



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 04:06 PM UTC

PDB ID : 1AHX / pdb_00001ahx
Title : ASPARTATE AMINOTRANSFERASE HEXAMUTANT
Authors : Malashkevich, V.N.; Jansonius, J.N.
Deposited on : 1995-02-21
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)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

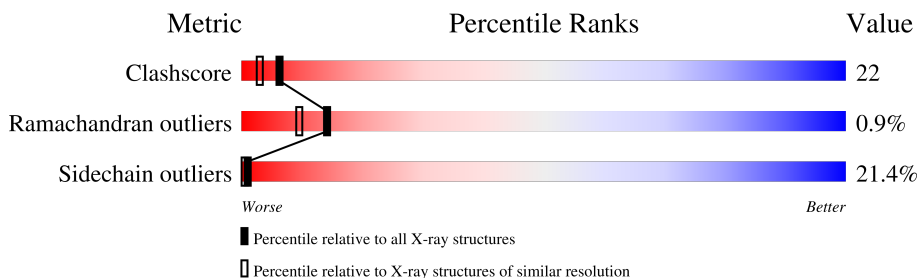
1 Overall quality at a glance

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))
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	396	 60% 28% 10% •
1	B	396	 55% 32% 10% •

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6723 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.

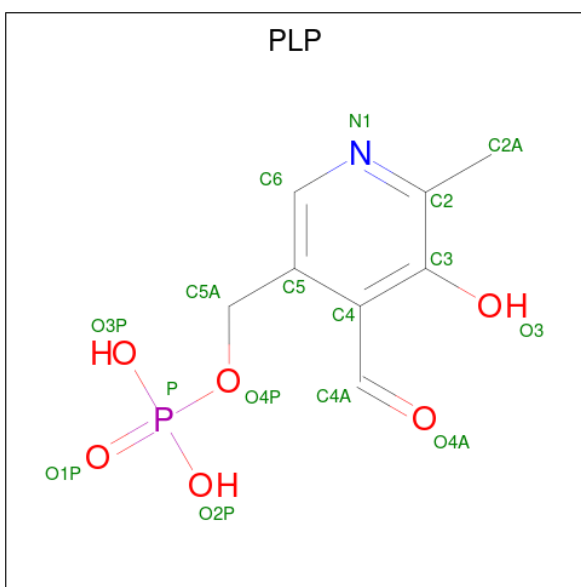
- Molecule 1 is a protein called ASPARTATE AMINOTRANSFERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	396	Total	C	N	O	S	0	0	0
			3071	1942	533	583	13			
1	B	396	Total	C	N	O	S	0	0	0
			3071	1942	533	583	13			

There are 12 discrepancies between the modelled and reference sequences:

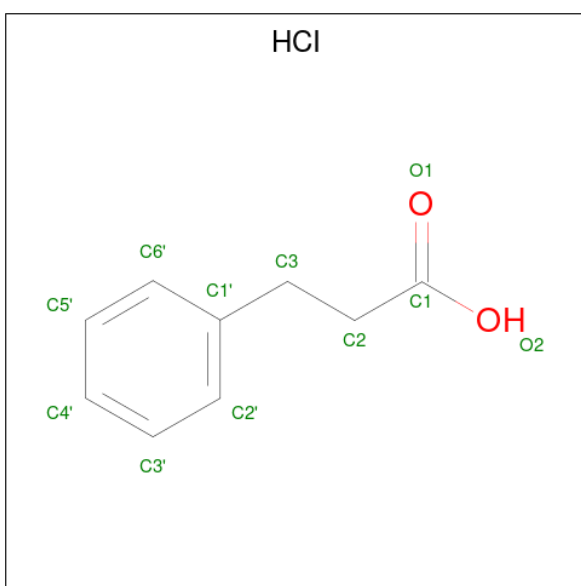
Chain	Residue	Modelled	Actual	Comment	Reference
A	39	LEU	VAL	conflict	UNP P00509
A	41	TYR	LYS	conflict	UNP P00509
A	47	ILE	THR	conflict	UNP P00509
A	69	LEU	ASN	conflict	UNP P00509
A	109	SER	THR	conflict	UNP P00509
A	297	SER	ASN	conflict	UNP P00509
B	39	LEU	VAL	conflict	UNP P00509
B	41	TYR	LYS	conflict	UNP P00509
B	47	ILE	THR	conflict	UNP P00509
B	69	LEU	ASN	conflict	UNP P00509
B	109	SER	THR	conflict	UNP P00509
B	297	SER	ASN	conflict	UNP P00509

- 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 HYDROCINNAMIC ACID (CCD ID: HCI) (formula: $C_9H_{10}O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			11	9	2		
3	B	1	Total	C	O	0	0
			11	9	2		

- Molecule 4 is water.

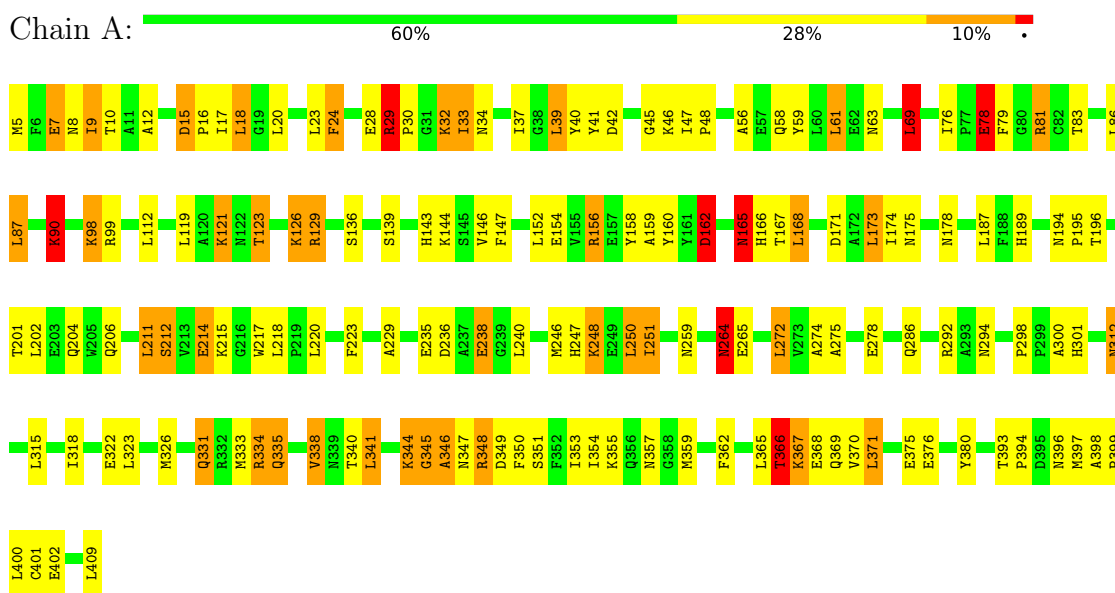
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	279	Total 279	O 279	0	0
4	B	250	Total 250	O 250	0	0

