Full wwPDB X-ray Structure Validation Report (i)

Oct 23, 2021 – 03:36 PM EDT

PDB ID	:	1QU4
Title	:	CRYSTAL STRUCTURE OF TRYPANOSOMA BRUCEI ORNITHINE DECARBOXYLASE
Authors	:	Grishin, N.V.; Osterman, A.L.; Brooks, H.B.; Phillips, M.A.; Goldsmith, E.J.
Deposited on	:	1999-07-06
Resolution	:	2.90 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 following versions of software and data (see references (i)) were used in the production of this report:

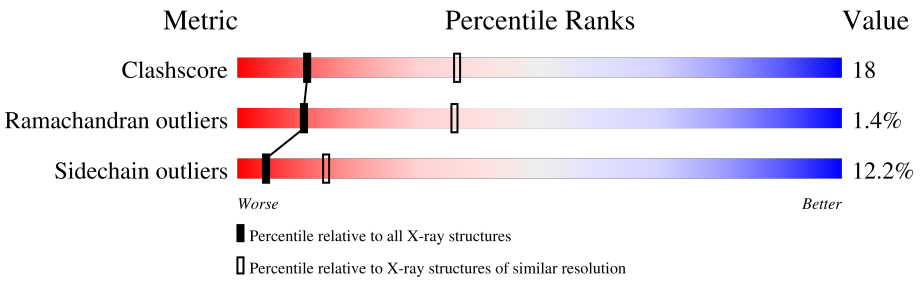
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.23.2

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 2.90 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))
Clashscore	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)

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%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	425	50% 25% 8% • 16%
1	B	425	48% 27% 8% • 16%
1	C	425	52% 24% 6% • 16%
1	D	425	50% 26% 7% • 16%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 11176 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.

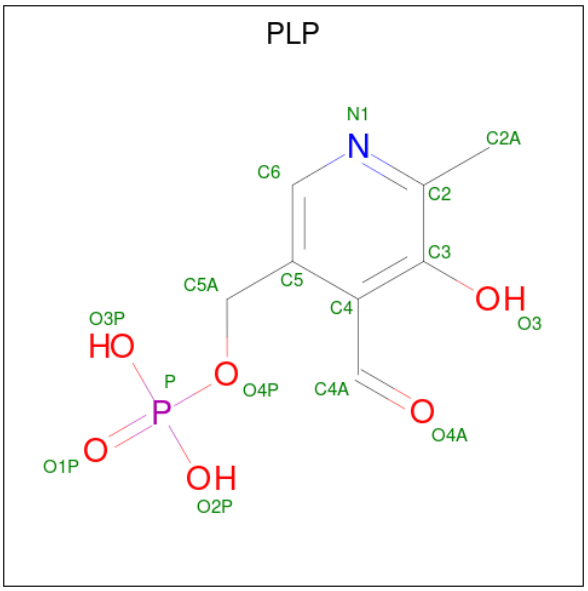
- Molecule 1 is a protein called ORNITHINE DECARBOXYLASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	356	2779	1786	460	518	15	0	0	0
1	B	356	2779	1786	460	518	15	0	0	0
1	C	356	2779	1786	460	518	15	0	0	0
1	D	356	2779	1786	460	518	15	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	LYS	engineered mutation	UNP P07805
A	2	ALA	SER	engineered mutation	UNP P07805
B	1	GLY	LYS	engineered mutation	UNP P07805
B	2	ALA	SER	engineered mutation	UNP P07805
C	1	GLY	LYS	engineered mutation	UNP P07805
C	2	ALA	SER	engineered mutation	UNP P07805
D	1	GLY	LYS	engineered mutation	UNP P07805
D	2	ALA	SER	engineered mutation	UNP P07805

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



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		
2	C	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
2	D	1	Total	C	N	O	P	0	0
			15	8	1	5	1		

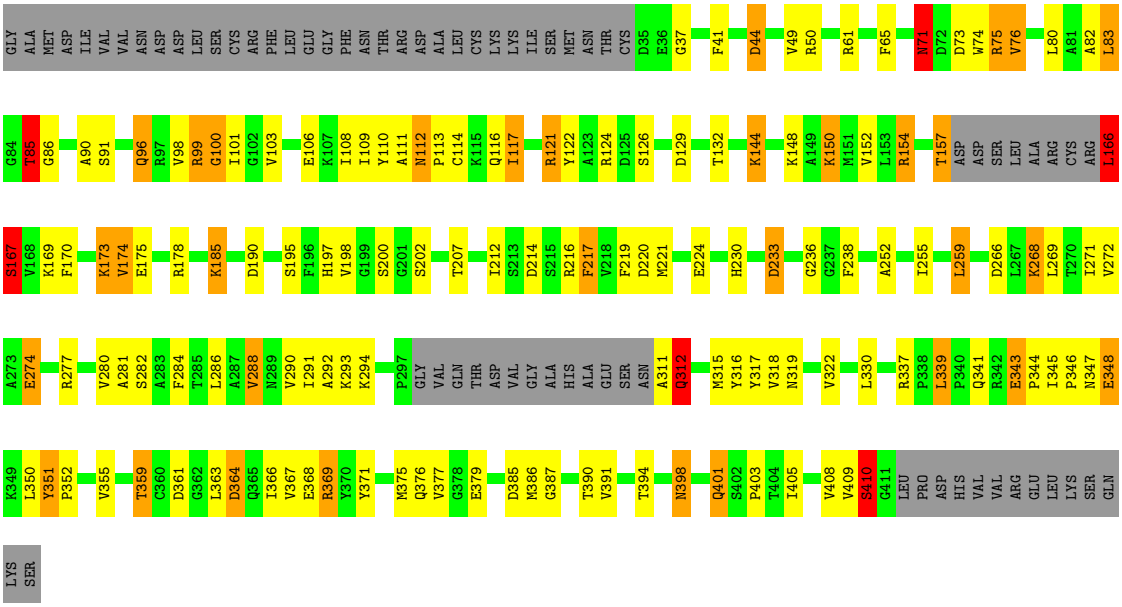
3 Residue-property plots (i)

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. 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. 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.

Note EDS was not executed.

