



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 07:06 PM UTC

PDB ID : 2ZY2 / pdb_00002zy2
Title : dodecameric L-aspartate beta-decarboxylase
Authors : Chen, H.-J.; Ko, T.-P.; Lee, C.-Y.; Wang, N.-C.; Wang, A.H.-J.
Deposited on : 2009-01-13
Resolution : 3.30 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

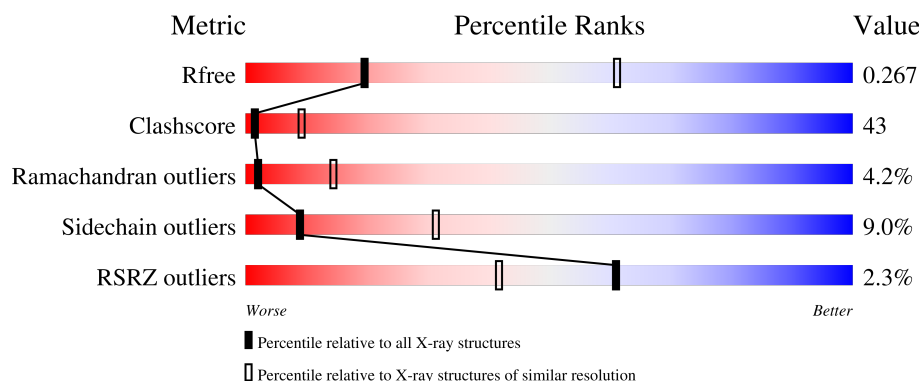
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

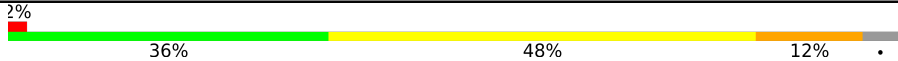
The reported resolution of this entry is 3.30 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1169 (3.32-3.28)
Clashscore	190562	1209 (3.32-3.28)
Ramachandran outliers	187476	1188 (3.32-3.28)
Sidechain outliers	187428	1187 (3.32-3.28)
RSRZ outliers	180081	1169 (3.32-3.28)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	544	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4147 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.

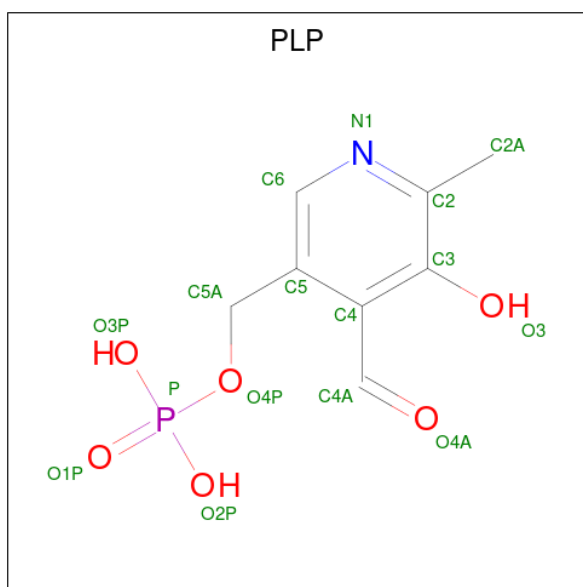
- Molecule 1 is a protein called L-aspartate 4-carboxylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	521	4095	2611	706	762	16	0	0	0

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	533	LYS	-	expression tag	UNP Q53IZ1
A	534	LEU	-	expression tag	UNP Q53IZ1
A	535	ALA	-	expression tag	UNP Q53IZ1
A	536	ALA	-	expression tag	UNP Q53IZ1
A	537	ALA	-	expression tag	UNP Q53IZ1
A	538	LEU	-	expression tag	UNP Q53IZ1
A	539	GLU	-	expression tag	UNP Q53IZ1
A	540	HIS	-	expression tag	UNP Q53IZ1
A	541	HIS	-	expression tag	UNP Q53IZ1
A	542	HIS	-	expression tag	UNP Q53IZ1
A	543	HIS	-	expression tag	UNP Q53IZ1
A	544	HIS	-	expression tag	UNP Q53IZ1
A	545	HIS	-	expression tag	UNP Q53IZ1