3 Residue-property plots

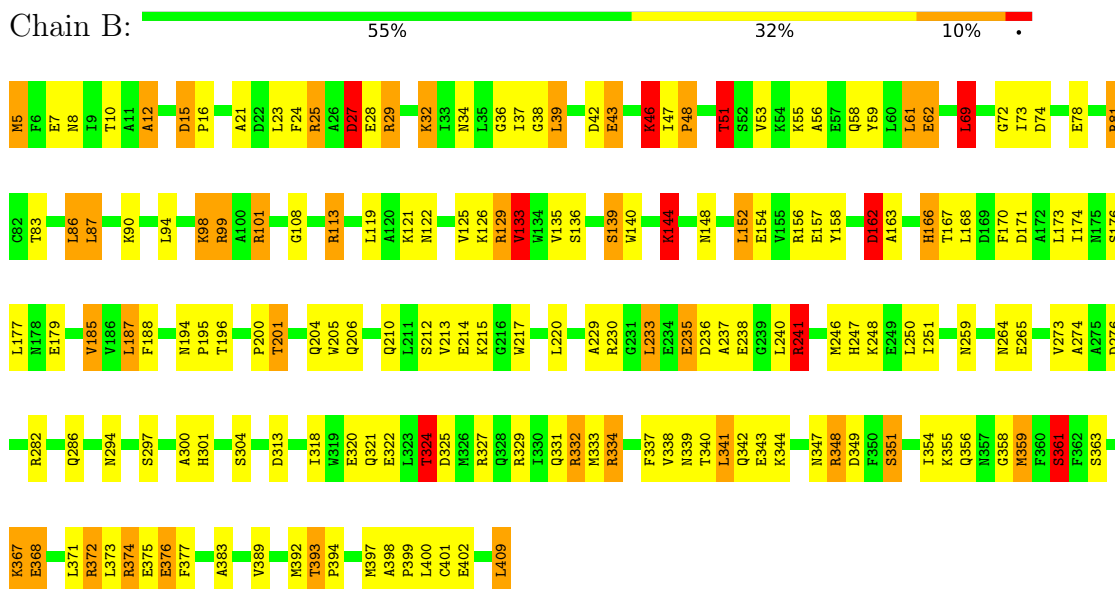
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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: ASPARTATE AMINOTRANSFERASE



• Molecule 1: ASPARTATE AMINOTRANSFERASE



4 Data and refinement statistics

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	84.98Å 78.69Å 89.28Å 90.00° 118.32° 90.00°	Depositor
Resolution (Å)	8.00 – 2.00	Depositor
% Data completeness (in resolution range)	93.5 (8.00-2.00)	Depositor
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	TNT	Depositor
R, R_{free}	0.226 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6723	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: HCl, 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	1.22	5/3133 (0.2%)	1.57	32/4244 (0.8%)
1	B	1.19	1/3133 (0.0%)	1.64	45/4244 (1.1%)
All	All	1.21	6/6266 (0.1%)	1.61	77/8488 (0.9%)

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 (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	123	THR	C-N	-8.24	1.22	1.33
1	A	345	GLY	C-N	-7.80	1.23	1.33
1	A	346	ALA	CA-C	7.18	1.61	1.52
1	A	265	GLU	CD-OE1	5.41	1.35	1.25
1	B	320	GLU	CD-OE1	5.32	1.35	1.25
1	A	123	THR	N-CA	5.23	1.52	1.46