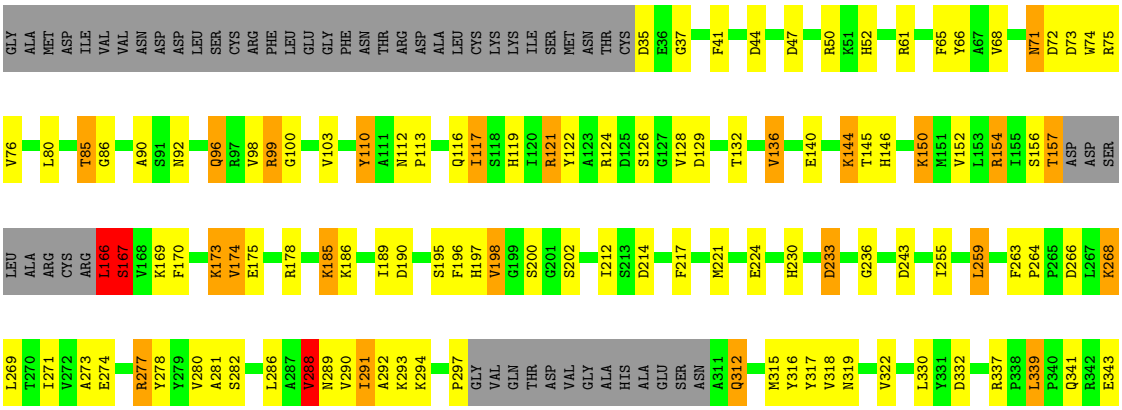
• Molecule 1: ORNITHINE DECARBOXYLASE

Chain A: 50% 25% 8% • 16%



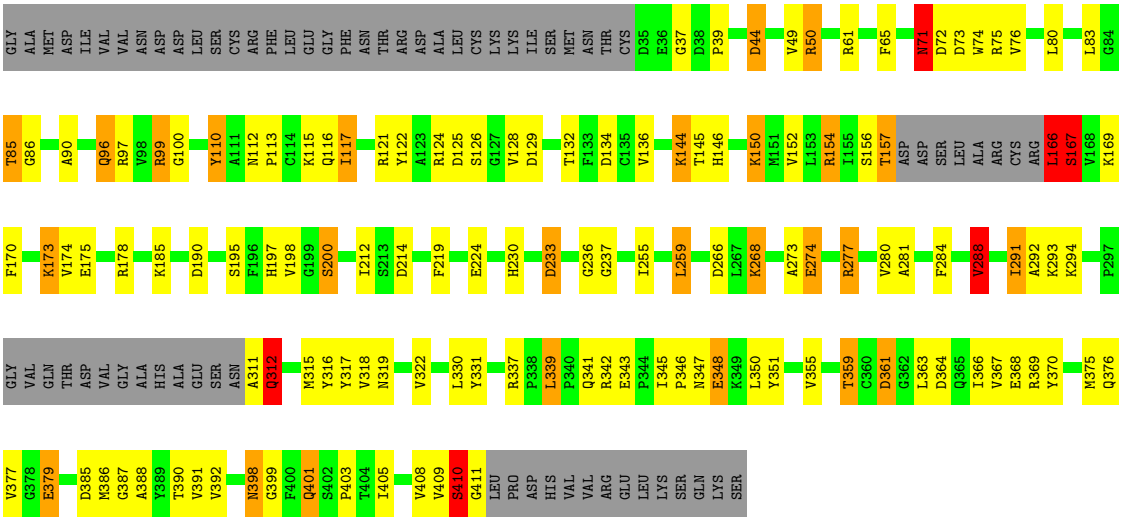
• Molecule 1: ORNITHINE DECARBOXYLASE

Chain B: 48% 27% 8% • 16%



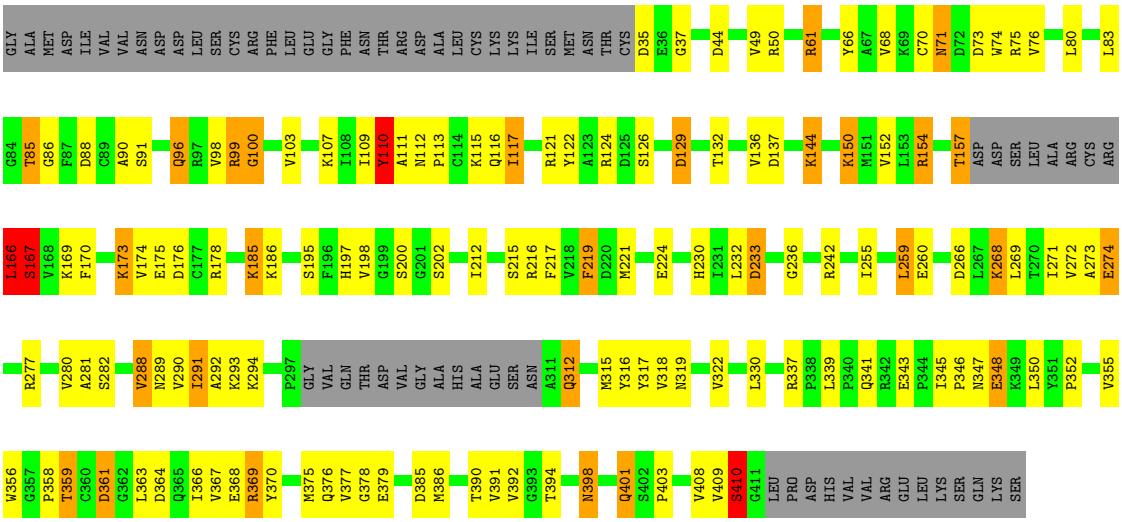
• Molecule 1: ORNITHINE DECARBOXYLASE

Chain C: 52% 24% 6% • 16%



• Molecule 1: ORNITHINE DECARBOXYLASE

Chain D: 50% 26% 7% • 16%



4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	66.80Å 151.70Å 85.35Å 90.00° 102.30° 90.00°	Depositor
Resolution (Å)	20.00 – 2.90	Depositor
% Data completeness (in resolution range)	(Not available) (20.00-2.90)	Depositor
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	REFMAC	Depositor
R, R_{free}	0.245 , 0.268	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	11176	wwPDB-VP
Average B, all atoms (Å^2)	30.0	wwPDB-VP

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: 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	0.66	0/2848	1.63	42/3867 (1.1%)
1	B	0.67	0/2848	1.66	43/3867 (1.1%)
1	C	0.67	0/2848	1.59	35/3867 (0.9%)
1	D	0.67	0/2848	1.60	31/3867 (0.8%)
All	All	0.67	0/11392	1.62	151/15468 (1.0%)

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
1	B	0	1
1	C	0	1
1	D	0	1
All	All	0	4

There are no bond length outliers.