- 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		

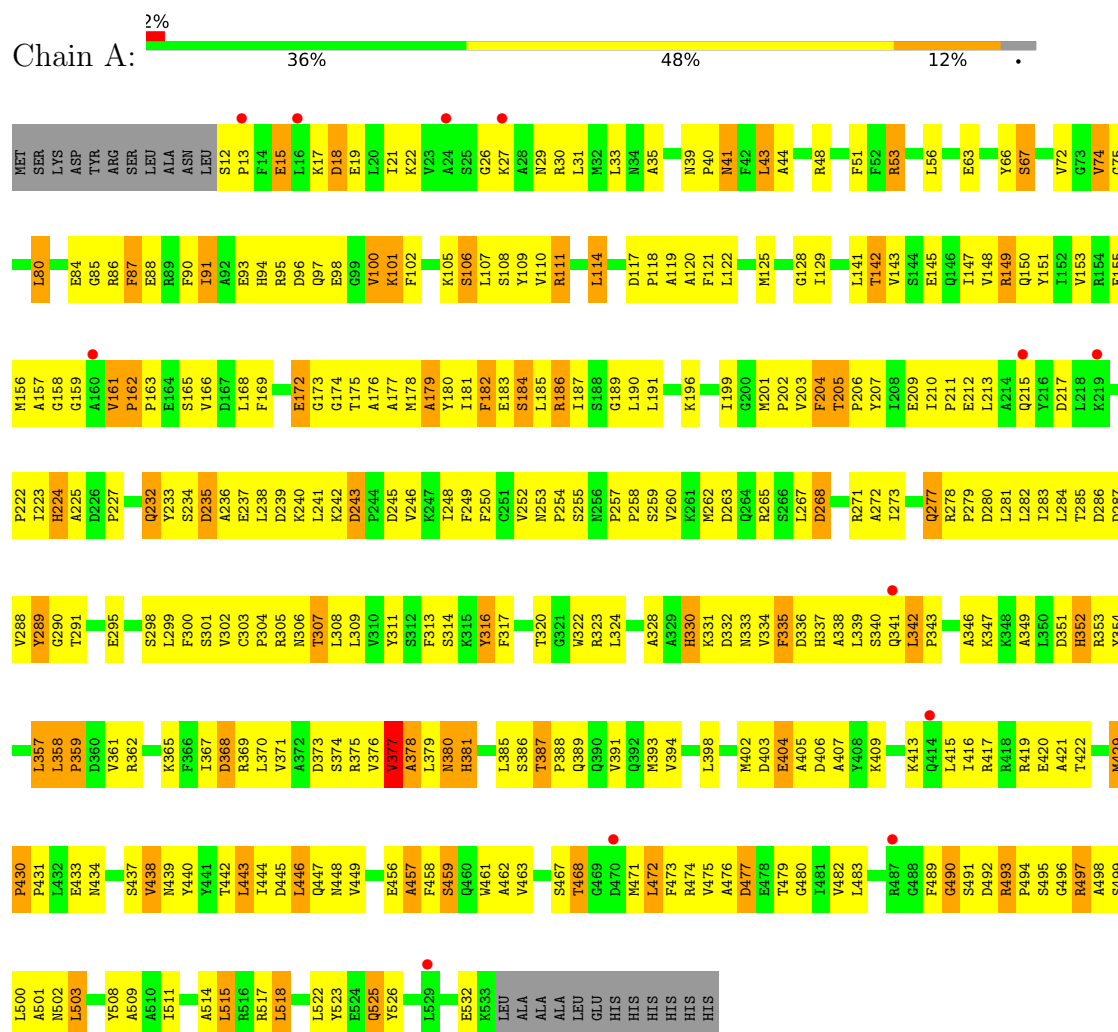
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	37	Total	O	0	0
			37	37		

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 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: L-aspartate 4-carboxylase



4 Data and refinement statistics

Property	Value	Source
Space group	F 4 3 2	Depositor
Cell constants a, b, c, α , β , γ	298.90Å 298.90Å 298.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 3.30 30.00 – 3.30	Depositor EDS
% Data completeness (in resolution range)	90.4 (30.00-3.30) 90.2 (30.00-3.30)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.27 (at 3.18Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.228 , 0.293 0.218 , 0.267	Depositor DCC
R_{free} test set	837 reflections (4.84%)	wwPDB-VP
Wilson B-factor (Å ²)	85.2	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 65.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	4147	wwPDB-VP
Average B, all atoms (Å ²)	77.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.12% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 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	0.85	1/4183 (0.0%)	1.23	35/5665 (0.6%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	91	ILE	CA-CB	-6.24	1.47	1.54

All (35) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	72	VAL	N-CA-C	12.14	121.95	110.53
1	A	314	SER	N-CA-C	11.08	123.36	111.28
1	A	162	PRO	N-CA-C	-9.21	99.47	110.70
1	A	430	PRO	N-CA-C	7.52	117.69	110.47
1	A	224	HIS	N-CA-C	7.40	121.12	110.24
1	A	87	PHE	N-CA-C	-7.22	103.34	111.07
1	A	532	GLU	N-CA-C	-7.14	104.56	113.28
1	A	161	VAL	N-CA-C	6.93	123.84	108.88
1	A	438	VAL	N-CA-C	-6.74	106.08	113.43
1	A	15	GLU	N-CA-C	-6.64	105.21	113.38
1	A	430	PRO	CA-C-N	6.52	127.99	119.84
1	A	430	PRO	C-N-CA	6.52	127.99	119.84
1	A	111	ARG	N-CA-C	6.37	121.31	112.45
1	A	316	TYR	N-CA-C	6.30	118.14	111.28
1	A	67	SER	N-CA-C	6.03	123.64	110.80
1	A	302	VAL	N-CA-C	5.99	116.73	110.62
1	A	243	ASP	CA-C-N	5.71	126.97	119.84
1	A	243	ASP	C-N-CA	5.71	126.97	119.84
1	A	490	GLY	CA-C-N	5.70	131.51	122.61
1	A	490	GLY	C-N-CA	5.70	131.51	122.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	357	LEU	N-CA-C	5.68	117.15	111.07
1	A	491	SER	N-CA-C	-5.61	105.51	112.47
1	A	43	LEU	N-CA-C	5.58	116.89	108.46
1	A	101	LYS	N-CA-C	-5.57	105.21	111.28
1	A	295	GLU	N-CA-C	-5.47	100.97	109.72
1	A	493	ARG	CA-C-N	-5.41	114.22	119.90
1	A	493	ARG	C-N-CA	-5.41	114.22	119.90
1	A	517	ARG	N-CA-C	-5.37	105.43	111.28
1	A	352	HIS	N-CA-C	-5.27	105.21	111.69
1	A	377	VAL	N-CA-C	5.24	120.23	109.34
1	A	303	CYS	CA-C-N	5.16	126.29	119.84
1	A	303	CYS	C-N-CA	5.16	126.29	119.84
1	A	173	GLY	CA-C-O	-5.12	117.88	121.88
1	A	114	LEU	N-CA-C	-5.03	106.99	113.23
1	A	27	LYS	N-CA-C	-5.01	100.12	110.80