All (77) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	27	ASP	N-CA-CB	9.46	123.80	110.17
1	A	165	ASN	N-CA-CB	8.21	122.55	110.56
1	A	162	ASP	CA-CB-CG	8.04	120.64	112.60
1	B	341	LEU	N-CA-C	-7.51	103.03	111.14
1	B	363	SER	N-CA-C	7.28	121.42	112.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	300	ALA	N-CA-C	7.25	118.97	111.14
1	A	300	ALA	N-CA-C	7.06	118.76	111.14
1	A	250	LEU	N-CA-CB	-7.04	99.07	111.39
1	A	345	GLY	O-C-N	-7.04	113.56	122.70
1	A	166	HIS	CA-CB-CG	-7.00	106.81	113.80
1	B	46	LYS	CB-CA-C	6.84	122.93	109.66
1	B	171	ASP	CA-CB-CG	-6.73	105.87	112.60
1	B	166	HIS	CA-CB-CG	-6.59	107.20	113.80
1	A	357	ASN	CA-CB-CG	-6.50	106.10	112.60
1	A	338	VAL	N-CA-CB	6.49	118.14	110.55
1	B	247	HIS	N-CA-C	6.43	120.54	110.32
1	A	264	ASN	N-CA-C	6.31	120.83	113.20
1	A	29	ARG	CA-C-N	6.25	127.65	119.84
1	A	29	ARG	C-N-CA	6.25	127.65	119.84
1	B	196	THR	N-CA-C	6.18	118.98	111.82
1	B	51	THR	N-CA-CB	6.17	119.29	110.16
1	B	162	ASP	CA-CB-CG	6.09	118.69	112.60
1	B	376	GLU	N-CA-CB	-6.09	101.18	110.26
1	B	133	VAL	N-CA-CB	6.06	119.77	111.41
1	A	366	THR	N-CA-CB	-6.05	101.09	110.29
1	B	324	THR	N-CA-CB	6.01	118.95	110.12
1	A	298	PRO	N-CA-C	6.00	118.03	110.70
1	A	175	ASN	CA-CB-CG	-5.97	106.63	112.60
1	B	162	ASP	CB-CA-C	5.96	121.42	111.30
1	B	313	ASP	CA-CB-CG	-5.91	106.69	112.60
1	B	69	LEU	CB-CA-C	-5.86	98.75	110.42
1	B	250	LEU	N-CA-CB	5.84	121.37	111.57
1	A	196	THR	N-CA-C	5.83	117.72	111.36
1	B	297	SER	CB-CA-C	5.79	118.95	109.97
1	B	334	ARG	N-CA-CB	5.79	118.72	110.16
1	A	175	ASN	CB-CA-C	5.77	120.66	110.85
1	B	72	GLY	N-CA-C	-5.69	104.97	112.82
1	B	238	GLU	N-CA-C	5.67	117.91	111.11
1	B	108	GLY	N-CA-C	-5.65	107.65	114.66
1	B	359	MET	N-CA-C	5.63	119.87	112.89
1	A	359	MET	N-CA-C	5.62	119.86	112.89
1	B	334	ARG	CB-CA-C	5.60	120.36	110.85
1	A	42	ASP	CA-CB-CG	5.58	118.18	112.60
1	A	238	GLU	N-CA-C	5.55	117.77	111.11
1	B	313	ASP	N-CA-C	5.54	117.76	111.11
1	B	15	ASP	CA-C-N	5.53	126.75	119.84
1	B	15	ASP	C-N-CA	5.53	126.75	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	347	ASN	CA-CB-CG	-5.42	107.18	112.60
1	B	144	LYS	CB-CA-C	5.40	119.76	110.79
1	A	15	ASP	CA-C-N	5.38	125.45	119.32
1	A	15	ASP	C-N-CA	5.38	125.45	119.32
1	B	409	LEU	N-CA-CB	5.34	119.59	110.50
1	A	357	ASN	CB-CA-C	-5.29	100.57	109.50
1	B	46	LYS	N-CA-C	5.26	118.15	109.85
1	B	393	THR	O-C-N	5.23	125.06	121.71
1	B	140	TRP	CB-CA-C	5.21	118.42	109.82
1	A	69	LEU	N-CA-CB	-5.16	101.77	110.49
1	A	341	LEU	N-CA-C	-5.16	105.35	110.97
1	B	48	PRO	N-CA-C	5.15	119.13	111.41
1	A	81	ARG	NE-CZ-NH2	5.13	123.82	119.20
1	B	368	GLU	N-CA-CB	5.13	118.90	110.39
1	A	162	ASP	CB-CA-C	5.11	119.90	111.31
1	B	48	PRO	CB-CA-C	-5.11	104.25	110.95
1	B	361	SER	CB-CA-C	5.09	117.67	110.24
1	A	63	ASN	CA-CB-CG	-5.09	107.51	112.60
1	B	163	ALA	N-CA-C	5.08	116.82	111.28
1	B	46	LYS	CB-CG-CD	5.07	122.97	111.30
1	A	171	ASP	CA-CB-CG	-5.07	107.53	112.60
1	B	51	THR	CB-CA-C	5.06	119.45	110.85
1	B	94	LEU	N-CA-C	-5.06	105.77	111.28
1	A	78	GLU	CB-CA-C	-5.04	102.42	110.79
1	B	241	ARG	CG-CD-NE	5.03	123.07	112.00
1	A	376	GLU	N-CA-CB	-5.01	102.79	110.26
1	A	24	PHE	CA-CB-CG	-5.00	108.80	113.80
1	B	12	ALA	CA-C-N	-5.00	115.41	120.31
1	B	12	ALA	C-N-CA	-5.00	115.41	120.31
1	A	7	GLU	N-CA-C	5.00	117.38	111.33

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	334	ARG	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	3071	0	3020	125	0
1	B	3071	0	3020	156	0
2	A	15	0	6	0	0
2	B	15	0	6	0	0
3	A	11	0	9	1	0
3	B	11	0	9	0	0
4	A	279	0	0	6	0
4	B	250	0	0	21	0
All	All	6723	0	6070	272	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 22.