All (151) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	216	ARG	NE-CZ-NH1	16.85	128.72	120.30
1	B	154	ARG	NE-CZ-NH1	-15.09	112.76	120.30
1	D	154	ARG	NE-CZ-NH1	-15.02	112.79	120.30
1	B	277	ARG	NE-CZ-NH1	13.95	127.28	120.30
1	B	99	ARG	NE-CZ-NH2	-13.20	113.70	120.30
1	C	154	ARG	NE-CZ-NH1	-13.05	113.77	120.30
1	C	277	ARG	NE-CZ-NH1	11.46	126.03	120.30
1	D	99	ARG	NE-CZ-NH2	-11.08	114.76	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	190	ASP	CB-CG-OD2	-10.96	108.43	118.30
1	D	154	ARG	NE-CZ-NH2	10.77	125.68	120.30
1	D	99	ARG	NE-CZ-NH1	10.65	125.63	120.30
1	C	61	ARG	NE-CZ-NH2	-10.62	114.99	120.30
1	B	277	ARG	NE-CZ-NH2	-10.47	115.07	120.30
1	C	277	ARG	NE-CZ-NH2	-10.16	115.22	120.30
1	B	124	ARG	NE-CZ-NH1	9.56	125.08	120.30
1	D	277	ARG	NE-CZ-NH1	8.86	124.73	120.30
1	C	266	ASP	CB-CG-OD2	-8.77	110.41	118.30
1	A	124	ARG	NE-CZ-NH2	-8.76	115.92	120.30
1	A	99	ARG	NE-CZ-NH2	-8.71	115.94	120.30
1	D	61	ARG	NE-CZ-NH2	-8.57	116.01	120.30
1	B	233	ASP	CB-CG-OD1	8.50	125.95	118.30
1	C	99	ARG	NE-CZ-NH2	-8.41	116.09	120.30
1	B	371	TYR	CB-CG-CD2	-8.35	115.99	121.00
1	B	369	ARG	NE-CZ-NH2	-8.29	116.15	120.30
1	B	61	ARG	NE-CZ-NH2	-8.27	116.17	120.30
1	D	124	ARG	NE-CZ-NH1	8.05	124.33	120.30
1	A	61	ARG	NE-CZ-NH1	8.02	124.31	120.30
1	B	190	ASP	CB-CG-OD2	-8.02	111.08	118.30
1	A	44	ASP	CB-CG-OD1	7.98	125.48	118.30
1	B	110	TYR	CB-CG-CD1	7.90	125.74	121.00
1	D	216	ARG	NE-CZ-NH1	7.83	124.21	120.30
1	C	342	ARG	NE-CZ-NH2	-7.72	116.44	120.30
1	D	266	ASP	CB-CG-OD2	-7.68	111.39	118.30
1	B	121	ARG	NE-CZ-NH2	-7.44	116.58	120.30
1	B	266	ASP	CB-CG-OD2	-7.39	111.65	118.30
1	C	190	ASP	CB-CG-OD2	-7.26	111.76	118.30
1	A	44	ASP	CB-CG-OD2	-7.24	111.79	118.30
1	D	176	ASP	CB-CG-OD2	7.19	124.77	118.30
1	A	124	ARG	NE-CZ-NH1	7.11	123.85	120.30
1	A	154	ARG	NE-CZ-NH1	-7.10	116.75	120.30
1	A	220	ASP	CB-CG-OD2	-7.09	111.92	118.30
1	D	277	ARG	CD-NE-CZ	7.06	133.48	123.60
1	A	75	ARG	NE-CZ-NH1	7.04	123.82	120.30
1	B	273	ALA	N-CA-CB	7.02	119.92	110.10
1	D	110	TYR	CB-CG-CD1	7.02	125.21	121.00
1	C	44	ASP	CB-CG-OD1	6.99	124.59	118.30
1	D	96	GLN	CA-CB-CG	6.96	128.70	113.40
1	A	288	VAL	N-CA-CB	-6.95	96.20	111.50
1	B	364	ASP	CB-CG-OD1	6.93	124.54	118.30
1	A	214	ASP	CB-CG-OD1	6.88	124.49	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	288	VAL	N-CA-CB	-6.78	96.59	111.50
1	B	154	ARG	CD-NE-CZ	-6.76	114.14	123.60
1	A	277	ARG	NE-CZ-NH2	-6.75	116.92	120.30
1	A	121	ARG	NE-CZ-NH2	-6.73	116.94	120.30
1	A	96	GLN	CA-CB-CG	6.63	127.98	113.40
1	C	124	ARG	CD-NE-CZ	6.62	132.87	123.60
1	A	233	ASP	CB-CG-OD1	6.61	124.25	118.30
1	C	233	ASP	CB-CG-OD1	6.54	124.19	118.30
1	C	50	ARG	NE-CZ-NH2	-6.52	117.04	120.30
1	B	389	TYR	CG-CD2-CE2	6.42	126.44	121.30
1	A	371	TYR	CB-CG-CD2	-6.29	117.23	121.00
1	D	233	ASP	CB-CG-OD1	6.28	123.95	118.30
1	A	124	ARG	CD-NE-CZ	6.25	132.35	123.60
1	A	216	ARG	NE-CZ-NH2	-6.23	117.18	120.30
1	B	196	PHE	CB-CG-CD2	-6.22	116.44	120.80
1	C	72	ASP	CB-CG-OD1	-6.22	112.70	118.30
1	D	99	ARG	CD-NE-CZ	-6.18	114.94	123.60
1	A	252	ALA	N-CA-CB	6.17	118.73	110.10
1	C	233	ASP	CB-CG-OD2	-6.15	112.76	118.30
1	D	288	VAL	N-CA-CB	-6.11	98.07	111.50
1	C	214	ASP	CB-CG-OD1	6.07	123.77	118.30
1	B	96	GLN	CA-CB-CG	6.04	126.68	113.40
1	D	107	LYS	CB-CG-CD	6.01	127.23	111.60
1	A	361	ASP	CB-CG-OD2	-5.94	112.95	118.30
1	A	190	ASP	CB-CG-OD1	5.92	123.63	118.30
1	D	167	SER	CA-C-O	5.91	132.51	120.10
1	B	166	LEU	CA-CB-CG	5.88	128.82	115.30
1	A	233	ASP	CB-CG-OD2	-5.86	113.03	118.30
1	B	389	TYR	CB-CG-CD1	5.83	124.50	121.00
1	B	368	GLU	OE1-CD-OE2	-5.83	116.31	123.30
1	A	277	ARG	NE-CZ-NH1	5.83	123.21	120.30
1	B	72	ASP	CB-CG-OD2	5.82	123.54	118.30
1	B	278	TYR	CB-CG-CD2	-5.76	117.54	121.00
1	D	274	GLU	OE1-CD-OE2	-5.75	116.41	123.30
1	A	207	THR	CA-CB-CG2	-5.72	104.39	112.40
1	A	272	VAL	N-CA-CB	-5.70	98.95	111.50
1	A	274	GLU	OE1-CD-OE2	-5.69	116.48	123.30
1	D	100	GLY	CA-C-O	-5.67	110.40	120.60
1	B	233	ASP	CB-CG-OD2	-5.64	113.22	118.30
1	B	99	ARG	CD-NE-CZ	-5.61	115.74	123.60
1	A	166	LEU	CA-CB-CG	5.60	128.19	115.30
1	A	217	PHE	CD1-CE1-CZ	5.60	126.82	120.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	166	LEU	CA-CB-CG	5.59	128.16	115.30
1	A	371	TYR	CA-CB-CG	-5.58	102.80	113.40
1	B	371	TYR	CA-CB-CG	-5.56	102.83	113.40
1	B	167	SER	CA-C-O	5.56	131.78	120.10
1	A	167	SER	CA-C-O	5.55	131.75	120.10
1	A	148	LYS	CA-CB-CG	5.52	125.54	113.40
1	D	166	LEU	CA-CB-CG	5.50	127.96	115.30
1	C	96	GLN	CA-CB-CG	5.50	125.51	113.40
1	B	72	ASP	CB-CG-OD1	-5.49	113.36	118.30
1	C	379	GLU	O-C-N	-5.49	113.92	122.70
1	B	371	TYR	CB-CG-CD1	5.49	124.29	121.00
1	D	219	PHE	CB-CG-CD1	-5.48	116.96	120.80
1	A	364	ASP	CB-CG-OD2	-5.47	113.38	118.30
1	D	124	ARG	CD-NE-CZ	5.47	131.26	123.60
1	A	339	LEU	CA-CB-CG	5.46	127.85	115.30
1	B	288	VAL	N-CA-CB	-5.46	99.50	111.50
1	C	266	ASP	O-C-N	-5.43	114.01	122.70
1	A	106	GLU	OE1-CD-OE2	5.39	129.77	123.30
1	D	392	VAL	CG1-CB-CG2	5.39	119.53	110.90
1	D	129	ASP	CB-CG-OD1	5.39	123.15	118.30
1	C	266	ASP	CB-CG-OD1	5.39	123.15	118.30
1	C	97	ARG	NE-CZ-NH2	-5.37	117.61	120.30
1	B	364	ASP	CB-CG-OD2	-5.37	113.47	118.30
1	A	85	THR	N-CA-CB	-5.36	100.12	110.30
1	C	331	TYR	CA-CB-CG	5.35	123.57	113.40
1	B	368	GLU	N-CA-CB	5.33	120.20	110.60
1	C	110	TYR	CB-CG-CD1	5.33	124.20	121.00
1	C	273	ALA	N-CA-CB	5.32	117.55	110.10
1	B	52	HIS	CA-CB-CG	-5.30	104.59	113.60
1	C	110	TYR	CB-CG-CD2	-5.29	117.83	121.00
1	D	219	PHE	CB-CG-CD2	5.25	124.48	120.80
1	B	121	ARG	NE-CZ-NH1	5.24	122.92	120.30
1	A	272	VAL	CB-CA-C	5.23	121.34	111.40
1	C	361	ASP	CB-CG-OD2	-5.23	113.59	118.30
1	B	266	ASP	N-CA-CB	-5.22	101.20	110.60
1	C	61	ARG	NE-CZ-NH1	5.20	122.90	120.30
1	C	167	SER	CA-C-O	5.17	130.96	120.10
1	D	273	ALA	N-CA-CB	5.17	117.34	110.10
1	C	154	ARG	NE-CZ-NH2	5.16	122.88	120.30
1	B	47	ASP	CB-CG-OD2	5.15	122.94	118.30
1	B	99	ARG	NH1-CZ-NH2	5.14	125.06	119.40
1	B	214	ASP	CB-CG-OD1	5.14	122.93	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	385	ASP	CB-CG-OD1	-5.14	113.68	118.30
1	B	154	ARG	NE-CZ-NH2	5.13	122.86	120.30
1	A	369	ARG	NE-CZ-NH2	-5.12	117.74	120.30
1	B	339	LEU	CA-CB-CG	5.10	127.03	115.30
1	B	332	ASP	CB-CG-OD2	5.10	122.89	118.30
1	A	220	ASP	CB-CG-OD1	5.09	122.88	118.30
1	C	274	GLU	OE1-CD-OE2	-5.09	117.19	123.30
1	B	198	VAL	CA-CB-CG2	-5.08	103.28	110.90
1	C	339	LEU	CA-CB-CG	5.07	126.97	115.30
1	D	266	ASP	N-CA-CB	-5.07	101.47	110.60
1	D	70	CYS	CA-CB-SG	-5.07	104.87	114.00
1	A	82	ALA	CB-CA-C	-5.06	102.51	110.10
1	A	266	ASP	O-C-N	-5.04	114.64	122.70
1	C	342	ARG	NE-CZ-NH1	5.04	122.82	120.30
1	C	125	ASP	CB-CG-OD2	5.04	122.83	118.30
1	D	369	ARG	NE-CZ-NH2	-5.02	117.79	120.30
1	D	361	ASP	CB-CG-OD2	-5.00	113.80	118.30

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	167	SER	Peptide
1	B	167	SER	Peptide
1	C	167	SER	Peptide
1	D	167	SER	Peptide

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	2779	0	2729	101	0
1	B	2779	0	2729	112	0
1	C	2779	0	2729	102	0
1	D	2779	0	2729	106	0
2	A	15	0	7	1	0
2	B	15	0	7	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	15	0	7	1	0
2	D	15	0	7	1	0
All	All	11176	0	10944	389	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 18.