There are no chirality outliers.

There are no planarity outliers.

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	4095	0	4080	353	0
2	A	15	0	7	1	0
3	A	37	0	0	0	0
All	All	4147	0	4087	353	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 43.

All (353) 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:525:GLN:HE21	1:A:525:GLN:HA	1.15	1.09
1:A:141:LEU:HD11	1:A:387:THR:HG22	1.42	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:53:ARG:HG2	1:A:100:VAL:HG22	1.45	0.96
1:A:262:MET:HE1	1:A:299:LEU:HD21	1.51	0.90
1:A:205:THR:OG1	1:A:206:PRO:HD3	1.76	0.86
1:A:288:VAL:HG13	1:A:289:TYR:HD1	1.39	0.85
1:A:525:GLN:HA	1:A:525:GLN:NE2	1.92	0.84
1:A:309:LEU:HB3	1:A:328:ALA:HB3	1.59	0.84
1:A:333:ASN:ND2	1:A:335:PHE:HB2	1.94	0.82
1:A:443:LEU:HD11	1:A:495:SER:HB2	1.62	0.82
1:A:429:MET:HB3	1:A:430:PRO:HD2	1.62	0.82
1:A:472:LEU:HD13	1:A:483:LEU:O	1.79	0.81
1:A:183:GLU:HG3	1:A:187:ILE:HD11	1.63	0.81
1:A:446:LEU:HD12	1:A:446:LEU:O	1.82	0.80
1:A:419:ARG:HD3	1:A:508:TYR:HE2	1.46	0.80
1:A:468:THR:OG1	1:A:494:PRO:HA	1.82	0.79
1:A:415:LEU:O	1:A:419:ARG:HG3	1.82	0.79
1:A:156:MET:HG3	1:A:309:LEU:HD21	1.63	0.79
1:A:225:ALA:O	1:A:227:PRO:HD3	1.82	0.78
1:A:176:ALA:HB1	1:A:180:TYR:CE2	2.17	0.78
1:A:183:GLU:O	1:A:187:ILE:HG12	1.82	0.78
1:A:288:VAL:C	1:A:290:GLY:H	1.91	0.77
1:A:376:VAL:HG23	1:A:376:VAL:O	1.84	0.77
1:A:145:GLU:O	1:A:149:ARG:HB3	1.85	0.77
1:A:283:ILE:HB	1:A:307:THR:HG23	1.65	0.77
1:A:255:SER:OG	1:A:258:PRO:HB2	1.84	0.76
1:A:288:VAL:HG13	1:A:289:TYR:CD1	2.20	0.76
1:A:525:GLN:HE21	1:A:525:GLN:CA	1.91	0.75
1:A:497:ARG:HG3	1:A:497:ARG:HH11	1.51	0.75
1:A:87:PHE:CZ	1:A:91:ILE:HD11	2.22	0.75
1:A:253:ASN:O	1:A:287:ASP:HA	1.87	0.75
1:A:105:LYS:C	1:A:402:MET:HE1	2.12	0.75
1:A:222:PRO:HB2	1:A:224:HIS:CE1	2.23	0.73
1:A:288:VAL:HG13	1:A:289:TYR:H	1.54	0.73
1:A:394:VAL:O	1:A:398:LEU:HD12	1.89	0.73
1:A:301:SER:O	1:A:304:PRO:HD3	1.89	0.72
1:A:19:GLU:HA	1:A:22:LYS:HG2	1.71	0.72
1:A:497:ARG:HH11	1:A:497:ARG:CG	2.02	0.72
1:A:106:SER:N	1:A:402:MET:HE1	2.04	0.72
1:A:186:ARG:HG3	1:A:186:ARG:HH11	1.53	0.72
1:A:419:ARG:HD3	1:A:508:TYR:CE2	2.25	0.72
1:A:358:LEU:HB2	1:A:359:PRO:HD2	1.70	0.71
1:A:330:HIS:ND1	1:A:331:LYS:N	2.37	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:334:VAL:HG23	1:A:335:PHE:N	2.06	0.71
1:A:125:MET:HE2	1:A:125:MET:HA	1.73	0.70
1:A:281:LEU:HD12	1:A:282:LEU:H	1.56	0.69
1:A:149:ARG:HD2	1:A:163:PRO:O	1.92	0.69
1:A:172:GLU:OE1	1:A:172:GLU:N	2.23	0.69
1:A:66:TYR:CE1	1:A:74:VAL:HG11	2.26	0.69
1:A:298:SER:O	1:A:301:SER:HB3	1.92	0.69
1:A:278:ARG:HH21	1:A:280:ASP:CG	2.01	0.68