All (272) 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:46:LYS:HD2	1:A:47:ILE:H	1.23	1.04
1:A:366:THR:HG22	1:A:369:GLN:H	1.25	0.99
1:B:29:ARG:HH11	1:B:29:ARG:HG3	1.29	0.95
1:A:18:LEU:HD12	1:A:37:ILE:HD12	1.49	0.94
1:B:359:MET:HE2	4:B:456:HOH:O	1.68	0.93
1:A:397:MET:HE3	1:A:397:MET:HA	1.49	0.92
1:B:98:LYS:HE2	1:B:98:LYS:HA	1.57	0.87
1:B:389:VAL:HG13	1:B:392:MET:CE	2.08	0.84
1:A:248:LYS:CG	1:A:275:ALA:HB2	2.10	0.81
1:B:389:VAL:HG22	1:B:392:MET:HE2	1.60	0.81
1:A:126:LYS:HE2	1:A:129:ARG:NH1	1.96	0.81
1:A:366:THR:HG22	1:A:369:GLN:N	1.97	0.79
1:A:366:THR:HG21	4:A:583:HOH:O	1.82	0.79
1:A:165:ASN:N	1:A:165:ASN:HD22	1.79	0.79
1:A:312:ASN:ND2	1:A:315:LEU:H	1.81	0.78
1:A:165:ASN:HD22	1:A:165:ASN:H	1.31	0.78
1:B:38:GLY:C	1:B:359:MET:HE1	2.09	0.77
1:A:121:LYS:NZ	1:A:121:LYS:HB3	1.96	0.77
1:A:397:MET:HE2	1:A:401:CYS:SG	2.23	0.77
1:B:389:VAL:HG13	1:B:392:MET:HE2	1.67	0.76
1:A:45:GLY:HA3	4:A:672:HOH:O	1.86	0.76
1:B:348:ARG:HG2	1:B:348:ARG:HH11	1.51	0.74
1:B:201:THR:HG23	1:B:204:GLN:OE1	1.88	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:90:LYS:HG2	4:A:463:HOH:O	1.87	0.73
1:A:159:ALA:O	1:A:173:LEU:HD23	1.89	0.73
1:B:398:ALA:O	1:B:402:GLU:HG3	1.89	0.73
1:B:46:LYS:HD2	1:B:47:ILE:H	1.54	0.72
1:B:42:ASP:HB2	1:B:43:GLU:OE1	1.90	0.72
1:B:98:LYS:HA	1:B:98:LYS:CE	2.20	0.72
1:B:201:THR:HG23	1:B:204:GLN:CD	2.15	0.71
1:B:332:ARG:HG2	1:B:333:MET:HE2	1.72	0.71
1:A:294:ASN:HD21	1:B:294:ASN:HD21	1.39	0.71
1:A:312:ASN:HD22	1:A:315:LEU:H	1.37	0.71
1:B:397:MET:HE2	1:B:401:CYS:SG	2.31	0.71
1:A:393:THR:HB	1:A:394:PRO:HD2	1.73	0.70
1:B:136:SER:O	1:B:139:SER:HB2	1.91	0.70
1:A:41:TYR:CE2	1:A:47:ILE:HD11	2.26	0.69
1:A:235:GLU:O	1:A:238:GLU:HG3	1.92	0.69
1:B:200:PRO:HG2	1:B:205:TRP:CE2	2.28	0.68
1:A:366:THR:CG2	1:A:369:GLN:H	2.03	0.68
1:B:43:GLU:CD	1:B:43:GLU:H	2.01	0.68
1:A:46:LYS:HD2	1:A:47:ILE:N	2.04	0.67
1:B:133:VAL:HB	1:B:185:VAL:HG23	1.76	0.67
1:A:248:LYS:HG3	1:A:275:ALA:HB2	1.78	0.66
1:B:87:LEU:O	1:B:241:ARG:NH1	2.29	0.66
1:B:24:PHE:CZ	1:B:32:LYS:HG3	2.31	0.66
1:A:46:LYS:CD	1:A:47:ILE:H	2.06	0.65
1:A:251:ILE:HD13	1:A:272:LEU:HD23	1.78	0.65
1:B:99:ARG:NH2	4:B:481:HOH:O	2.29	0.65
1:B:29:ARG:NH2	1:B:374:ARG:O	2.29	0.65
1:A:78:GLU:OE1	1:A:81:ARG:NH2	2.29	0.65
1:B:187:LEU:HD12	1:B:188:PHE:N	2.12	0.65
1:B:321:GLN:NE2	1:B:325:ASP:OD1	2.30	0.65
1:A:18:LEU:CD1	1:A:37:ILE:HD12	2.27	0.65
1:A:162:ASP:OD2	1:A:165:ASN:ND2	2.30	0.65
1:B:21:ALA:O	1:B:25:ARG:HD2	1.97	0.65
1:A:99:ARG:NH2	4:A:476:HOH:O	2.30	0.64
1:A:29:ARG:HG3	4:A:571:HOH:O	1.98	0.64
1:B:27:ASP:OD2	1:B:29:ARG:NH1	2.29	0.64
1:B:81:ARG:NH1	4:B:641:HOH:O	2.31	0.63
1:A:398:ALA:HB3	1:A:399:PRO:HD3	1.79	0.63
1:A:37:ILE:HG23	1:A:39:LEU:HD22	1.79	0.63
1:A:126:LYS:HE2	1:A:129:ARG:HH12	1.63	0.63
1:B:46:LYS:O	1:B:48:PRO:HD3	1.97	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:332:ARG:HD2	4:B:547:HOH:O	1.98	0.62
1:B:29:ARG:HG3	1:B:29:ARG:NH1	2.08	0.62
1:B:344:LYS:NZ	1:B:402:GLU:OE2	2.30	0.62
1:B:393:THR:HB	1:B:394:PRO:HD2	1.79	0.62
1:A:136:SER:O	1:A:139:SER:HB3	1.99	0.62
1:B:99:ARG:HG2	1:B:274:ALA:O	1.99	0.62
1:B:201:THR:HG21	4:B:510:HOH:O	1.99	0.61
1:B:389:VAL:HG13	1:B:392:MET:HE3	1.82	0.61
1:B:46:LYS:HD2	1:B:47:ILE:HG13	1.82	0.61
1:B:241:ARG:CG	1:B:241:ARG:HH11	2.13	0.61
1:A:366:THR:HG22	1:A:369:GLN:HB2	1.83	0.61
1:B:241:ARG:HH11	1:B:241:ARG:HG3	1.65	0.61
1:B:348:ARG:HG2	1:B:348:ARG:NH1	2.14	0.61
1:A:340:THR:O	1:A:344:LYS:HB2	2.01	0.60
1:B:348:ARG:HH11	1:B:348:ARG:CG	2.13	0.60
1:B:389:VAL:O	1:B:392:MET:HG3	2.02	0.60
1:B:372:ARG:O	1:B:376:GLU:HB3	2.01	0.60
1:B:29:ARG:HH11	1:B:29:ARG:CG	2.08	0.59
1:A:121:LYS:HB3	1:A:121:LYS:HZ2	1.68	0.59
1:B:376:GLU:HG2	1:B:377:PHE:CE1	2.37	0.59
1:A:129:ARG:CD	1:A:156:ARG:HG3	2.33	0.58
1:A:398:ALA:O	1:A:402:GLU:HG3	2.03	0.58
1:B:397:MET:HE3	1:B:400:LEU:HD13	1.85	0.58
1:B:5:MET:N	1:B:7:GLU:OE1	2.36	0.58
1:B:229:ALA:HB3	1:B:236:ASP:OD1	2.04	0.58
1:A:318:ILE:O	1:A:322:GLU:HG3	2.04	0.58
1:B:58:GLN:O	1:B:62:GLU:HG3	2.04	0.58