All (389) 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:166:LEU:HD13	1:A:167:SER:H	1.22	1.04
1:C:166:LEU:HD13	1:C:167:SER:H	1.20	1.03
1:A:366:ILE:HG22	1:A:367:VAL:HG23	1.42	1.01
1:D:166:LEU:HD13	1:D:167:SER:H	1.24	0.98
1:D:366:ILE:HG22	1:D:367:VAL:HG23	1.42	0.98
1:B:166:LEU:HD13	1:B:167:SER:H	1.25	0.96
1:B:366:ILE:HG22	1:B:367:VAL:HG23	1.47	0.95
1:A:319:ASN:HD22	1:B:116:GLN:NE2	1.64	0.94
1:C:366:ILE:HG22	1:C:367:VAL:HG23	1.49	0.94
1:A:319:ASN:HD22	1:B:116:GLN:HE22	1.14	0.93
1:C:319:ASN:HD22	1:D:116:GLN:NE2	1.66	0.92
1:C:319:ASN:HD22	1:D:116:GLN:HE22	1.14	0.91
1:A:116:GLN:NE2	1:B:319:ASN:HD22	1.67	0.91
1:C:116:GLN:NE2	1:D:319:ASN:HD22	1.70	0.88
1:A:116:GLN:HE22	1:B:319:ASN:HD22	1.21	0.87
1:C:116:GLN:HE22	1:D:319:ASN:HD22	1.19	0.87
1:A:173:LYS:HZ1	1:A:174:VAL:H	1.21	0.86
1:B:288:VAL:HG13	1:B:318:VAL:HB	1.57	0.85
1:D:117:ILE:HD11	1:D:121:ARG:NH2	1.92	0.85
1:D:73:ASP:HB3	1:D:76:VAL:HG13	1.60	0.83
1:A:73:ASP:HB3	1:A:76:VAL:HG13	1.61	0.82
1:A:359:THR:HB	1:A:364:ASP:OD2	1.79	0.82
1:D:288:VAL:HG13	1:D:318:VAL:HB	1.62	0.81
1:B:292:ALA:HB3	1:B:317:TYR:HB2	1.60	0.81
1:C:359:THR:HB	1:C:364:ASP:OD2	1.80	0.81
1:A:117:ILE:HD11	1:A:121:ARG:NH2	1.94	0.81
1:C:173:LYS:HZ1	1:C:174:VAL:H	1.28	0.81
1:A:288:VAL:HG13	1:A:318:VAL:HB	1.61	0.81
1:A:173:LYS:HE3	1:A:175:GLU:OE2	1.83	0.79
1:B:359:THR:HB	1:B:364:ASP:OD2	1.83	0.78
1:A:292:ALA:HB3	1:A:317:TYR:HB2	1.64	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:117:ILE:HD11	1:B:121:ARG:NH2	1.99	0.78
1:C:288:VAL:HG13	1:C:318:VAL:HB	1.66	0.78
1:B:73:ASP:HB3	1:B:76:VAL:HG13	1.66	0.77
1:D:359:THR:HB	1:D:364:ASP:OD2	1.85	0.77
1:C:73:ASP:HB3	1:C:76:VAL:HG13	1.66	0.77
1:B:113:PRO:HG2	1:B:170:PHE:CD2	2.21	0.76
1:C:157:THR:H	1:C:166:LEU:HD11	1.53	0.73
1:D:173:LYS:HE3	1:D:175:GLU:OE2	1.88	0.73
1:A:113:PRO:HG2	1:A:170:PHE:CD2	2.23	0.72
1:A:294:LYS:HB2	1:A:315:MET:HB2	1.73	0.70
1:C:292:ALA:HB3	1:C:317:TYR:HB2	1.72	0.70
1:A:166:LEU:CD1	1:A:167:SER:H	2.03	0.70
1:B:173:LYS:HE3	1:B:175:GLU:OE2	1.92	0.69
1:B:293:LYS:HE2	1:B:375:MET:O	1.92	0.69
1:C:166:LEU:HD13	1:C:167:SER:N	2.02	0.69
1:D:113:PRO:HG2	1:D:170:PHE:CD2	2.28	0.69
1:A:166:LEU:HD13	1:A:167:SER:N	2.04	0.68
1:D:157:THR:H	1:D:166:LEU:HD11	1.57	0.68
1:C:117:ILE:HD11	1:C:121:ARG:NH2	2.08	0.68
1:D:293:LYS:HE2	1:D:375:MET:O	1.94	0.68
1:A:157:THR:H	1:A:166:LEU:HD11	1.59	0.67
1:A:293:LYS:HE2	1:A:375:MET:O	1.95	0.67
1:D:157:THR:HG21	1:D:198:VAL:HA	1.77	0.67
1:B:157:THR:H	1:B:166:LEU:HD11	1.58	0.67
1:B:132:THR:HG22	1:B:152:VAL:HB	1.78	0.66
1:B:167:SER:HB2	1:B:169:LYS:H	1.60	0.66
1:C:346:PRO:O	1:C:347:ASN:HB2	1.95	0.66
1:D:132:THR:HG22	1:D:152:VAL:HB	1.77	0.66
1:D:255:ILE:HG22	1:D:259:LEU:HD22	1.78	0.66
1:C:173:LYS:NZ	1:C:174:VAL:H	1.93	0.66
1:C:294:LYS:HB2	1:C:315:MET:HB2	1.79	0.65
1:A:346:PRO:O	1:A:347:ASN:HB2	1.96	0.65
1:A:71:ASN:C	1:A:71:ASN:HD22	2.00	0.64
1:D:292:ALA:HB3	1:D:317:TYR:HB2	1.78	0.64
1:B:173:LYS:HZ1	1:B:174:VAL:H	1.45	0.64
1:C:175:GLU:CD	1:C:175:GLU:H	2.01	0.64
1:A:132:THR:HG22	1:A:152:VAL:HB	1.80	0.64
1:D:173:LYS:HZ1	1:D:174:VAL:H	1.46	0.64
1:C:293:LYS:HE2	1:C:375:MET:O	1.98	0.63
1:D:85:THR:HG23	1:D:86:GLY:O	1.98	0.63
1:B:157:THR:HG21	1:B:198:VAL:HA	1.81	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:117:ILE:HD12	1:A:117:ILE:O	1.98	0.63
1:D:348:GLU:HG2	1:D:350:LEU:HD13	1.80	0.63
1:C:113:PRO:HG2	1:C:170:PHE:CD2	2.34	0.63
1:C:85:THR:HG23	1:C:86:GLY:O	1.99	0.63
1:C:255:ILE:HG22	1:C:259:LEU:HD22	1.78	0.62
1:A:348:GLU:HG2	1:A:350:LEU:HD13	1.81	0.62
1:B:386:MET:HE3	1:B:390:THR:HG21	1.82	0.62
1:D:197:HIS:CD2	1:D:236:GLY:H	2.17	0.62
1:A:157:THR:HG21	1:A:198:VAL:HA	1.81	0.62
1:D:212:ILE:HD13	1:D:259:LEU:HD13	1.81	0.62
1:B:230:HIS:HB2	1:B:268:LYS:O	1.99	0.62
1:B:71:ASN:C	1:B:71:ASN:HD22	2.03	0.62
1:D:80:LEU:HB3	1:D:85:THR:HG21	1.81	0.62
1:A:316:TYR:CE2	1:A:375:MET:HB2	2.35	0.61
1:B:294:LYS:HB2	1:B:315:MET:HB2	1.82	0.61
1:D:166:LEU:HD13	1:D:167:SER:N	2.07	0.61
1:B:173:LYS:NZ	1:B:174:VAL:H	1.99	0.61
1:D:346:PRO:O	1:D:347:ASN:HB2	2.00	0.61
1:A:80:LEU:HB3	1:A:85:THR:HG21	1.81	0.61
1:C:167:SER:HB2	1:C:169:LYS:H	1.65	0.61
1:C:212:ILE:HD13	1:C:259:LEU:HD13	1.82	0.61
1:B:269:LEU:HD21	1:B:271:ILE:HD11	1.81	0.60
1:B:288:VAL:CG1	1:B:318:VAL:HB	2.29	0.60
1:C:132:THR:HG22	1:C:152:VAL:HB	1.83	0.60
1:C:167:SER:HB2	1:C:169:LYS:N	2.16	0.60
1:D:175:GLU:CD	1:D:175:GLU:H	2.05	0.60
1:A:212:ILE:HD13	1:A:259:LEU:HD13	1.84	0.60
1:A:173:LYS:NZ	1:A:174:VAL:H	1.97	0.60
1:C:197:HIS:CD2	1:C:236:GLY:H	2.20	0.60
1:B:167:SER:HB2	1:B:169:LYS:N	2.17	0.60
1:C:157:THR:HG21	1:C:198:VAL:HA	1.83	0.60
1:C:173:LYS:HE3	1:C:175:GLU:OE2	2.02	0.60
1:D:166:LEU:HD22	1:D:167:SER:OG	2.02	0.59
1:A:166:LEU:HD22	1:A:167:SER:OG	2.01	0.59
1:C:316:TYR:CE2	1:C:375:MET:HB2	2.37	0.59
1:D:316:TYR:CE2	1:D:375:MET:HB2	2.37	0.59
1:A:85:THR:HG23	1:A:86:GLY:O	2.02	0.59
1:C:166:LEU:CD1	1:C:167:SER:H	2.04	0.59
1:B:346:PRO:O	1:B:347:ASN:HB2	2.01	0.59
1:A:230:HIS:HB2	1:A:268:LYS:O	2.02	0.59
1:C:288:VAL:CG1	1:C:318:VAL:HB	2.33	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:230:HIS:HB2	1:D:268:LYS:O	2.03	0.59
1:A:90:ALA:HB3	1:B:398:ASN:ND2	2.17	0.59
1:D:50:ARG:HH12	1:D:410:SER:HB3	1.67	0.59
1:D:269:LEU:HD21	1:D:271:ILE:HD11	1.85	0.59
1:A:175:GLU:CD	1:A:175:GLU:H	2.07	0.59
1:A:197:HIS:CD2	1:A:236:GLY:H	2.22	0.58
1:C:166:LEU:HD22	1:C:167:SER:OG	2.03	0.58
1:C:230:HIS:HB2	1:C:268:LYS:O	2.03	0.58
1:B:197:HIS:CD2	1:B:236:GLY:H	2.20	0.58
1:B:85:THR:HG23	1:B:86:GLY:O	2.03	0.58
1:C:99:ARG:HH11	1:C:126:SER:HB3	1.68	0.58
1:A:167:SER:HB2	1:A:169:LYS:N	2.19	0.58
1:C:99:ARG:NH1	1:C:126:SER:HB3	2.19	0.58
1:B:348:GLU:HG2	1:B:350:LEU:HD13	1.85	0.57
1:C:348:GLU:HG2	1:C:350:LEU:HD13	1.86	0.57
1:B:255:ILE:HG22	1:B:259:LEU:HD22	1.87	0.57
1:C:117:ILE:HD12	1:C:117:ILE:O	2.04	0.57
