O	1.91	0.54
1:A:385:LEU:HD12	1:A:385:LEU:H	1.71	0.54
1:D:91:MET:HB2	3:D:501:3VQ:CAE	2.37	0.54
1:D:98:GLU:HB3	1:D:99:PRO:HD3	1.88	0.54
1:B:11[A]:GLU:HG2	1:B:12:GLN:N	2.23	0.53
1:B:264:GLY:HA2	1:B:345:ILE:HG21	1.89	0.53
1:B:283:LYS:NZ	2:B:502:PLP:O3	2.42	0.53
1:C:163:LEU:HD22	1:D:162:PHE:CD2	2.43	0.53
1:D:241[B]:ARG:NH1	1:D:277:ASP:OD1	2.38	0.53
1:A:40:ALA:HB1	1:B:86:VAL:O	2.09	0.53
1:D:66:THR:HB	1:D:288:GLY:HA3	1.91	0.53
1:D:140:ARG:NH2	1:D:148:ARG:HB3	2.24	0.53
1:A:389:THR:HB	1:A:390:PRO:HD3	1.91	0.53
1:B:360:ARG:HE	1:B:368:VAL:HB	1.74	0.53
1:A:41:ALA:HA	1:A:46:LEU:HA	1.91	0.52
1:A:244:CYS:HB3	1:A:249:VAL:O	2.09	0.52
1:C:87:MET:HB2	1:D:40:ALA:HA	1.90	0.52
1:D:241[A]:ARG:NH2	1:D:275:SER:H	2.07	0.52
1:C:27:SER:HB2	1:D:306:SER:HB3	1.91	0.52
1:B:139:TRP:CD2	1:B:147:LYS:HD3	2.44	0.52
1:C:30:ARG:HA	1:C:30:ARG:NE	2.25	0.52
1:C:380:ASP:OD1	1:C:381:ARG:HG2	2.09	0.52
1:C:308:GLY:C	1:C:310:ALA:HB3	2.30	0.52
1:C:150:LEU:HD23	1:C:216:ALA:HB3	1.92	0.52
1:C:81:THR:HG22	1:D:81:THR:HG22	1.91	0.51
1:D:111:THR:HG21	1:D:296:LEU:HD22	1.92	0.51
1:A:39:VAL:HG13	1:A:39:VAL:O	2.11	0.51
1:B:151:MET:HB3	1:B:217:VAL:HG22	1.91	0.51
1:B:78:GLN:NE2	1:D:395:ARG:HA	2.25	0.51
1:B:61:MET:HE3	1:B:399:LEU:HA	1.93	0.51
1:B:407:TYR:CE2	1:B:409:MET:HE3	2.46	0.51
1:D:110:ILE:HG21	1:D:337:LEU:HD11	1.92	0.51
1:D:356:LEU:HD22	1:D:377:ILE:HD11	1.93	0.51
1:A:63:SER:HB3	1:B:91:MET:N	2.26	0.51
1:B:244:CYS:HB3	1:B:249:VAL:O	2.11	0.51
1:A:97:HIS:CE1	1:A:100:ALA:HB2	2.46	0.50
1:C:238:HIS:HA	1:C:274:VAL:HG11	1.92	0.50
1:B:234:PRO:O	1:B:272:ALA:HB2	2.11	0.50
1:C:9:THR:HG22	1:C:12:GLN:OE1	2.12	0.50
1:B:407:TYR:HE2	1:B:409:MET:HE3	1.76	0.50
1:D:140:ARG:NH2	1:D:145:PRO:O	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:97:HIS:HD2	1:B:100:ALA:H	1.59	0.49
1:C:50:ARG:NH2	1:C:394:ASP:OD1	2.35	0.49
1:A:283:LYS:HE2	1:B:318:THR:OG1	2.13	0.49
1:B:395:ARG:NE	1:B:428:GLU:HG3	2.27	0.49
1:A:55:ILE:HG13	1:A:55:ILE:O	2.13	0.49
1:A:192:PRO:HG2	1:A:236:TYR:OH	2.12	0.49
1:B:125:SER:HB3	1:B:161:THR:HG23	1.94	0.49
1:C:308:GLY:HA2	1:C:309:ALA:C	2.33	0.49
1:C:162:PHE:HA	1:C:165:MET:HE2	1.93	0.49
1:B:61:MET:CE	1:B:399:LEU:HA	2.43	0.49
1:A:218:VAL:HG22	1:A:252:ILE:HB	1.94	0.49
1:A:348:LEU:O	1:A:352:LEU:HB2	2.13	0.49
1:A:428:GLU:OE2	1:A:431:ARG:NH2	2.45	0.49
1:B:98:GLU:HB3	1:B:99:PRO:HD3	1.95	0.49
1:C:111:THR:HG21	1:C:296:LEU:HD22	1.94	0.49
1:C:136:LEU:O	1:C:140:ARG:HG3	2.12	0.49
1:B:153:TRP:HZ3	1:B:240:LEU:HD11	1.77	0.49
1:C:43:GLY:O	1:C:71:HIS:N	2.43	0.49