1:B:101:ARG:HG3	1:B:101:ARG:HH11	1.67	0.58
1:B:265:GLU:HB3	4:B:601:HOH:O	2.03	0.57
1:A:154:GLU:OE2	1:A:156:ARG:HD2	2.05	0.57
1:A:201:THR:OG1	1:A:204:GLN:HG3	2.05	0.57
1:B:389:VAL:CG2	1:B:392:MET:HE2	2.31	0.57
1:A:46:LYS:O	1:A:48:PRO:HD3	2.05	0.57
1:A:366:THR:HB	1:A:369:GLN:OE1	2.05	0.56
1:B:46:LYS:HD2	1:B:47:ILE:N	2.19	0.56
1:A:248:LYS:HD2	1:A:275:ALA:CB	2.36	0.56
1:B:101:ARG:HG3	1:B:101:ARG:NH1	2.21	0.56
1:A:211:LEU:O	1:A:214:GLU:N	2.40	0.55
1:B:173:LEU:O	1:B:176:SER:HB2	2.07	0.55
1:B:237:ALA:HB1	1:B:241:ARG:NH1	2.21	0.55
1:B:170:PHE:CE2	1:B:174:ILE:HD11	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:389:VAL:CG1	1:B:392:MET:HE2	2.36	0.55
1:A:123:THR:HB	4:B:412:HOH:O	2.06	0.55
1:B:24:PHE:CZ	1:B:34:ASN:HB2	2.42	0.55
1:A:220:LEU:HG	1:A:251:ILE:HB	1.89	0.54
1:B:327:ARG:O	1:B:331:GLN:HG3	2.07	0.54
1:A:126:LYS:NZ	1:A:154:GLU:OE1	2.35	0.54
1:A:248:LYS:CD	1:A:275:ALA:HB2	2.38	0.54
1:B:324:THR:HG21	4:B:529:HOH:O	2.08	0.53
1:A:264:ASN:C	1:A:264:ASN:HD22	2.14	0.53
1:A:398:ALA:N	1:A:399:PRO:HD2	2.23	0.52
1:B:230:ARG:NH2	1:B:235:GLU:HB2	2.24	0.52
1:A:349:ASP:CG	1:A:351:SER:HG	2.18	0.52
1:B:397:MET:CE	1:B:400:LEU:HD22	2.39	0.52
1:B:144:LYS:HD2	1:B:148:ASN:OD1	2.10	0.52
1:B:129:ARG:HD3	1:B:154:GLU:OE2	2.10	0.52
1:B:179:GLU:O	1:B:179:GLU:HG3	2.08	0.52
1:A:248:LYS:HD2	1:A:275:ALA:HB2	1.92	0.52
1:A:61:LEU:HD12	1:B:61:LEU:HD12	1.92	0.51
1:B:332:ARG:NH2	4:B:606:HOH:O	2.30	0.51
1:B:28:GLU:OE1	1:B:28:GLU:HA	2.09	0.51
1:B:210:GLN:HA	1:B:246:MET:CE	2.40	0.51
1:B:212:SER:HB2	1:B:217:TRP:HE3	1.75	0.51
1:A:126:LYS:HE2	1:A:129:ARG:CZ	2.40	0.51
1:A:76:ILE:O	1:A:79:PHE:HB3	2.09	0.51
1:A:33:ILE:CD1	1:A:396:ASN:HB2	2.41	0.50
1:B:53:VAL:O	1:B:56:ALA:HB3	2.11	0.50
1:B:133:VAL:HB	1:B:185:VAL:CG2	2.41	0.50
1:B:170:PHE:O	1:B:173:LEU:HB3	2.12	0.50
1:B:321:GLN:HB2	4:B:625:HOH:O	2.10	0.50
1:B:37:ILE:HG23	1:B:39:LEU:HD22	1.94	0.50
1:B:367:LYS:HE3	1:B:383:ALA:O	2.12	0.49
1:A:187:LEU:C	1:A:187:LEU:HD23	2.38	0.49
1:B:397:MET:HE3	1:B:400:LEU:HD22	1.95	0.48
1:B:398:ALA:N	1:B:399:PRO:HD2	2.28	0.48
1:A:350:PHE:HB3	1:A:353:ILE:HD12	1.95	0.48
1:A:397:MET:HA	1:A:397:MET:CE	2.34	0.48
1:B:129:ARG:HD3	1:B:154:GLU:CD	2.38	0.48
1:B:331:GLN:NE2	4:B:548:HOH:O	2.43	0.48
1:A:12:ALA:HB2	1:B:286:GLN:NE2	2.29	0.48
1:B:349:ASP:OD1	1:B:351:SER:OG	2.31	0.48
1:B:83:THR:HG22	1:B:87:LEU:HD22	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:389:VAL:HG22	1:B:392:MET:CE	2.38	0.47
1:B:294:ASN:C	1:B:294:ASN:HD22	2.23	0.47
1:A:366:THR:HG22	1:A:369:GLN:CB	2.44	0.47
1:B:113:ARG:HA	1:B:113:ARG:HD3	1.75	0.47
1:B:56:ALA:O	1:B:59:TYR:HB3	2.14	0.47
1:B:201:THR:HG23	1:B:204:GLN:CG	2.45	0.47
1:A:5:MET:N	1:A:7:GLU:OE1	2.48	0.47
1:A:165:ASN:N	1:A:165:ASN:ND2	2.53	0.47
1:B:51:THR:HG21	4:B:589:HOH:O	2.14	0.47
1:B:237:ALA:CB	1:B:241:ARG:NH1	2.78	0.47
1:B:37:ILE:N	4:B:563:HOH:O	2.29	0.47
1:B:318:ILE:O	1:B:322:GLU:HG3	2.14	0.47
1:B:46:LYS:C	1:B:48:PRO:HD3	2.40	0.47
1:B:389:VAL:CB	1:B:392:MET:HE2	2.45	0.46
1:B:101:ARG:HD2	1:B:101:ARG:HA	1.74	0.46
1:A:229:ALA:HB3	1:A:236:ASP:OD1	2.15	0.46
1:B:389:VAL:HA	1:B:392:MET:HG3	1.98	0.46
1:A:146:VAL:HG23	1:A:147:PHE:N	2.31	0.46
1:B:74:ASP:N	1:B:74:ASP:OD1	2.42	0.46
1:B:187:LEU:HD12	1:B:187:LEU:C	2.40	0.46
1:B:212:SER:CB	1:B:217:TRP:HE3	2.29	0.46
1:B:332:ARG:HB2	4:B:586:HOH:O	2.15	0.46
1:A:29:ARG:O	1:A:32:LYS:HG2	2.16	0.46
1:A:397:MET:HE3	1:A:397:MET:CA	2.33	0.45
1:A:78:GLU:CD	1:A:81:ARG:HH21	2.24	0.45
1:B:101:ARG:HH11	1:B:101:ARG:CG	2.29	0.45
1:B:389:VAL:HA	1:B:392:MET:HE2	1.99	0.45
1:A:345:GLY:O	1:A:346:ALA:C	2.58	0.45
1:B:332:ARG:NE	4:B:586:HOH:O	2.46	0.45
1:A:398:ALA:HB3	1:A:399:PRO:CD	2.45	0.45
1:B:83:THR:O	1:B:87:LEU:HB2	2.17	0.45
1:B:158:TYR:CD1	1:B:173:LEU:CD1	3.00	0.45
1:A:24:PHE:HD1	1:A:380:TYR:CG	2.34	0.45
1:B:135:VAL:O	1:B:157:GLU:HA	2.17	0.45
1:B:162:ASP:O	1:B:166:HIS:N	2.50	0.45
1:B:220:LEU:HD13	1:B:251:ILE:CG2	2.46	0.45
1:A:158:TYR:CD1	1:A:173:LEU:HD21	2.52	0.45
1:A:396:ASN:O	1:A:399:PRO:HD2	2.16	0.45
1:B:348:ARG:HD3	4:B:617:HOH:O	2.15	0.45