1:C:157:THR:H	1:C:166:LEU:CD1	2.17	0.57
1:D:154:ARG:HA	1:D:195:SER:O	2.04	0.57
1:D:167:SER:HB2	1:D:169:LYS:H	1.69	0.57
1:A:398:ASN:ND2	1:B:90:ALA:HB3	2.20	0.57
1:B:80:LEU:HB3	1:B:85:THR:HG21	1.86	0.57
1:D:173:LYS:NZ	1:D:174:VAL:H	2.02	0.56
1:C:319:ASN:ND2	1:D:116:GLN:NE2	2.48	0.56
1:B:212:ILE:HD13	1:B:259:LEU:HD13	1.88	0.56
1:B:316:TYR:CE2	1:B:375:MET:HB2	2.40	0.56
1:D:99:ARG:HH11	1:D:126:SER:HB3	1.71	0.56
1:B:175:GLU:CD	1:B:175:GLU:H	2.09	0.56
1:B:166:LEU:HD22	1:B:167:SER:OG	2.06	0.56
1:A:99:ARG:HH11	1:A:126:SER:HB3	1.71	0.55
1:D:294:LYS:HB2	1:D:315:MET:HB2	1.89	0.55
1:D:96:GLN:HG2	1:D:122:TYR:OH	2.06	0.55
1:A:99:ARG:NH1	1:A:126:SER:HB3	2.22	0.55
1:A:255:ILE:HG22	1:A:259:LEU:HD22	1.89	0.55
1:D:167:SER:HB2	1:D:169:LYS:N	2.22	0.55
1:C:49:VAL:HG22	1:C:83:LEU:HD21	1.88	0.55
1:D:157:THR:H	1:D:166:LEU:CD1	2.19	0.55
1:B:96:GLN:HG2	1:B:122:TYR:OH	2.07	0.55
1:D:288:VAL:CG1	1:D:318:VAL:HB	2.36	0.55
1:A:157:THR:H	1:A:166:LEU:CD1	2.20	0.54
1:D:71:ASN:HD22	1:D:71:ASN:C	2.09	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:398:ASN:ND2	1:D:90:ALA:HB3	2.22	0.54
1:B:65:PHE:O	1:B:274:GLU:HA	2.08	0.54
1:A:288:VAL:CG1	1:A:318:VAL:HB	2.34	0.54
1:B:157:THR:H	1:B:166:LEU:CD1	2.20	0.54
1:C:157:THR:HB	1:C:166:LEU:HG	1.90	0.54
1:B:50:ARG:HH12	1:B:410:SER:HB3	1.73	0.53
1:B:99:ARG:HH11	1:B:126:SER:HB3	1.73	0.53
1:C:90:ALA:HB3	1:D:398:ASN:ND2	2.23	0.53
1:A:167:SER:HB2	1:A:169:LYS:H	1.73	0.53
1:A:90:ALA:CB	1:B:398:ASN:HD21	2.22	0.53
1:A:386:MET:HE3	1:A:390:THR:HG21	1.91	0.53
1:D:166:LEU:CD1	1:D:167:SER:H	2.11	0.52
1:B:99:ARG:NH1	1:B:126:SER:HB3	2.25	0.52
1:D:255:ILE:CG2	1:D:259:LEU:HD22	2.39	0.52
1:A:291:ILE:HD13	1:A:319:ASN:HB3	1.91	0.51
1:B:349:LYS:HD3	1:B:350:LEU:H	1.75	0.51
1:C:178:ARG:HH22	1:C:224:GLU:CD	2.13	0.51
1:A:50:ARG:HH12	1:A:410:SER:HB3	1.75	0.51
1:B:359:THR:HG22	1:B:361:ASP:H	1.75	0.51
1:C:121:ARG:HH12	1:D:35:ASP:CG	2.14	0.51
1:A:217:PHE:CD2	1:A:221:MET:HE3	2.45	0.51
1:B:157:THR:HB	1:B:166:LEU:HG	1.92	0.51
1:B:166:LEU:CD1	1:B:167:SER:H	2.11	0.51
1:C:169:LYS:HB2	1:D:356:TRP:CZ3	2.46	0.51
1:A:348:GLU:HG2	1:A:350:LEU:CD1	2.41	0.50
1:B:401:GLN:HA	1:B:401:GLN:HE21	1.77	0.50
1:C:280:VAL:O	1:C:281:ALA:C	2.49	0.50
1:D:409:VAL:HG22	1:D:409:VAL:O	2.11	0.50
1:A:359:THR:O	1:B:169:LYS:NZ	2.38	0.50
1:C:274:GLU:O	2:C:600:PLP:H6	2.11	0.50
1:C:50:ARG:HH12	1:C:410:SER:HB3	1.76	0.50
1:C:99:ARG:O	1:C:100:GLY:C	2.49	0.50
1:C:280:VAL:O	1:C:387:GLY:HA3	2.11	0.50
1:D:359:THR:HG22	1:D:361:ASP:H	1.75	0.50
1:D:348:GLU:HG2	1:D:350:LEU:CD1	2.42	0.50
1:C:173:LYS:HZ2	1:C:173:LYS:HA	1.77	0.49
1:D:157:THR:HB	1:D:166:LEU:HG	1.94	0.49
1:D:173:LYS:HZ2	1:D:173:LYS:HA	1.78	0.49
1:D:391:VAL:O	1:D:394:THR:HG23	2.12	0.49
1:C:71:ASN:HD22	1:C:73:ASP:H	1.58	0.49
1:A:274:GLU:O	2:A:600:PLP:H6	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:96:GLN:HG2	1:C:122:TYR:OH	2.13	0.49
1:C:348:GLU:HG2	1:C:350:LEU:CD1	2.41	0.49
1:A:121:ARG:HH12	1:B:35:ASP:CG	2.16	0.49
1:A:157:THR:HB	1:A:166:LEU:HG	1.95	0.49
1:B:129:ASP:O	1:B:150:LYS:N	2.41	0.49
1:D:280:VAL:O	1:D:281:ALA:C	2.51	0.49
1:A:269:LEU:HD21	1:A:271:ILE:HD11	1.94	0.49
1:A:41:PHE:CZ	1:A:286:LEU:HD13	2.48	0.48
1:B:154:ARG:HA	1:B:195:SER:O	2.13	0.48
1:B:44:ASP:HA	1:B:408:VAL:HG13	1.95	0.48
1:C:71:ASN:HD22	1:C:71:ASN:C	2.16	0.48
1:A:195:SER:HB3	1:A:233:ASP:HB3	1.96	0.48
1:B:322:VAL:HB	1:B:330:LEU:CD2	2.44	0.48
1:A:178:ARG:HH22	1:A:224:GLU:CD	2.17	0.48
1:B:166:LEU:HD13	1:B:167:SER:N	2.09	0.48
1:B:289:ASN:HD21	1:B:378:GLY:HA2	1.77	0.48
1:C:80:LEU:HB3	1:C:85:THR:HG21	1.95	0.48
1:B:280:VAL:O	1:B:281:ALA:C	2.52	0.48
1:D:195:SER:HA	1:D:233:ASP:O	2.13	0.48
1:D:274:GLU:O	2:D:600:PLP:H6	2.14	0.48
1:A:217:PHE:HD2	1:A:221:MET:HE3	1.79	0.48
1:B:178:ARG:HH22	1:B:224:GLU:CD	2.17	0.48
1:D:318:VAL:O	1:D:358:PRO:HD3	2.13	0.48
1:A:71:ASN:HD22	1:A:73:ASP:H	1.62	0.47
1:D:44:ASP:HA	1:D:408:VAL:HG13	1.95	0.47
1:A:90:ALA:HB3	1:B:398:ASN:HD21	1.78	0.47
1:A:98:VAL:HG23	1:A:103:VAL:HB	1.96	0.47
1:B:144:LYS:HD3	1:B:144:LYS:N	2.30	0.47
1:A:99:ARG:O	1:A:100:GLY:C	2.52	0.47
1:C:117:ILE:HD13	1:C:145:THR:OG1	2.15	0.47
1:D:386:MET:HE3	1:D:390:THR:HG21	1.97	0.47
1:A:319:ASN:ND2	1:B:116:GLN:NE2	2.47	0.47
1:B:195:SER:HA	1:B:233:ASP:O	2.13	0.47
1:C:322:VAL:HB	1:C:330:LEU:CD2	2.45	0.47
1:D:99:ARG:NH1	1:D:126:SER:HB3	2.30	0.47
1:A:255:ILE:CG2	1:A:259:LEU:HD22	2.44	0.47
1:A:376:GLN:O	1:A:379:GLU:HG3	2.15	0.47
1:B:156:SER:OG	1:B:173:LYS:HD2	2.14	0.47
1:D:376:GLN:O	1:D:379:GLU:HG3	2.15	0.47
1:B:185:LYS:HD2	1:B:185:LYS:HA	1.73	0.47
1:B:391:VAL:O	1:B:394:THR:HG23	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:154:ARG:HA	1:A:195:SER:O	2.15	0.47
1:A:391:VAL:O	1:A:394:THR:HG23	2.15	0.47
1:B:157:THR:N	1:B:166:LEU:HD11	2.29	0.47
1:C:116:GLN:HA	1:D:291:ILE:HB	1.96	0.47
1:B:274:GLU:O	2:B:600:PLP:H6	2.16	0.46
1:C:154:ARG:HA	1:C:195:SER:O	2.15	0.46
1:A:280:VAL:O	1:A:281:ALA:C	2.53	0.46
1:D:185:LYS:HA	1:D:185:LYS:HD2	1.74	0.46
1:A:109:ILE:HG22	1:A:111:ALA:HB2	1.97	0.46
1:A:116:GLN:HA	1:B:291:ILE:HB	1.96	0.46
1:A:337:ARG:HH21	1:A:337:ARG:HG3	1.81	0.46
1:A:96:GLN:HG2	1:A:122:TYR:OH	2.16	0.46
1:A:322:VAL:HB	1:A:330:LEU:CD2	2.46	0.46
1:B:217:PHE:HE2	1:B:221:MET:HE2	1.81	0.46
1:C:195:SER:CB	1:C:233:ASP:HB3	2.45	0.46
1:B:367:VAL:HG11	1:B:370:TYR:HB2	1.98	0.46
1:B:349:LYS:HD3	1:B:350:LEU:N	2.29	0.46
1:B:41:PHE:CZ	1:B:286:LEU:HD13	2.51	0.46
1:B:66:TYR:CE2	1:B:68:VAL:HA	2.50	0.46
1:B:255:ILE:CG2	1:B:259:LEU:HD22	2.45	0.46
1:B:316:TYR:O	1:B:355:VAL:HA	2.16	0.46
1:C:376:GLN:O	1:C:379:GLU:HG3	2.15	0.46
1:D:290:VAL:HG22	1:D:377:VAL:HA	1.98	0.46
1:C:391:VAL:HG23	1:C:392:VAL:N	2.30	0.45
1:A:398:ASN:HD21	1:B:90:ALA:HB3	1.81	0.45
1:A:195:SER:CB	1:A:233:ASP:HB3	2.46	0.45
1:C:44:ASP:HA	1:C:408:VAL:HG13	1.98	0.45