1:C:244:CYS:HB3	1:C:249:VAL:O	2.11	0.49
1:C:359:ALA:HB2	1:C:427:VAL:HG22	1.94	0.49
1:B:158:HIS:O	1:B:164:ALA:HB1	2.12	0.49
1:B:50:ARG:NH1	1:B:394:ASP:OD1	2.46	0.49
1:A:27:SER:HB2	1:B:306:SER:HB3	1.95	0.48
1:B:149:ARG:HB2	1:B:214:LEU:HD23	1.95	0.48
1:C:253:PHE:HB2	1:C:276:PRO:HG3	1.94	0.48
1:B:380:ASP:OD1	1:B:381:ARG:HG3	2.12	0.48
1:D:92:PHE:N	3:D:501:3VQ:H3	2.18	0.48
1:A:239:ASP:O	1:A:243:ILE:HG13	2.14	0.48
1:A:348:LEU:HD11	1:A:412:TYR:HA	1.94	0.48
1:B:262:ARG:HG3	1:B:374:ILE:HD11	1.95	0.48
1:C:306:SER:HB3	1:D:27:SER:HB2	1.94	0.48
1:A:38:ALA:O	1:A:39:VAL:HB	2.12	0.48
1:C:239:ASP:O	1:C:243:ILE:HG13	2.13	0.48
1:D:149:ARG:HB2	1:D:214:LEU:HD23	1.95	0.48
1:A:58:LEU:O	1:A:60:ALA:HB3	2.13	0.48
1:A:221:PRO:HA	1:A:237:LEU:HD21	1.95	0.48
1:A:362:LEU:HD11	1:A:431:ARG:NE	2.29	0.48
1:A:20:HIS:ND1	1:B:116:ASP:O	2.37	0.48
1:A:341:TRP:O	1:A:345:ILE:HG12	2.13	0.48
1:A:258:THR:HB	1:A:268:ALA:HB2	1.96	0.47
1:A:84:LEU:HD22	1:B:80:LEU:HD23	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:43:GLY:N	1:D:71:HIS:O	2.46	0.47
1:C:163:LEU:HD22	1:D:162:PHE:CE2	2.49	0.47
1:C:289:TYR:HE2	1:D:84:LEU:HD11	1.79	0.47
1:C:257:ALA:HB2	2:C:501:PLP:O3	2.14	0.47
1:B:384:ASP:HB3	1:B:387:VAL:HG22	1.94	0.47
1:C:153:TRP:CZ3	1:C:224:GLN:HG2	2.49	0.47
1:A:17:ASP:HA	1:A:21:LEU:HD12	1.97	0.47
1:A:279:MET:N	1:A:296:LEU:O	2.45	0.47
1:C:103:LEU:HD23	1:C:120:PHE:CE2	2.50	0.47
1:A:130:VAL:O	1:A:134:MET:HG3	2.15	0.47
1:B:395:ARG:HE	1:B:428:GLU:HG3	1.79	0.47
1:A:66:THR:HB	1:A:288:GLY:HA2	1.96	0.47
1:D:369:ARG:HH12	1:D:378:GLU:HB2	1.79	0.47
1:D:389:THR:HB	1:D:390:PRO:HD3	1.96	0.47
1:C:371:CYS:O	1:C:374:ILE:HB	2.14	0.46
1:A:418:GLU:O	1:A:422:ILE:HG13	2.15	0.46
1:B:255:GLU:OE1	1:B:258:THR:OG1	2.31	0.46
1:C:66:THR:HB	1:C:288:GLY:HA2	1.98	0.46
1:B:57:VAL:HG12	1:B:396:GLY:HA2	1.97	0.46
1:C:254:ASP:OD1	2:C:501:PLP:H2A2	2.16	0.46
1:B:40:ALA:HB1	1:B:42:HIS:NE2	2.30	0.46
1:A:60:ALA:HB2	1:A:422:ILE:HD13	1.96	0.46
1:B:147:LYS:HE2	1:B:214:LEU:O	2.15	0.46
1:B:309:ALA:C	1:B:311:GLY:H	2.18	0.46
1:C:223:VAL:HB	1:C:258:THR:HG22	1.97	0.46
1:B:130:VAL:O	1:B:134:MET:HG3	2.15	0.46
1:B:221:PRO:HB2	1:B:268:ALA:HB3	1.97	0.46
1:A:138:TYR:CD1	1:A:301:VAL:HA	2.51	0.46
1:B:381:ARG:CZ	1:B:433:VAL:HG13	2.46	0.46
1:D:286:THR:HG22	1:D:329:SER:HB2	1.97	0.46
1:C:395:ARG:HG2	1:C:395:ARG:HH21	1.80	0.45
1:A:65:TRP:HB2	1:A:283:LYS:CD	2.47	0.45
1:A:162:PHE:HD2	1:B:129:GLU:OE2	1.99	0.45
1:A:61:MET:HE3	1:A:400:ARG:N	2.31	0.45
1:C:107:LEU:O	1:C:111:THR:OG1	2.12	0.45
1:D:17:ASP:HA	1:D:21:LEU:HD12	1.97	0.45