1:A:126:LYS:O	1:A:126:LYS:HG2	2.17	0.44
1:B:170:PHE:CE2	1:B:174:ILE:CD1	3.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:18:LEU:HD13	3:A:411:HCl:C5'	2.47	0.44
1:A:47:ILE:HG13	1:B:69:LEU:HD21	1.99	0.44
1:B:200:PRO:HG2	1:B:205:TRP:CZ2	2.53	0.44
1:A:121:LYS:HB3	1:A:121:LYS:HZ3	1.78	0.44
1:A:212:SER:HB2	1:A:217:TRP:HE3	1.82	0.44
1:B:47:ILE:HA	1:B:48:PRO:HD2	1.82	0.44
1:A:8:ASN:N	1:A:8:ASN:OD1	2.36	0.44
1:A:158:TYR:CD1	1:A:173:LEU:CD2	3.01	0.44
1:A:212:SER:OG	1:A:247:HIS:NE2	2.49	0.44
1:A:366:THR:HG23	1:A:368:GLU:H	1.82	0.44
1:B:337:PHE:HB2	1:B:392:MET:HE1	1.98	0.44
1:A:69:LEU:O	1:B:264:ASN:HB3	2.18	0.44
1:A:333:MET:HA	1:A:333:MET:HE2	1.99	0.44
1:B:329:ARG:NH1	1:B:329:ARG:HG2	2.32	0.44
1:A:9:ILE:HD13	1:B:122:ASN:HB3	1.99	0.43
1:A:69:LEU:HD23	1:A:69:LEU:HA	1.47	0.43
1:A:41:TYR:CZ	1:A:47:ILE:HD11	2.53	0.43
1:A:194:ASN:HA	1:A:195:PRO:HA	1.81	0.43
1:B:158:TYR:CD1	1:B:173:LEU:HD13	2.53	0.43
1:B:344:LYS:CD	1:B:402:GLU:HG2	2.48	0.43
1:A:286:GLN:CD	1:B:12:ALA:HB2	2.44	0.43
1:A:335:GLN:H	1:A:335:GLN:HG2	1.56	0.43
1:A:367:LYS:H	1:A:367:LYS:HG2	1.58	0.43
1:A:398:ALA:N	1:A:399:PRO:CD	2.81	0.43
1:A:211:LEU:HD23	1:A:211:LEU:HA	1.61	0.43
1:B:27:ASP:OD1	1:B:27:ASP:N	2.48	0.43
1:B:398:ALA:N	1:B:399:PRO:CD	2.82	0.43
1:A:56:ALA:O	1:A:59:TYR:HB3	2.19	0.43
1:B:201:THR:HG22	4:B:618:HOH:O	2.18	0.43
1:A:24:PHE:CZ	1:A:34:ASN:HB2	2.54	0.43
1:B:86:LEU:HA	1:B:86:LEU:HD23	1.75	0.43
1:B:210:GLN:NE2	1:B:214:GLU:OE2	2.52	0.43
1:B:324:THR:HG22	4:B:479:HOH:O	2.19	0.43
1:A:312:ASN:HD22	1:A:312:ASN:C	2.27	0.42
1:A:20:LEU:HD23	1:A:20:LEU:HA	1.82	0.42
1:A:7:GLU:O	1:B:282:ARG:NH2	2.52	0.42
1:A:167:THR:OG1	1:A:168:LEU:N	2.52	0.42
1:A:212:SER:HB2	1:A:217:TRP:CE3	2.54	0.42
1:B:133:VAL:HA	1:B:185:VAL:HG23	2.00	0.42
1:A:15:ASP:HA	1:A:16:PRO:HD3	1.92	0.42
1:A:189:HIS:CD2	1:A:194:ASN:H	2.37	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:340:THR:O	1:B:344:LYS:HG3	2.20	0.42
1:A:17:ILE:O	1:A:20:LEU:HB2	2.19	0.42
1:B:348:ARG:H	1:B:348:ARG:HG3	1.48	0.42
1:B:356:GLN:OE1	1:B:361:SER:HA	2.19	0.42
1:A:40:TYR:CD1	1:A:40:TYR:C	2.98	0.42
1:B:144:LYS:HD2	4:B:629:HOH:O	2.19	0.42
1:B:177:LEU:HD23	1:B:177:LEU:HA	1.85	0.42
1:A:143:HIS:O	1:A:147:PHE:HD2	2.03	0.41
1:A:323:LEU:HD12	1:A:326:MET:HE3	2.02	0.41
1:A:348:ARG:H	1:A:348:ARG:HG2	1.60	0.41
1:B:78:GLU:O	1:B:78:GLU:HG3	2.20	0.41
1:B:15:ASP:HA	1:B:16:PRO:HD3	1.88	0.41
1:B:98:LYS:HE2	1:B:98:LYS:CA	2.36	0.41
1:B:374:ARG:NH1	4:B:649:HOH:O	2.52	0.41
1:A:396:ASN:C	1:A:399:PRO:HD2	2.45	0.41
1:B:344:LYS:HD3	1:B:402:GLU:HG2	2.03	0.41
1:A:331:GLN:O	1:A:335:GLN:HG2	2.20	0.41
1:A:348:ARG:CZ	1:A:409:LEU:HD22	2.50	0.41
1:A:371:LEU:HD12	1:A:371:LEU:O	2.21	0.41
1:B:38:GLY:CA	1:B:359:MET:HE1	2.50	0.41
1:A:29:ARG:HA	1:A:30:PRO:HD2	1.82	0.41
1:A:98:LYS:HD2	4:A:464:HOH:O	2.19	0.41
1:A:46:LYS:CG	1:A:47:ILE:N	2.84	0.41
1:B:210:GLN:HG3	1:B:214:GLU:OE2	2.21	0.41
1:B:334:ARG:NH2	1:B:358:GLY:O	2.54	0.41
1:A:278:GLU:O	1:A:278:GLU:HG2	2.11	0.41
1:B:210:GLN:HA	1:B:246:MET:HE3	2.03	0.41
1:B:212:SER:CB	1:B:217:TRP:CE3	3.04	0.41
1:B:334:ARG:HB3	1:B:389:VAL:HG11	2.03	0.41
1:B:393:THR:HA	1:B:394:PRO:HD3	1.85	0.41
1:A:160:TYR:O	1:A:168:LEU:HD23	2.21	0.41
1:B:359:MET:CE	4:B:456:HOH:O	2.44	0.41
1:A:81:ARG:HH11	1:A:81:ARG:HD3	1.72	0.40
1:B:170:PHE:CE1	1:B:204:GLN:HB3	2.55	0.40
1:A:9:ILE:CG2	1:B:286:GLN:HG3	2.51	0.40
1:B:125:VAL:CG1	1:B:185:VAL:HG22	2.52	0.40
1:A:393:THR:HB	1:A:394:PRO:CD	2.49	0.40
1:A:409:LEU:HD23	1:A:409:LEU:HA	1.82	0.40
1:B:152:LEU:HA	1:B:152:LEU:HD12	1.65	0.40
1:B:339:ASN:HD22	1:B:339:ASN:HA	1.60	0.40
1:B:213:VAL:HG21	1:B:246:MET:HB3	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:83:THR:O	1:A:87:LEU:HB2	2.21	0.40
1:A:99:ARG:HD2	1:A:274:ALA:O	2.21	0.40
1:B:194:ASN:HA	1:B:195:PRO:HA	1.83	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	394/396 (100%)	369 (94%)	22 (6%)	3 (1%)	16	11
1	B	394/396 (100%)	369 (94%)	21 (5%)	4 (1%)	12	8
All	All	788/792 (100%)	738 (94%)	43 (6%)	7 (1%)	14	9