1:D:178:ARG:HH22	1:D:224:GLU:CD	2.20	0.45
1:B:71:ASN:HD22	1:B:73:ASP:H	1.63	0.45
1:C:359:THR:O	1:D:169:LYS:NZ	2.37	0.45
1:D:215:SER:O	1:D:219:PHE:HB2	2.17	0.45
1:A:173:LYS:HZ1	1:A:174:VAL:HG13	1.81	0.45
1:A:343:GLU:HA	1:A:344:PRO:HD3	1.89	0.45
1:D:322:VAL:HB	1:D:330:LEU:CD2	2.47	0.45
1:A:351:TYR:HB3	1:A:352:PRO:HD2	1.99	0.45
1:B:348:GLU:HG2	1:B:350:LEU:CD1	2.47	0.45
1:A:116:GLN:NE2	1:B:319:ASN:ND2	2.51	0.45
1:B:117:ILE:HD12	1:B:145:THR:HG21	1.99	0.45
1:C:359:THR:HG22	1:C:361:ASP:H	1.81	0.45
1:B:282:SER:HA	1:B:385:ASP:HA	1.99	0.45
1:C:401:GLN:HA	1:C:401:GLN:HE21	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:409:VAL:HG22	1:A:409:VAL:O	2.16	0.44
1:C:195:SER:HA	1:C:233:ASP:O	2.18	0.44
1:C:359:THR:CG2	1:C:361:ASP:H	2.31	0.44
1:D:129:ASP:O	1:D:150:LYS:N	2.45	0.44
1:D:337:ARG:HH21	1:D:337:ARG:HG3	1.82	0.44
1:B:376:GLN:O	1:B:377:VAL:C	2.56	0.44
1:A:280:VAL:O	1:A:387:GLY:HA3	2.17	0.44
1:C:200:SER:HB3	1:C:277:ARG:HE	1.83	0.44
1:A:44:ASP:HA	1:A:408:VAL:HG13	1.99	0.44
1:C:128:VAL:O	1:C:146:HIS:HE1	2.01	0.44
1:D:61:ARG:NH2	1:D:260:GLU:OE1	2.44	0.44
1:C:134:ASP:OD1	1:D:294:LYS:NZ	2.51	0.43
1:D:98:VAL:HG23	1:D:103:VAL:HB	2.00	0.43
1:C:330:LEU:HD22	1:C:330:LEU:H	1.84	0.43
1:C:386:MET:HE3	1:C:390:THR:HG21	2.01	0.43
1:B:113:PRO:HG2	1:B:170:PHE:CE2	2.54	0.43
1:A:71:ASN:ND2	1:A:73:ASP:H	2.15	0.43
1:B:157:THR:HG22	1:B:166:LEU:HD12	1.99	0.43
1:D:71:ASN:HD22	1:D:73:ASP:H	1.64	0.43
1:D:144:LYS:HD3	1:D:144:LYS:N	2.33	0.43
1:D:330:LEU:H	1:D:330:LEU:HD22	1.82	0.43
1:C:398:ASN:HD21	1:D:90:ALA:HB3	1.82	0.43
1:B:50:ARG:HH12	1:B:410:SER:CB	2.32	0.43
1:B:367:VAL:CG1	1:B:370:TYR:HB2	2.47	0.43
1:D:117:ILE:HD12	1:D:117:ILE:O	2.19	0.43
1:D:282:SER:HA	1:D:385:ASP:HA	2.01	0.43
1:D:99:ARG:HH11	1:D:99:ARG:HD3	1.72	0.43
1:B:99:ARG:HH11	1:B:99:ARG:HD3	1.58	0.43
1:C:284:PHE:HE2	1:C:405:ILE:HD13	1.84	0.43
1:D:50:ARG:HH12	1:D:410:SER:CB	2.32	0.43
1:D:359:THR:CG2	1:D:361:ASP:H	2.31	0.43
1:A:71:ASN:C	1:A:71:ASN:ND2	2.70	0.43
1:C:399:GLY:HA3	1:D:91:SER:OG	2.19	0.43
1:A:49:VAL:HG22	1:A:83:LEU:HD21	2.01	0.42
1:A:99:ARG:O	1:A:101:ILE:N	2.52	0.42
1:C:255:ILE:CG2	1:C:259:LEU:HD22	2.45	0.42
1:A:195:SER:HA	1:A:233:ASP:O	2.18	0.42
1:A:401:GLN:HE21	1:A:401:GLN:HA	1.84	0.42
1:B:71:ASN:ND2	1:B:73:ASP:H	2.17	0.42
1:B:98:VAL:HG23	1:B:103:VAL:HB	2.01	0.42
1:B:195:SER:CB	1:B:233:ASP:HB3	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:99:ARG:HH11	1:A:99:ARG:HD3	1.67	0.42
1:C:169:LYS:HE3	1:D:356:TRP:HB3	2.02	0.42
1:C:185:LYS:HA	1:C:185:LYS:HD2	1.85	0.42
1:B:217:PHE:CE2	1:B:221:MET:HE2	2.54	0.42
1:B:337:ARG:HH21	1:B:337:ARG:HG3	1.84	0.42
1:B:409:VAL:O	1:B:409:VAL:HG22	2.19	0.42
1:C:388:ALA:O	1:C:390:THR:HG23	2.19	0.42
1:C:200:SER:HA	1:C:237:GLY:HA2	2.02	0.42
1:D:401:GLN:HE21	1:D:401:GLN:HA	1.85	0.42
1:B:189:ILE:HD13	1:B:189:ILE:HA	1.92	0.42
1:C:144:LYS:HD3	1:C:144:LYS:N	2.34	0.42
1:D:157:THR:HG22	1:D:166:LEU:HD12	2.00	0.42
1:A:98:VAL:HG22	1:A:108:ILE:HD11	2.02	0.42
1:C:65:PHE:O	1:C:274:GLU:HA	2.18	0.42
1:C:178:ARG:NH2	1:C:224:GLU:OE1	2.51	0.42
1:D:49:VAL:HG22	1:D:83:LEU:HD21	2.02	0.42
1:D:289:ASN:HD21	1:D:378:GLY:HA2	1.84	0.42
1:A:290:VAL:HG22	1:A:377:VAL:HA	2.02	0.42
1:C:157:THR:N	1:C:166:LEU:HD11	2.28	0.42
1:D:136:VAL:O	1:D:137:ASP:C	2.58	0.42
1:B:92:ASN:H	1:B:119:HIS:CD2	2.38	0.42
1:B:200:SER:HB3	1:B:277:ARG:HH21	1.85	0.42
1:D:367:VAL:HG11	1:D:370:TYR:HB2	2.02	0.42
1:D:66:TYR:CG	1:D:80:LEU:HD13	2.54	0.42
1:A:185:LYS:HA	1:A:185:LYS:HD2	1.86	0.41
1:A:284:PHE:HE2	1:A:405:ILE:HD13	1.85	0.41
1:C:376:GLN:O	1:C:377:VAL:C	2.58	0.41
1:D:195:SER:HB3	1:D:233:ASP:HB3	2.02	0.41
1:A:73:ASP:CB	1:A:76:VAL:HG13	2.43	0.41
1:B:391:VAL:HG23	1:B:392:VAL:N	2.36	0.41
1:C:115:LYS:HE2	1:C:115:LYS:HB2	1.88	0.41
1:C:116:GLN:NE2	1:D:319:ASN:ND2	2.53	0.41
1:D:88:ASP:OD1	1:D:88:ASP:C	2.58	0.41
1:A:112:ASN:ND2	1:A:114:CYS:H	2.17	0.41
1:B:293:LYS:NZ	1:B:374:GLU:OE1	2.53	0.41
1:C:90:ALA:CB	1:D:398:ASN:HD21	2.34	0.41
1:D:109:ILE:HG22	1:D:111:ALA:HB2	2.02	0.41
1:B:136:VAL:O	1:B:140:GLU:HG3	2.21	0.41
1:D:232:LEU:HD23	1:D:271:ILE:HD12	2.02	0.41
1:A:282:SER:HA	1:A:385:ASP:HA	2.01	0.41
1:B:386:MET:HE3	1:B:386:MET:HB3	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:157:THR:HG22	1:C:166:LEU:HD12	2.02	0.41
1:D:217:PHE:CD2	1:D:221:MET:HE3	2.55	0.41
1:B:243:ASP:OD1	1:B:243:ASP:N	2.53	0.41
1:D:195:SER:CB	1:D:233:ASP:HB3	2.50	0.41
1:B:41:PHE:CE2	1:B:286:LEU:HD13	2.55	0.41
1:B:71:ASN:C	1:B:71:ASN:ND2	2.73	0.41
1:B:173:LYS:HZ2	1:B:173:LYS:HA	1.86	0.41
1:C:367:VAL:CG1	1:C:370:TYR:HB2	2.50	0.41
1:A:65:PHE:O	1:A:274:GLU:HA	2.20	0.41
1:C:311:ALA:O	1:C:312:GLN:C	2.59	0.41
1:C:409:VAL:O	1:C:411:GLY:N	2.54	0.41
1:D:217:PHE:HD2	1:D:221:MET:HE3	1.85	0.41
1:D:367:VAL:CG1	1:D:370:TYR:HB2	2.50	0.41
1:A:311:ALA:O	1:A:312:GLN:C	2.60	0.41
1:A:129:ASP:O	1:A:150:LYS:N	2.51	0.40
1:B:128:VAL:O	1:B:146:HIS:HE1	2.04	0.40
1:C:39:PRO:HD3	1:C:319:ASN:ND2	2.36	0.40
1:C:291:ILE:HD13	1:C:319:ASN:HB3	2.02	0.40
1:D:110:TYR:CZ	1:D:115:LYS:HG2	2.57	0.40
1:D:217:PHE:HE2	1:D:221:MET:HE2	1.86	0.40
1:A:91:SER:OG	1:B:399:GLY:HA3	2.21	0.40
1:B:195:SER:HB3	1:B:233:ASP:HB3	2.03	0.40
1:C:73:ASP:CB	1:C:76:VAL:HG13	2.45	0.40
1:C:156:SER:OG	1:C:173:LYS:HD2	2.21	0.40
1:C:337:ARG:HH21	1:C:337:ARG:HG3	1.87	0.40
1:A:144:LYS:N	1:A:144:LYS:HD3	2.36	0.40
1:B:263:PHE:N	1:B:264:PRO:CD	2.84	0.40
1:D:66:TYR:CE2	1:D:68:VAL:HA	2.56	0.40
1:C:129:ASP:O	1:C:150:LYS:N	2.52	0.40
1:B:66:TYR:CG	1:B:80:LEU:HD13	2.56	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	350/425 (82%)	324 (93%)	21 (6%)	5 (1%)	11	36
1	B	350/425 (82%)	319 (91%)	26 (7%)	5 (1%)	11	36
1	C	350/425 (82%)	325 (93%)	21 (6%)	4 (1%)	14	42
1	D	350/425 (82%)	324 (93%)	21 (6%)	5 (1%)	11	36
All	All	1400/1700 (82%)	1292 (92%)	89 (6%)	19 (1%)	11	36