1:A:210:HIS:O	1:A:214:LEU:HG	2.17	0.45
1:B:383:VAL:HG21	1:B:406:VAL:HG23	1.98	0.45
1:A:27:SER:HB2	1:B:306:SER:CB	2.47	0.45
1:D:193:ARG:HA	1:D:232:HIS:HA	1.98	0.45
1:B:151:MET:HA	1:B:186:VAL:O	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:40:ALA:HB1	1:D:42:HIS:CE1	2.52	0.45
1:D:111:THR:HB	1:D:115:LEU:HD12	1.98	0.45
1:A:46:LEU:CG	1:A:59:ASP:HB2	2.46	0.45
1:C:154:ARG:HG3	1:C:188:ALA:O	2.17	0.45
1:C:290:LEU:HD22	1:D:290:LEU:HD22	1.99	0.45
1:A:135:ALA:O	1:A:138:TYR:HB3	2.17	0.45
1:B:187:PHE:O	1:B:206:GLN:NE2	2.48	0.45
1:B:340:ASP:OD2	1:B:343:THR:HB	2.17	0.44
1:D:92:PHE:H	3:D:501:3VQ:CAC	2.17	0.44
1:A:53:GLN:HA	1:A:54:PRO:HD3	1.72	0.44
1:A:229:MET:HB2	1:A:405:LEU:HD13	1.98	0.44
1:C:348:LEU:HD11	1:C:412:TYR:HA	1.99	0.44
1:D:151:MET:O	1:D:217:VAL:HA	2.18	0.44
1:D:397:VAL:HG21	1:D:422:ILE:HA	1.99	0.44
1:A:161:THR:O	1:A:165:MET:HG3	2.18	0.44
1:B:110:ILE:HG21	1:B:337:LEU:HD11	1.98	0.44
1:B:153:TRP:C	1:B:153:TRP:CD1	2.90	0.44
1:D:256:ILE:O	1:D:283:LYS:HB2	2.16	0.44
1:D:369:ARG:NH1	1:D:378:GLU:OE1	2.49	0.44
1:B:344:ARG:HB2	1:B:344:ARG:CZ	2.48	0.44
1:D:401:PRO:HG3	1:D:406:VAL:HG12	1.99	0.44
1:A:324:LEU:O	1:A:328:VAL:HG23	2.17	0.44
1:C:109:ASP:OD2	1:C:109:ASP:N	2.51	0.44
1:D:254:ASP:OD1	1:D:256:ILE:HD12	2.17	0.44
1:B:122:ASP:O	1:B:291:SER:OG	2.24	0.44
1:D:241[A]:ARG:HD2	1:D:245:ARG:HH22	1.83	0.44
1:B:48:LEU:O	1:B:55:ILE:HG12	2.16	0.44
1:A:21:LEU:HD22	1:B:92:PHE:HE2	1.83	0.44
1:B:108:VAL:HG22	1:B:116:ASP:HA	2.00	0.44
1:C:21:LEU:HD21	1:D:104:ALA:HB2	2.00	0.44
1:A:414:CYS:HA	1:A:418:GLU:OE1	2.18	0.43
1:A:290:LEU:HD22	1:B:290:LEU:HD22	1.99	0.43
1:A:97:HIS:NE2	1:A:321:ALA:O	2.51	0.43
1:A:340:ASP:OD2	1:A:343:THR:OG1	2.25	0.43
1:A:395:ARG:HD2	1:A:425:ALA:HA	2.00	0.43
1:C:150:LEU:HD22	1:C:218:VAL:CG2	2.49	0.43
1:A:312:ALA:HB1	1:B:26:SER:O	2.19	0.43
1:B:301:VAL:O	1:B:305:ILE:HG12	2.17	0.43
1:B:128:VAL:HG21	1:B:158:HIS:O	2.19	0.43
1:C:399:LEU:HD12	1:C:399:LEU:HA	1.83	0.43
1:B:243:ILE:O	1:B:247:TYR:HD1	2.02	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:104:ALA:HB2	1:B:21:LEU:HD21	2.00	0.43
1:C:308:GLY:O	1:C:310:ALA:HB3	2.19	0.43
1:C:402:PHE:HB3	1:C:407:TYR:CE1	2.53	0.43
1:C:403:ARG:HB3	1:C:404:ASN:H	1.67	0.43
1:A:41:ALA:HB3	1:B:87:MET:HG3	2.00	0.42
1:C:408:ALA:C	1:C:409:MET:HG3	2.36	0.42
1:D:105:LYS:HD3	1:D:105:LYS:HA	1.61	0.42
1:B:50:ARG:NH2	1:B:390:PRO:HB3	2.34	0.42
1:B:97:HIS:CD2	1:B:100:ALA:H	2.37	0.42
1:D:378:GLU:HA	1:D:405:LEU:HD23	2.00	0.42
1:A:27:SER:HB2	1:B:306:SER:OG	2.19	0.42