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	69	LEU
1	B	233	LEU
1	A	90	LYS
1	B	301	HIS
1	A	69	LEU
1	A	301	HIS
1	B	36	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	320/320 (100%)	253 (79%)	67 (21%)	1	0
1	B	320/320 (100%)	250 (78%)	70 (22%)	1	0
All	All	640/640 (100%)	503 (79%)	137 (21%)	1	0

All (137) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	9	ILE
1	A	10	THR
1	A	18	LEU
1	A	23	LEU
1	A	28	GLU
1	A	29	ARG
1	A	32	LYS
1	A	33	ILE
1	A	39	LEU
1	A	58	GLN
1	A	61	LEU
1	A	69	LEU
1	A	78	GLU
1	A	86	LEU
1	A	87	LEU
1	A	90	LYS
1	A	98	LYS
1	A	112	LEU
1	A	119	LEU
1	A	121	LYS
1	A	126	LYS
1	A	129	ARG
1	A	144	LYS
1	A	152	LEU
1	A	156	ARG
1	A	162	ASP
1	A	165	ASN
1	A	168	LEU
1	A	173	LEU
1	A	174	ILE
1	A	178	ASN
1	A	202	LEU
1	A	206	GLN
1	A	211	LEU

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Mol	Chain	Res	Type
1	A	212	SER
1	A	214	GLU
1	A	215	LYS
1	A	218	LEU
1	A	223	PHE
1	A	240	LEU
1	A	246	MET
1	A	248	LYS
1	A	250	LEU
1	A	251	ILE
1	A	259	ASN
1	A	264	ASN
1	A	272	LEU
1	A	292	ARG
1	A	312	ASN
1	A	331	GLN
1	A	334	ARG
1	A	335	GLN
1	A	338	VAL
1	A	341	LEU
1	A	344	LYS
1	A	347	ASN
1	A	348	ARG
1	A	354	ILE
1	A	355	LYS
1	A	362	PHE
1	A	365	LEU
1	A	366	THR
1	A	367	LYS
1	A	370	VAL
1	A	371	LEU
1	A	375	GLU
1	A	400	LEU
1	B	5	MET
1	B	8	ASN
1	B	10	THR
1	B	23	LEU
1	B	25	ARG
1	B	27	ASP
1	B	29	ARG
1	B	32	LYS
1	B	39	LEU