All (19) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	312	GLN
1	B	312	GLN
1	C	312	GLN
1	D	312	GLN
1	A	37	GLY
1	A	410	SER
1	B	37	GLY
1	B	410	SER
1	C	37	GLY
1	C	410	SER
1	D	100	GLY
1	D	410	SER
1	A	71	ASN
1	A	100	GLY
1	D	37	GLY
1	C	71	ASN
1	D	242	ARG
1	B	377	VAL
1	B	100	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	302/362 (83%)	264 (87%)	38 (13%)	4 13
1	B	302/362 (83%)	264 (87%)	38 (13%)	4 13
1	C	302/362 (83%)	267 (88%)	35 (12%)	5 16
1	D	302/362 (83%)	266 (88%)	36 (12%)	5 15
All	All	1208/1448 (83%)	1061 (88%)	147 (12%)	5 15

All (147) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	71	ASN
1	A	74	TRP
1	A	75	ARG
1	A	76	VAL
1	A	83	LEU
1	A	85	THR
1	A	110	TYR
1	A	112	ASN
1	A	117	ILE
1	A	144	LYS
1	A	150	LYS
1	A	157	THR
1	A	166	LEU
1	A	173	LYS
1	A	174	VAL
1	A	185	LYS
1	A	200	SER
1	A	202	SER
1	A	219	PHE
1	A	238	PHE
1	A	259	LEU
1	A	268	LYS
1	A	312	GLN
1	A	339	LEU
1	A	341	GLN
1	A	343	GLU
1	A	345	ILE
1	A	348	GLU
1	A	351	TYR
1	A	355	VAL
1	A	359	THR
1	A	363	LEU
1	A	368	GLU