1:C:161:THR:O	1:C:165:MET:HG3	2.19	0.42
1:B:121:SER:O	1:B:292:LEU:HD12	2.20	0.42
1:A:147:LYS:NZ	1:A:214:LEU:O	2.39	0.42
1:C:402:PHE:HB3	1:C:407:TYR:HE1	1.83	0.42
1:D:138:TYR:CE2	1:D:142:ARG:HD3	2.54	0.42
1:A:62:SER:HB3	1:A:67:ALA:H	1.85	0.42
1:A:169:ASP:O	1:A:171:HIS:N	2.50	0.42
1:A:169:ASP:OD2	1:A:171:HIS:HB2	2.20	0.42
1:A:170:PRO:O	1:A:171:HIS:CG	2.73	0.42
1:B:126:VAL:O	1:B:130:VAL:HG23	2.20	0.42
1:B:154:ARG:O	1:B:190:GLN:OE1	2.38	0.42
1:D:65:TRP:CE2	1:D:409:MET:SD	3.12	0.42
1:B:97:HIS:NE2	1:B:100:ALA:HB2	2.35	0.42
1:D:9:THR:OG1	1:D:12:GLN:HG3	2.19	0.42
1:A:73:HIS:HA	1:A:74:PRO:HD3	1.89	0.42
1:D:73:HIS:HA	1:D:74:PRO:HD3	1.96	0.42
1:C:22:TRP:CD1	1:D:119:PHE:HB2	2.55	0.42
1:C:150:LEU:HD12	1:C:185:GLN:NE2	2.34	0.42
1:C:165:MET:HE3	1:C:182:LEU:HD21	2.02	0.42
1:C:233:ASP:HA	1:C:234:PRO:HD3	1.91	0.42
1:A:365:VAL:HG13	1:A:377:ILE:HG23	2.02	0.41
1:A:422:ILE:O	1:A:426:MET:HG3	2.19	0.41
1:D:66:THR:HB	1:D:288:GLY:CA	2.49	0.41
1:D:282:GLY:O	1:D:284:ALA:N	2.52	0.41
1:A:193:ARG:NE	1:A:194:ASP:OD1	2.53	0.41
1:C:103:LEU:HD23	1:C:120:PHE:CZ	2.55	0.41
1:A:117:THR:O	1:A:296:LEU:HA	2.19	0.41
1:D:89:HIS:HA	1:D:323:PRO:HG2	2.01	0.41
1:A:124:GLY:O	1:A:128:VAL:HG23	2.20	0.41
1:A:206:GLN:O	1:A:209:GLN:HG2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:241:ARG:HG3	1:B:245:ARG:HH12	1.85	0.41
1:C:66:THR:HB	1:C:288:GLY:CA	2.51	0.41
1:D:195:TYR:CE1	1:D:235:ARG:HG2	2.55	0.41
1:A:61:MET:O	1:A:411:PRO:HD3	2.20	0.41
1:A:170:PRO:HD3	1:A:187:PHE:CE2	2.56	0.41
1:B:306:SER:O	1:B:307:ALA:CB	2.69	0.41
1:C:191:VAL:HA	1:C:192:PRO:HD3	1.93	0.41
1:D:83:GLN:HG2	1:D:327:ALA:HB2	2.03	0.41
1:D:83:GLN:HG2	1:D:327:ALA:CB	2.50	0.41
1:D:93:GLY:H	3:D:501:3VQ:CAE	2.33	0.41
1:A:9:THR:HG22	1:A:12:GLN:OE1	2.21	0.41
1:A:98:GLU:HB3	1:A:99:PRO:HD3	2.03	0.41
1:A:107:LEU:HD23	1:A:107:LEU:HA	1.78	0.41
1:A:283:LYS:HE3	1:A:283:LYS:HB2	1.91	0.41
1:A:339:GLN:O	1:A:341:TRP:N	2.53	0.41
1:B:324:LEU:HD23	1:B:324:LEU:HA	1.94	0.41
1:C:210:HIS:O	1:C:213:GLU:HG2	2.21	0.41
1:C:315:HIS:HD2	1:C:317:PRO:HD3	1.86	0.41
1:D:252:ILE:HG12	1:D:278:ILE:HB	2.03	0.41
1:A:77:ASP:OD2	1:A:289:TYR:OH	2.30	0.41
1:B:221:PRO:HG3	1:B:253:PHE:CG	2.56	0.41
1:C:389:THR:OG1	1:C:390:PRO:HD3	2.21	0.41
1:B:223:VAL:HG22	1:B:231:PHE:CD2	2.56	0.40
1:D:110:ILE:HG13	1:D:267:PHE:HE1	1.86	0.40
1:A:46:LEU:HB2	1:A:48:LEU:HD21	2.03	0.40
1:A:367:ASP:OD1	1:A:368:VAL:N	2.54	0.40
1:C:322:ASN:HA	1:C:323:PRO:HD3	1.97	0.40
1:A:127:SER:HB3	1:A:293:ALA:HB1	2.03	0.40
1:C:63:SER:O	1:C:66:THR:OG1	2.33	0.40