1:A:201:MET:HB3	1:A:202:PRO:HA	1.74	0.68
1:A:29:ASN:HB3	1:A:482:VAL:HG23	1.76	0.67
1:A:94:HIS:HB3	1:A:97:GLN:OE1	1.93	0.67
1:A:288:VAL:O	1:A:290:GLY:N	2.27	0.67
1:A:204:PHE:HD2	1:A:204:PHE:O	1.77	0.67
1:A:334:VAL:O	1:A:337:HIS:N	2.27	0.67
1:A:367:ILE:HG23	1:A:368:ASP:N	2.10	0.67
1:A:434:ASN:HB3	1:A:437:SER:HB2	1.76	0.67
1:A:248:ILE:HG12	1:A:249:PHE:N	2.09	0.66
1:A:190:LEU:HD21	1:A:339:LEU:HD23	1.78	0.66
1:A:151:TYR:OH	1:A:291:THR:HG21	1.94	0.66
1:A:243:ASP:OD1	1:A:243:ASP:C	2.38	0.66
1:A:334:VAL:CG2	1:A:335:PHE:N	2.58	0.66
1:A:246:VAL:HG13	1:A:246:VAL:O	1.95	0.66
1:A:210:ILE:N	1:A:211:PRO:HD2	2.11	0.65
1:A:204:PHE:HE2	1:A:207:TYR:CD2	2.14	0.65
1:A:288:VAL:C	1:A:290:GLY:N	2.54	0.65
1:A:189:GLY:C	1:A:191:LEU:H	2.04	0.65
1:A:347:LYS:O	1:A:351:ASP:OD1	2.15	0.65
1:A:268:ASP:O	1:A:271:ARG:HB3	1.96	0.65
1:A:41:ASN:C	1:A:41:ASN:HD22	2.05	0.64
1:A:333:ASN:HD22	1:A:335:PHE:HB2	1.62	0.64
1:A:178:MET:O	1:A:180:TYR:N	2.30	0.64
1:A:26:GLY:O	1:A:30:ARG:NH1	2.31	0.64
1:A:475:VAL:CG1	1:A:476:ALA:N	2.60	0.64
1:A:176:ALA:HB1	1:A:180:TYR:HE2	1.63	0.64
1:A:445:ASP:O	1:A:449:VAL:HG23	1.98	0.64
1:A:459:SER:O	1:A:463:VAL:HG23	1.98	0.64
1:A:288:VAL:HG13	1:A:289:TYR:N	2.14	0.63
1:A:248:ILE:HG13	1:A:282:LEU:HB2	1.81	0.63
1:A:337:HIS:O	1:A:340:SER:HB2	1.98	0.62
1:A:174:GLY:O	1:A:177:ALA:HB3	2.00	0.62
1:A:181:ILE:HA	1:A:370:LEU:HD21	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:40:PRO:HA	1:A:501:ALA:O	2.00	0.61
1:A:93:GLU:O	1:A:93:GLU:HG2	1.99	0.61
1:A:525:GLN:NE2	1:A:525:GLN:CA	2.54	0.61
1:A:357:LEU:HB3	1:A:358:LEU:HD22	1.83	0.60
1:A:367:ILE:CG2	1:A:368:ASP:N	2.63	0.60
1:A:102:PHE:HE1	1:A:402:MET:SD	2.25	0.60
1:A:189:GLY:C	1:A:191:LEU:N	2.57	0.60
1:A:282:LEU:HD23	1:A:334:VAL:HG21	1.83	0.59
1:A:178:MET:HG3	1:A:207:TYR:HE1	1.68	0.59
1:A:15:GLU:HA	1:A:18:ASP:HB2	1.83	0.59
1:A:475:VAL:HG13	1:A:476:ALA:N	2.17	0.59
1:A:109:TYR:CE2	1:A:114:LEU:HD21	2.36	0.59
1:A:442:THR:HG22	1:A:498:ALA:HB3	1.83	0.59
1:A:351:ASP:OD2	1:A:362:ARG:NH1	2.36	0.58
1:A:340:SER:C	1:A:342:LEU:H	2.11	0.58
1:A:110:VAL:HG11	1:A:121:PHE:CG	2.39	0.58
1:A:446:LEU:HD12	1:A:446:LEU:C	2.28	0.58
1:A:282:LEU:CD2	1:A:334:VAL:HG21	2.34	0.57
1:A:467:SER:HA	1:A:494:PRO:HG3	1.85	0.57
1:A:17:LYS:O	1:A:21:ILE:HG13	2.04	0.57
1:A:149:ARG:HA	1:A:168:LEU:HD11	1.85	0.57
1:A:204:PHE:CE2	1:A:207:TYR:CD2	2.92	0.57
1:A:281:LEU:HD12	1:A:282:LEU:N	2.20	0.57
1:A:369:ARG:O	1:A:370:LEU:C	2.48	0.57
1:A:336:ASP:OD2	1:A:365:LYS:HG2	2.05	0.57
1:A:398:LEU:O	1:A:402:MET:HG3	2.04	0.56
1:A:254:PRO:HD2	1:A:289:TYR:HB2	1.88	0.56