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Mol	Chain	Res	Type
1	B	43	GLU
1	B	46	LYS
1	B	51	THR
1	B	55	LYS
1	B	61	LEU
1	B	62	GLU
1	B	69	LEU
1	B	73	ILE
1	B	81	ARG
1	B	86	LEU
1	B	87	LEU
1	B	90	LYS
1	B	98	LYS
1	B	99	ARG
1	B	101	ARG
1	B	113	ARG
1	B	119	LEU
1	B	121	LYS
1	B	126	LYS
1	B	129	ARG
1	B	133	VAL
1	B	139	SER
1	B	144	LYS
1	B	152	LEU
1	B	156	ARG
1	B	162	ASP
1	B	167	THR
1	B	168	LEU
1	B	185	VAL
1	B	187	LEU
1	B	201	THR
1	B	206	GLN
1	B	215	LYS
1	B	233	LEU
1	B	235	GLU
1	B	240	LEU
1	B	241	ARG
1	B	248	LYS
1	B	259	ASN
1	B	273	VAL
1	B	276	ASP
1	B	304	SER

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Mol	Chain	Res	Type
1	B	324	THR
1	B	332	ARG
1	B	338	VAL
1	B	341	LEU
1	B	342	GLN
1	B	343	GLU
1	B	348	ARG
1	B	351	SER
1	B	354	ILE
1	B	355	LYS
1	B	361	SER
1	B	367	LYS
1	B	368	GLU
1	B	371	LEU
1	B	372	ARG
1	B	373	LEU
1	B	374	ARG
1	B	375	GLU
1	B	409	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (27) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	84	GLN
1	A	122	ASN
1	A	142	ASN
1	A	165	ASN
1	A	189	HIS
1	A	206	GLN
1	A	226	GLN
1	A	259	ASN
1	A	264	ASN
1	A	312	ASN
1	A	328	GLN
1	A	339	ASN
1	A	357	ASN
1	A	388	ASN
1	B	63	ASN
1	B	84	GLN
1	B	96	ASN
1	B	122	ASN
1	B	206	GLN

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Mol	Chain	Res	Type
1	B	210	GLN
1	B	226	GLN
1	B	259	ASN
1	B	294	ASN
1	B	328	GLN
1	B	331	GLN
1	B	339	ASN
1	B	342	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 oligosaccharides 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$
3	HCI	B	411	-	11,11,11	0.98	1 (9%)	13,13,13	1.62	4 (30%)
3	HCI	A	411	-	11,11,11	1.05	1 (9%)	13,13,13	1.30	2 (15%)
2	PLP	A	410	1	15,15,16	1.34	3 (20%)	21,22,23	2.02	8 (38%)
2	PLP	B	410	1	15,15,16	1.64	4 (26%)	21,22,23	1.79	7 (33%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	HCI	B	411	-	-	2/5/5/5	0/1/1/1
3	HCI	A	411	-	-	2/5/5/5	0/1/1/1
2	PLP	A	410	1	-	2/6/6/8	0/1/1/1
2	PLP	B	410	1	-	3/6/6/8	0/1/1/1

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	410	PLP	C5-C4	4.45	1.45	1.40
2	A	410	PLP	C5-C4	2.89	1.43	1.40
3	A	411	HCI	C2-C1	2.72	1.56	1.50
2	A	410	PLP	C4A-C4	-2.57	1.46	1.51
3	B	411	HCI	C2-C1	2.53	1.56	1.50
2	B	410	PLP	C3-C2	2.44	1.43	1.41
2	A	410	PLP	C3-C2	2.39	1.43	1.41
2	B	410	PLP	C5A-C5	2.15	1.56	1.50
2	B	410	PLP	C4A-C4	-2.06	1.47	1.51

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	410	PLP	C6-C5-C4	4.84	122.07	118.10
3	A	411	HCI	O2-C1-C2	3.12	123.87	114.00
2	A	410	PLP	C2A-C2-C3	3.09	124.42	120.80
2	B	410	PLP	C3-C2-N1	-3.04	117.13	120.96
3	B	411	HCI	O2-C1-C2	2.95	123.31	114.00
2	A	410	PLP	C5-C6-N1	-2.92	119.09	123.83
3	A	411	HCI	O1-C1-C2	-2.81	114.17	123.09
2	B	410	PLP	C3-C4-C5	-2.68	115.38	118.59
2	B	410	PLP	C6-N1-C2	2.62	123.96	119.20
2	A	410	PLP	C6-N1-C2	2.62	123.96	119.20
2	A	410	PLP	C3-C4-C5	-2.59	115.48	118.59
2	B	410	PLP	C2A-C2-C3	2.57	123.80	120.80
3	B	411	HCI	C5'-C6'-C1'	2.54	124.19	120.61
2	B	410	PLP	C6-C5-C4	2.54	120.18	118.10
2	B	410	PLP	C5-C6-N1	-2.46	119.83	123.83
3	B	411	HCI	C4'-C5'-C6'	-2.33	117.36	120.24
2	A	410	PLP	C3-C2-N1	-2.32	118.04	120.96

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	410	PLP	O3P-P-O1P	2.24	119.55	110.83
3	B	411	HCI	O1-C1-C2	-2.20	116.12	123.09
2	B	410	PLP	C4A-C4-C5	2.18	123.19	120.94
2	A	410	PLP	O4P-C5A-C5	2.10	113.30	109.36

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	410	PLP	C4-C5-C5A-O4P
2	A	410	PLP	C6-C5-C5A-O4P
2	B	410	PLP	C6-C5-C5A-O4P
2	B	410	PLP	C5A-O4P-P-O1P
3	B	411	HCI	O1-C1-C2-C3
3	B	411	HCI	O2-C1-C2-C3
2	B	410	PLP	C5A-O4P-P-O2P
3	A	411	HCI	O2-C1-C2-C3
3	A	411	HCI	O1-C1-C2-C3

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	411	HCI	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

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.