All (2) 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)
4:C:620:HOH:O	4:D:622:HOH:O[1_565]	2.11	0.09
1:C:209:GLN:NE2	1:D:141:GLY:O[2_655]	2.19	0.01

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	414/457 (91%)	374 (90%)	32 (8%)	8 (2%)	8 13
1	B	415/457 (91%)	385 (93%)	21 (5%)	9 (2%)	6 10
1	C	413/457 (90%)	376 (91%)	31 (8%)	6 (2%)	10 18
1	D	409/457 (90%)	373 (91%)	30 (7%)	6 (2%)	10 18
All	All	1651/1828 (90%)	1508 (91%)	114 (7%)	29 (2%)	8 14

All (29) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	39	VAL
1	B	283	LYS
1	D	283	LYS
1	A	41	ALA
1	A	283	LYS
1	B	307	ALA
1	D	166	SER
1	D	268	ALA
1	A	61	MET
1	A	306	SER
1	D	170	PRO
1	A	31	GLU
1	B	59	ASP
1	C	171	HIS
1	D	115	LEU
1	A	225	GLY
1	B	78	GLN
1	B	176	SER
1	B	228	GLY
1	B	305	ILE
1	C	310	ALA
1	C	316	GLY

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Mol	Chain	Res	Type
1	D	222	VAL
1	A	171	HIS
1	B	28	ILE
1	B	310	ALA
1	C	282	GLY
1	C	401	PRO
1	C	170	PRO