1:A:169:PHE:CE1	1:A:371:VAL:HG22	2.41	0.56
1:A:153:VAL:O	1:A:158:GLY:N	2.38	0.56
1:A:225:ALA:HB2	1:A:233:TYR:CE2	2.41	0.56
1:A:499:SER:HB3	1:A:502:ASN:OD1	2.06	0.56
1:A:182:PHE:O	1:A:183:GLU:C	2.49	0.56
1:A:98:GLU:HA	1:A:101:LYS:HE3	1.88	0.55
1:A:199:ILE:HG22	1:A:201:MET:HG2	1.88	0.55
1:A:305:ARG:HG2	1:A:332:ASP:O	2.06	0.55
1:A:405:ALA:O	1:A:406:ASP:HB2	2.07	0.55
1:A:347:LYS:HB3	1:A:362:ARG:HE	1.72	0.55
1:A:386:SER:OG	1:A:389:GLN:HB2	2.06	0.55
1:A:257:PRO:HG2	1:A:258:PRO:HD3	1.89	0.55
1:A:468:THR:O	1:A:471:MET:HB2	2.06	0.55
1:A:180:TYR:CE1	1:A:374:SER:HB2	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:252:VAL:HG22	1:A:286:ASP:HB3	1.89	0.54
1:A:98:GLU:O	1:A:101:LYS:HG2	2.08	0.54
1:A:117:ASP:HB3	1:A:120:ALA:HB3	1.88	0.54
1:A:184:SER:OG	1:A:373:ASP:OD2	2.14	0.54
1:A:387:THR:O	1:A:391:VAL:HG23	2.08	0.54
1:A:41:ASN:HD21	1:A:419:ARG:HH22	1.56	0.54
1:A:44:ALA:O	1:A:48:ARG:NH1	2.41	0.54
1:A:361:VAL:HG12	1:A:361:VAL:O	2.07	0.54
1:A:394:VAL:HG12	1:A:398:LEU:CD1	2.38	0.53
1:A:199:ILE:O	1:A:201:MET:HG3	2.09	0.53
1:A:243:ASP:O	1:A:246:VAL:HG12	2.08	0.53
1:A:305:ARG:CG	1:A:332:ASP:O	2.56	0.53
1:A:246:VAL:O	1:A:246:VAL:CG1	2.56	0.53
1:A:365:LYS:O	1:A:369:ARG:HG3	2.09	0.53
1:A:237:GLU:O	1:A:240:LYS:HG3	2.09	0.53
1:A:313:PHE:CD1	1:A:393:MET:HE2	2.44	0.53
1:A:41:ASN:ND2	1:A:419:ARG:HH12	2.07	0.52
1:A:178:MET:C	1:A:180:TYR:N	2.67	0.52
1:A:186:ARG:HH11	1:A:186:ARG:CG	2.20	0.52
1:A:289:TYR:HD1	1:A:289:TYR:H	1.56	0.52
1:A:342:LEU:HD13	1:A:343:PRO:HD2	1.92	0.52
1:A:375:ARG:O	1:A:376:VAL:HG22	2.09	0.52
1:A:379:LEU:O	1:A:380:ASN:C	2.52	0.52
1:A:53:ARG:HG2	1:A:100:VAL:CG2	2.27	0.52
1:A:183:GLU:CG	1:A:187:ILE:HD11	2.38	0.52
1:A:461:TRP:CD1	1:A:526:TYR:HD1	2.27	0.52
1:A:479:THR:OG1	1:A:480:GLY:N	2.42	0.52
1:A:210:ILE:N	1:A:211:PRO:CD	2.72	0.52
1:A:236:ALA:O	1:A:239:ASP:HB2	2.10	0.52
1:A:41:ASN:C	1:A:41:ASN:ND2	2.66	0.52
1:A:109:TYR:HE2	1:A:114:LEU:HD21	1.75	0.52
1:A:324:LEU:HD13	1:A:393:MET:HB2	1.91	0.51
1:A:385:LEU:HD12	1:A:386:SER:H	1.74	0.51
1:A:386:SER:HG	1:A:389:GLN:CD	2.14	0.51
1:A:93:GLU:O	1:A:93:GLU:CG	2.58	0.51
1:A:346:ALA:O	1:A:349:ALA:HB3	2.11	0.51
1:A:143:VAL:O	1:A:147:ILE:HG13	2.10	0.51
1:A:180:TYR:O	1:A:184:SER:HB2	2.10	0.51
1:A:369:ARG:C	1:A:371:VAL:N	2.65	0.51
1:A:406:ASP:O	1:A:407:ALA:C	2.51	0.51
1:A:334:VAL:O	1:A:335:PHE:C	2.54	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:342:LEU:O	1:A:347:LYS:NZ	2.42	0.51
1:A:371:VAL:O	1:A:374:SER:OG	2.27	0.51
1:A:33:LEU:HD13	1:A:482:VAL:HG11	1.93	0.50
1:A:87:PHE:CE2	1:A:91:ILE:HD11	2.45	0.50
1:A:174:GLY:O	1:A:175:THR:C	2.53	0.50