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Mol	Chain	Res	Type
1	A	369	ARG
1	A	398	ASN
1	A	401	GLN
1	A	403	PRO
1	A	410	SER
1	B	71	ASN
1	B	74	TRP
1	B	75	ARG
1	B	85	THR
1	B	110	TYR
1	B	112	ASN
1	B	117	ILE
1	B	136	VAL
1	B	144	LYS
1	B	150	LYS
1	B	157	THR
1	B	166	LEU
1	B	173	LYS
1	B	174	VAL
1	B	185	LYS
1	B	186	LYS
1	B	202	SER
1	B	259	LEU
1	B	268	LYS
1	B	288	VAL
1	B	290	VAL
1	B	291	ILE
1	B	297	PRO
1	B	312	GLN
1	B	339	LEU
1	B	341	GLN
1	B	343	GLU
1	B	345	ILE
1	B	348	GLU
1	B	355	VAL
1	B	359	THR
1	B	363	LEU
1	B	368	GLU
1	B	369	ARG
1	B	398	ASN
1	B	401	GLN
1	B	403	PRO

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Mol	Chain	Res	Type
1	B	410	SER
1	C	71	ASN
1	C	74	TRP
1	C	75	ARG
1	C	85	THR
1	C	110	TYR
1	C	112	ASN
1	C	117	ILE
1	C	136	VAL
1	C	144	LYS
1	C	150	LYS
1	C	157	THR
1	C	166	LEU
1	C	173	LYS
1	C	200	SER
1	C	219	PHE
1	C	259	LEU
1	C	268	LYS
1	C	288	VAL
1	C	291	ILE
1	C	312	GLN
1	C	339	LEU
1	C	341	GLN
1	C	343	GLU
1	C	345	ILE
1	C	348	GLU
1	C	351	TYR
1	C	355	VAL
1	C	359	THR
1	C	363	LEU
1	C	368	GLU
1	C	369	ARG
1	C	398	ASN
1	C	401	GLN
1	C	403	PRO
1	C	410	SER
1	D	71	ASN
1	D	74	TRP
1	D	75	ARG
1	D	85	THR
1	D	110	TYR
1	D	112	ASN

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Mol	Chain	Res	Type
1	D	117	ILE
1	D	144	LYS
1	D	150	LYS
1	D	157	THR
1	D	166	LEU
1	D	173	LYS
1	D	185	LYS
1	D	186	LYS
1	D	200	SER
1	D	202	SER
1	D	259	LEU
1	D	268	LYS
1	D	272	VAL
1	D	291	ILE
1	D	312	GLN
1	D	339	LEU
1	D	341	GLN
1	D	343	GLU
1	D	345	ILE
1	D	348	GLU
1	D	352	PRO
1	D	355	VAL
1	D	359	THR
1	D	363	LEU
1	D	368	GLU
1	D	369	ARG
1	D	398	ASN
1	D	401	GLN
1	D	403	PRO
1	D	410	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (43) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	71	ASN
1	A	112	ASN
1	A	116	GLN
1	A	197	HIS
1	A	256	ASN
1	A	262	HIS
1	A	289	ASN
1	A	312	GLN

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Mol	Chain	Res	Type
1	A	341	GLN
1	A	398	ASN
1	B	71	ASN
1	B	112	ASN
1	B	116	GLN
1	B	197	HIS
1	B	256	ASN
1	B	262	HIS
1	B	289	ASN
1	B	312	GLN
1	B	341	GLN
1	B	398	ASN
1	C	71	ASN
1	C	112	ASN
1	C	116	GLN
1	C	146	HIS
1	C	197	HIS
1	C	256	ASN
1	C	262	HIS
1	C	289	ASN
1	C	312	GLN
1	C	341	GLN
1	C	398	ASN
1	C	401	GLN
1	D	71	ASN
1	D	112	ASN
1	D	116	GLN
1	D	197	HIS
1	D	256	ASN
1	D	262	HIS
1	D	289	ASN
1	D	312	GLN
1	D	341	GLN
1	D	398	ASN
1	D	401	GLN

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)

4 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	B	600	1	15,15,16	2.46	5 (33%)	20,22,23	3.31	5 (25%)
2	PLP	D	600	1	15,15,16	2.74	4 (26%)	20,22,23	3.44	6 (30%)
2	PLP	C	600	1	15,15,16	2.72	5 (33%)	20,22,23	2.35	5 (25%)
2	PLP	A	600	1	15,15,16	2.76	4 (26%)	20,22,23	2.65	7 (35%)

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	600	1	-	0/6/6/8	0/1/1/1
2	PLP	D	600	1	-	0/6/6/8	0/1/1/1
2	PLP	C	600	1	-	0/6/6/8	0/1/1/1
2	PLP	A	600	1	-	0/6/6/8	0/1/1/1

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	600	PLP	C5-C4	7.18	1.48	1.40
2	C	600	PLP	C5-C4	6.93	1.48	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	600	PLP	C4A-C4	6.74	1.65	1.51
2	D	600	PLP	C4A-C4	6.09	1.64	1.51
2	A	600	PLP	C5-C4	6.03	1.47	1.40
2	C	600	PLP	C4A-C4	5.89	1.63	1.51
2	B	600	PLP	C4A-C4	5.84	1.63	1.51
2	B	600	PLP	C5-C4	5.49	1.46	1.40
2	A	600	PLP	O3-C3	3.24	1.44	1.37
2	B	600	PLP	P-O4P	3.21	1.70	1.60
2	D	600	PLP	P-O4P	3.05	1.70	1.60
2	C	600	PLP	O3-C3	2.44	1.42	1.37
2	C	600	PLP	P-O4P	2.39	1.67	1.60
2	A	600	PLP	C2-N1	2.32	1.38	1.33
2	B	600	PLP	C2-N1	2.14	1.37	1.33
2	C	600	PLP	C2-N1	2.13	1.37	1.33
2	D	600	PLP	C2-N1	2.08	1.37	1.33
2	B	600	PLP	O3-C3	2.00	1.41	1.37

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	D	600	PLP	C4A-C4-C5	11.84	133.13	120.94
2	B	600	PLP	C4A-C4-C5	11.49	132.77	120.94
2	A	600	PLP	C4A-C4-C5	7.59	128.75	120.94
2	C	600	PLP	C4A-C4-C5	6.75	127.89	120.94
2	B	600	PLP	O3-C3-C2	5.30	129.04	117.49
2	D	600	PLP	C4A-C4-C3	-5.03	111.97	120.50
2	B	600	PLP	C4A-C4-C3	-5.03	111.98	120.50
2	D	600	PLP	O3-C3-C2	4.76	127.87	117.49
2	C	600	PLP	O3-C3-C2	4.66	127.65	117.49
2	A	600	PLP	O3-C3-C2	4.28	126.81	117.49
2	D	600	PLP	C3-C4-C5	-3.57	114.88	118.74
2	A	600	PLP	C4A-C4-C3	-3.57	114.45	120.50
2	B	600	PLP	O3-C3-C4	-3.41	109.14	118.10
2	B	600	PLP	C3-C4-C5	-3.24	115.24	118.74
2	C	600	PLP	C4A-C4-C3	-3.20	115.07	120.50
2	D	600	PLP	O3-C3-C4	-3.01	110.19	118.10
2	A	600	PLP	O2P-P-O4P	-2.99	98.78	106.73
2	A	600	PLP	C6-C5-C4	2.88	120.42	118.16
2	D	600	PLP	O2P-P-O4P	-2.87	99.10	106.73
2	C	600	PLP	C2A-C2-C3	2.80	124.35	120.89
2	A	600	PLP	C2A-C2-C3	2.56	124.05	120.89
2	A	600	PLP	O3P-P-O4P	2.52	113.43	106.73

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	C	600	PLP	O4P-P-O1P	2.27	112.86	106.47

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	600	PLP	1	0
2	D	600	PLP	1	0
2	C	600	PLP	1	0
2	A	600	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 (i)

6.1 Protein, DNA and RNA chains (i)

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains (i)

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.