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	315/346 (91%)	307 (98%)	8 (2%)	47	73
1	B	316/346 (91%)	306 (97%)	10 (3%)	39	65
1	C	316/346 (91%)	306 (97%)	10 (3%)	39	65
1	D	313/346 (90%)	305 (97%)	8 (3%)	46	72
All	All	1260/1384 (91%)	1224 (97%)	36 (3%)	44	69

All (36) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	30	ARG
1	A	50	ARG
1	A	61	MET
1	A	92	PHE
1	A	122	ASP
1	A	179	THR
1	A	432	LEU
1	A	433	VAL
1	B	11[A]	GLU
1	B	11[B]	GLU
1	B	36	VAL
1	B	92	PHE
1	B	127	SER
1	B	166	SER

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Mol	Chain	Res	Type
1	B	306	SER
1	B	381	ARG
1	B	393	LEU
1	B	409	MET
1	C	30	ARG
1	C	34	SER
1	C	74	PRO
1	C	86	VAL
1	C	92	PHE
1	C	121	SER
1	C	235	ARG
1	C	389	THR
1	C	395	ARG
1	C	409	MET
1	D	58	LEU
1	D	111	THR
1	D	116	ASP
1	D	153	TRP
1	D	170	PRO
1	D	194	ASP
1	D	241[A]	ARG
1	D	241[B]	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	78	GLN
1	B	303	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

6 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	$\#\|Z\| > 2$
2	PLP	C	501	1	15,15,16	2.70	3 (20%)	20,22,23	1.71	6 (30%)
3	3VQ	B	501	-	12,15,15	2.11	2 (16%)	11,20,20	1.56	2 (18%)
2	PLP	B	502	1	15,15,16	3.10	3 (20%)	20,22,23	1.59	1 (5%)
2	PLP	D	502	1	15,15,16	2.98	3 (20%)	20,22,23	1.92	5 (25%)
3	3VQ	D	501	-	12,15,15	2.39	1 (8%)	11,20,20	0.97	1 (9%)
2	PLP	A	501	1	15,15,16	3.26	3 (20%)	20,22,23	1.89	6 (30%)

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	C	501	1	-	0/6/6/8	0/1/1/1
3	3VQ	B	501	-	-	0/2/8/8	0/2/2/2
2	PLP	B	502	1	-	0/6/6/8	0/1/1/1
2	PLP	D	502	1	-	3/6/6/8	0/1/1/1
3	3VQ	D	501	-	-	0/2/8/8	0/2/2/2
2	PLP	A	501	1	-	5/6/6/8	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	C5-C4	8.94	1.50	1.40
2	D	502	PLP	C5-C4	8.20	1.49	1.40
2	B	502	PLP	C3-C2	7.81	1.48	1.40
2	B	502	PLP	C5-C4	7.80	1.49	1.40
3	D	501	3VQ	CAL-CAN	-7.72	1.31	1.49
2	A	501	PLP	C3-C2	7.64	1.48	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	501	PLP	C5-C4	7.10	1.48	1.40
2	D	502	PLP	C3-C2	6.76	1.47	1.40
3	B	501	3VQ	CAL-CAN	-6.53	1.34	1.49
2	C	501	PLP	C3-C2	6.36	1.47	1.40
2	A	501	PLP	C3-C4	4.06	1.48	1.40
2	B	502	PLP	C3-C4	3.89	1.48	1.40
2	C	501	PLP	C3-C4	3.49	1.47	1.40
2	D	502	PLP	C3-C4	3.38	1.47	1.40
3	B	501	3VQ	CAE-NAI	2.59	1.40	1.34