1:A:474:ARG:NH2	1:A:518:LEU:HB2	2.26	0.50
1:A:157:ALA:C	1:A:159:GLY:H	2.20	0.50
1:A:445:ASP:HB3	1:A:448:ASN:HD22	1.77	0.50
1:A:409:LYS:O	1:A:413:LYS:HG3	2.12	0.50
1:A:204:PHE:O	1:A:204:PHE:CD2	2.61	0.50
1:A:282:LEU:CD2	1:A:334:VAL:CG2	2.89	0.50
1:A:19:GLU:HA	1:A:22:LYS:CG	2.39	0.50
1:A:162:PRO:HG2	1:A:165:SER:OG	2.12	0.50
1:A:385:LEU:HD11	1:A:389:GLN:CD	2.36	0.50
1:A:445:ASP:OD2	1:A:448:ASN:ND2	2.45	0.50
1:A:190:LEU:CD2	1:A:339:LEU:HD23	2.40	0.49
1:A:316:TYR:HD2	1:A:317:PHE:CZ	2.30	0.49
1:A:443:LEU:HD12	1:A:443:LEU:C	2.38	0.49
1:A:39:ASN:OD1	1:A:320:THR:HG21	2.13	0.49
1:A:248:ILE:HG13	1:A:282:LEU:C	2.37	0.49
1:A:376:VAL:O	1:A:376:VAL:CG2	2.56	0.49
1:A:394:VAL:HG12	1:A:398:LEU:HD11	1.94	0.49
1:A:105:LYS:O	1:A:106:SER:C	2.56	0.49
1:A:174:GLY:O	1:A:177:ALA:N	2.45	0.49
1:A:182:PHE:O	1:A:185:LEU:N	2.45	0.49
1:A:223:ILE:CD1	1:A:241:LEU:HD21	2.42	0.49
1:A:473:PHE:O	1:A:477:ASP:HB2	2.12	0.49
1:A:475:VAL:HG11	1:A:483:LEU:HD12	1.94	0.49
1:A:278:ARG:C	1:A:280:ASP:H	2.20	0.48
1:A:514:ALA:O	1:A:515:LEU:C	2.56	0.48
1:A:334:VAL:CG2	1:A:335:PHE:H	2.25	0.48
1:A:394:VAL:CG1	1:A:398:LEU:HD11	2.44	0.48
1:A:232:GLN:CA	1:A:232:GLN:HE21	2.25	0.48
1:A:239:ASP:OD1	1:A:242:LYS:HE3	2.12	0.48
1:A:128:GLY:O	1:A:387:THR:HB	2.13	0.48
1:A:186:ARG:O	1:A:187:ILE:C	2.56	0.48
1:A:211:PRO:C	1:A:213:LEU:H	2.21	0.48
1:A:492:ASP:OD1	1:A:492:ASP:O	2.32	0.47
1:A:439:ASN:O	1:A:440:TYR:C	2.57	0.47
1:A:56:LEU:HD23	1:A:56:LEU:HA	1.63	0.47
1:A:80:LEU:O	1:A:80:LEU:HG	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:415:LEU:HD11	1:A:419:ARG:NH2	2.30	0.47
1:A:442:THR:CG2	1:A:498:ALA:HB3	2.45	0.47
1:A:490:GLY:C	1:A:492:ASP:N	2.71	0.47
1:A:518:LEU:C	1:A:518:LEU:HD23	2.39	0.47
1:A:31:LEU:HD11	1:A:35:ALA:HB3	1.97	0.47
1:A:257:PRO:N	1:A:258:PRO:CD	2.78	0.47
1:A:196:LYS:HB2	1:A:245:ASP:O	2.15	0.47
1:A:201:MET:O	1:A:233:TYR:HE2	1.97	0.47
1:A:265:ARG:HH11	1:A:265:ARG:HG2	1.80	0.47
1:A:406:ASP:HB3	1:A:409:LYS:HB3	1.97	0.47
1:A:248:ILE:HG13	1:A:282:LEU:O	2.14	0.47
1:A:308:LEU:HD23	1:A:308:LEU:HA	1.65	0.47
1:A:178:MET:C	1:A:180:TYR:H	2.24	0.46
1:A:334:VAL:O	1:A:336:ASP:N	2.48	0.46
1:A:358:LEU:HD23	1:A:358:LEU:N	2.30	0.46
1:A:472:LEU:N	1:A:472:LEU:HD23	2.30	0.46
1:A:205:THR:O	1:A:209:GLU:HG3	2.16	0.46
1:A:443:LEU:HD12	1:A:444:ILE:N	2.30	0.46
1:A:199:ILE:HG22	1:A:201:MET:CG	2.45	0.46
1:A:74:VAL:HG12	1:A:75:GLY:N	2.30	0.46
1:A:178:MET:O	1:A:179:ALA:C	2.57	0.46
1:A:175:THR:O	1:A:176:ALA:C	2.58	0.46
1:A:320:THR:O	1:A:323:ARG:HD2	2.14	0.46
1:A:203:VAL:HG12	1:A:204:PHE:N	2.31	0.46
1:A:492:ASP:O	1:A:493:ARG:HB3	2.15	0.46
1:A:248:ILE:HD11	1:A:284:LEU:HB2	1.97	0.46
1:A:257:PRO:CD	1:A:258:PRO:HD3	2.46	0.46
1:A:313:PHE:CE1	1:A:393:MET:HE2	2.51	0.46
1:A:248:ILE:HG13	1:A:282:LEU:CB	2.44	0.45
1:A:283:ILE:HG13	1:A:306:ASN:O	2.16	0.45
1:A:299:LEU:HD23	1:A:299:LEU:HA	1.64	0.45
1:A:102:PHE:CE1	1:A:402:MET:SD	3.08	0.45
1:A:456:GLU:O	1:A:459:SER:OG	2.35	0.45
1:A:254:PRO:HD3	1:A:290:GLY:HA2	1.98	0.45
1:A:340:SER:C	1:A:342:LEU:N	2.73	0.45
1:A:94:HIS:C	1:A:96:ASP:N	2.75	0.45
1:A:84:GLU:O	1:A:85:GLY:C	2.59	0.45
1:A:252:VAL:HG12	1:A:254:PRO:O	2.16	0.45
1:A:416:ILE:HG21	1:A:439:ASN:HB3	1.99	0.45
1:A:333:ASN:HD21	1:A:335:PHE:HB2	1.75	0.45
1:A:94:HIS:C	1:A:96:ASP:H	2.24	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:210:ILE:H	1:A:211:PRO:HD2	1.80	0.45
1:A:376:VAL:O	1:A:378:ALA:N	2.50	0.45
1:A:313:PHE:HB2	1:A:324:LEU:HB2	1.98	0.45
1:A:322:TRP:HB3	1:A:324:LEU:HG	1.99	0.45
1:A:379:LEU:O	1:A:381:HIS:N	2.50	0.45
1:A:94:HIS:O	1:A:96:ASP:N	2.49	0.45
1:A:278:ARG:C	1:A:280:ASP:N	2.75	0.45
1:A:172:GLU:HB2	1:A:176:ALA:HB2	1.98	0.45
1:A:203:VAL:CG1	1:A:204:PHE:N	2.79	0.45
1:A:489:PHE:HB3	1:A:490:GLY:H	1.53	0.45
1:A:86:ARG:NH1	1:A:86:ARG:HG3	2.32	0.44
1:A:285:THR:OG1	1:A:287:ASP:OD1	2.20	0.44
1:A:258:PRO:O	1:A:259:SER:HB2	2.18	0.44
1:A:298:SER:O	1:A:301:SER:N	2.34	0.44
1:A:362:ARG:HG3	1:A:362:ARG:HH11	1.82	0.44
1:A:106:SER:HA	1:A:402:MET:CE	2.47	0.44
1:A:415:LEU:HD11	1:A:419:ARG:HH21	1.82	0.44
1:A:260:VAL:HG12	1:A:437:SER:HA	1.99	0.44
1:A:475:VAL:C	1:A:477:ASP:H	2.25	0.44
1:A:222:PRO:HB2	1:A:224:HIS:HE1	1.78	0.44
1:A:238:LEU:O	1:A:241:LEU:HG	2.18	0.44
1:A:404:GLU:OE2	1:A:404:GLU:HA	2.17	0.44
1:A:86:ARG:HG3	1:A:86:ARG:HH11	1.81	0.44
1:A:232:GLN:HA	1:A:232:GLN:NE2	2.32	0.44
1:A:241:LEU:HA	1:A:246:VAL:HG11	2.00	0.44
1:A:358:LEU:N	1:A:358:LEU:CD2	2.81	0.43
1:A:377:VAL:O	1:A:379:LEU:N	2.51	0.43
1:A:43:LEU:O	1:A:43:LEU:HD12	2.18	0.43
1:A:471:MET:HE2	1:A:515:LEU:CD1	2.48	0.43
1:A:502:ASN:OD1	1:A:503:LEU:HD12	2.18	0.43
1:A:87:PHE:CE2	1:A:91:ILE:CD1	3.01	0.43
1:A:324:LEU:HB3	1:A:393:MET:HE3	1.99	0.43
1:A:444:ILE:N	1:A:496:GLY:O	2.44	0.43
1:A:66:TYR:CZ	1:A:74:VAL:HG11	2.54	0.43
1:A:204:PHE:CD2	1:A:204:PHE:C	2.97	0.43
1:A:33:LEU:HD13	1:A:482:VAL:CG1	2.48	0.43
1:A:66:TYR:CE1	1:A:74:VAL:CG1	2.99	0.43
1:A:217:ASP:OD2	1:A:217:ASP:C	2.62	0.43
1:A:422:THR:CG2	1:A:509:ALA:HB2	2.49	0.43
1:A:19:GLU:O	1:A:22:LYS:HB2	2.19	0.43
1:A:151:TYR:CE2	1:A:155:GLU:HG3	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:248:ILE:HG12	1:A:249:PHE:H	1.83	0.43
1:A:257:PRO:CG	1:A:258:PRO:HD3	2.49	0.43
1:A:41:ASN:ND2	1:A:419:ARG:HH22	2.15	0.43