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	D	502	PLP	C4A-C4-C5	5.44	126.54	120.94
2	A	501	PLP	C4A-C4-C5	4.71	125.78	120.94
2	B	502	PLP	C4A-C4-C5	4.34	125.41	120.94
2	C	501	PLP	C4A-C4-C5	3.50	124.54	120.94
3	B	501	3VQ	CAC-CAE-NAI	-3.02	118.49	123.43
3	B	501	3VQ	CAE-NAI-CAL	2.96	121.38	117.23
2	A	501	PLP	O4P-C5A-C5	2.78	114.64	109.35
2	D	502	PLP	O4P-C5A-C5	2.74	114.56	109.35
2	C	501	PLP	C2A-C2-N1	2.71	122.97	117.67
2	C	501	PLP	C2A-C2-C3	-2.70	117.56	120.89
2	A	501	PLP	C5A-C5-C6	-2.59	115.11	119.37
2	A	501	PLP	C6-N1-C2	2.51	123.81	119.17
2	C	501	PLP	C6-N1-C2	2.46	123.73	119.17
2	C	501	PLP	O3P-P-O2P	2.43	116.94	107.64
2	D	502	PLP	C2A-C2-C3	-2.43	117.89	120.89
2	D	502	PLP	C2A-C2-N1	2.43	122.41	117.67
2	A	501	PLP	C3-C4-C5	-2.34	116.21	118.74
2	D	502	PLP	C4A-C4-C3	-2.20	116.77	120.50
2	A	501	PLP	O2P-P-O4P	-2.14	101.03	106.73
3	D	501	3VQ	CAC-CAE-NAI	-2.06	120.07	123.43
2	C	501	PLP	O3P-P-O4P	-2.01	101.37	106.73

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	PLP	C4-C5-C5A-O4P
2	A	501	PLP	C6-C5-C5A-O4P
2	A	501	PLP	C5A-O4P-P-O1P

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Mol	Chain	Res	Type	Atoms
2	A	501	PLP	C5A-O4P-P-O2P
2	A	501	PLP	C5A-O4P-P-O3P
2	D	502	PLP	C4-C5-C5A-O4P
2	D	502	PLP	C6-C5-C5A-O4P
2	D	502	PLP	C5A-O4P-P-O2P

There are no ring outliers.

4 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	501	PLP	2	0
2	B	502	PLP	1	0
2	D	502	PLP	1	0
3	D	501	3VQ	8	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 (i)

6.1 Protein, DNA and RNA chains (i)

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	420/457 (91%)	-0.22	2 (0%)	91	91	30, 44, 60, 73	1 (0%)
1	B	422/457 (92%)	-0.21	3 (0%)	87	89	31, 43, 54, 70	1 (0%)
1	C	419/457 (91%)	-0.27	3 (0%)	87	89	29, 41, 59, 74	0
1	D	414/457 (90%)	-0.31	3 (0%)	87	89	26, 41, 52, 67	0
All	All	1675/1828 (91%)	-0.25	11 (0%)	87	89	26, 42, 57, 74	2 (0%)

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	432	LEU	4.1
1	D	37	VAL	3.2
1	A	237	LEU	3.1
1	B	7	GLY	2.7
1	B	119	PHE	2.6
1	C	261	GLY	2.6
1	A	203	PHE	2.4
1	B	427	VAL	2.3
1	D	119	PHE	2.1
1	C	186	VAL	2.1
1	D	20	HIS	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 monosaccharides 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	3VQ	B	501	14/14	0.94	0.12	36,44,52,52	0
2	PLP	D	502	15/16	0.96	0.13	28,31,38,39	0
2	PLP	A	501	15/16	0.96	0.09	32,37,42,42	0
2	PLP	B	502	15/16	0.97	0.09	27,34,37,39	0
3	3VQ	D	501	14/14	0.97	0.10	38,45,52,56	0
2	PLP	C	501	15/16	0.98	0.10	28,31,38,40	0

6.5 Other polymers (i)

There are no such residues in this entry.