1:A:353:ARG:NE	1:A:354:TYR:CE2	2.86	0.43
1:A:474:ARG:HG3	1:A:518:LEU:HD12	2.01	0.43
1:A:289:TYR:CD1	1:A:289:TYR:N	2.87	0.42
1:A:306:ASN:ND2	1:A:334:VAL:HG11	2.34	0.42
1:A:403:ASP:O	1:A:403:ASP:CG	2.60	0.42
1:A:416:ILE:O	1:A:417:ARG:C	2.62	0.42
1:A:12:SER:HB3	1:A:13:PRO:HD3	2.01	0.42
1:A:153:VAL:CG2	1:A:166:VAL:HG21	2.50	0.42
1:A:156:MET:HE3	1:A:311:TYR:CD1	2.55	0.42
1:A:190:LEU:HD21	1:A:339:LEU:CD2	2.47	0.42
1:A:232:GLN:CA	1:A:232:GLN:NE2	2.82	0.42
1:A:335:PHE:O	1:A:339:LEU:HG	2.20	0.42
1:A:278:ARG:O	1:A:280:ASP:N	2.52	0.42
1:A:143:VAL:HG12	1:A:147:ILE:HD11	2.02	0.42
1:A:254:PRO:HD2	1:A:289:TYR:C	2.45	0.42
1:A:369:ARG:O	1:A:371:VAL:N	2.52	0.42
1:A:462:ALA:HB1	1:A:522:LEU:HD13	2.01	0.42
1:A:474:ARG:CZ	1:A:518:LEU:HD12	2.50	0.42
1:A:29:ASN:HB3	1:A:482:VAL:CG2	2.47	0.42
1:A:298:SER:C	1:A:300:PHE:N	2.77	0.42
1:A:430:PRO:HA	1:A:431:PRO:HD3	1.74	0.42
1:A:419:ARG:HD2	1:A:500:LEU:O	2.20	0.42
1:A:458:PHE:CE1	1:A:523:TYR:HA	2.55	0.42
1:A:15:GLU:CA	1:A:18:ASP:HB2	2.49	0.41
1:A:141:LEU:O	1:A:142:THR:C	2.64	0.41
1:A:234:SER:O	1:A:235:ASP:C	2.62	0.41
1:A:41:ASN:HD21	1:A:419:ARG:NH2	2.18	0.41
1:A:106:SER:HA	1:A:402:MET:HE3	2.01	0.41
1:A:338:ALA:C	1:A:340:SER:H	2.28	0.41
1:A:90:PHE:CD1	1:A:90:PHE:C	2.98	0.41
1:A:201:MET:HB3	1:A:201:MET:HE2	1.94	0.41
1:A:223:ILE:HD11	1:A:241:LEU:HD21	2.01	0.41
1:A:289:TYR:HE1	2:A:900:PLP:HO3	1.67	0.41
1:A:367:ILE:HD12	1:A:367:ILE:HA	1.85	0.41
1:A:508:TYR:O	1:A:511:ILE:HB	2.21	0.41
1:A:41:ASN:CG	1:A:419:ARG:HH12	2.29	0.41
1:A:148:VAL:HG21	1:A:393:MET:HG2	2.01	0.41
1:A:246:VAL:CG1	1:A:278:ARG:HH12	2.34	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:118:PRO:HG2	1:A:119:ALA:H	1.86	0.41
1:A:161:VAL:HA	1:A:162:PRO:HD2	1.96	0.41
1:A:272:ALA:O	1:A:273:ILE:C	2.64	0.41
1:A:475:VAL:HG12	1:A:476:ALA:H	1.86	0.41
1:A:497:ARG:HG3	1:A:497:ARG:NH1	2.29	0.41
1:A:31:LEU:HD11	1:A:35:ALA:CB	2.50	0.41
1:A:457:ALA:HB1	1:A:526:TYR:OH	2.20	0.41
1:A:51:PHE:CE1	1:A:129:ILE:HG13	2.55	0.41
1:A:108:SER:O	1:A:111:ARG:N	2.54	0.41
1:A:150:GLN:HE21	1:A:150:GLN:HB2	1.74	0.41
1:A:339:LEU:HD13	1:A:369:ARG:CZ	2.51	0.41
1:A:420:GLU:O	1:A:421:ALA:C	2.64	0.41
1:A:444:ILE:O	1:A:496:GLY:N	2.50	0.41
1:A:475:VAL:CG1	1:A:476:ALA:H	2.32	0.41
1:A:87:PHE:CD2	1:A:122:LEU:HD11	2.55	0.41
1:A:267:LEU:O	1:A:268:ASP:C	2.64	0.41
1:A:413:LYS:O	1:A:416:ILE:N	2.51	0.41
1:A:277:GLN:O	1:A:278:ARG:HD2	2.21	0.40
1:A:106:SER:O	1:A:107:LEU:C	2.64	0.40
1:A:181:ILE:HA	1:A:370:LEU:CD2	2.49	0.40
1:A:304:PRO:O	1:A:330:HIS:HB2	2.20	0.40
1:A:178:MET:HE3	1:A:250:PHE:CZ	2.57	0.40
1:A:186:ARG:CG	1:A:186:ARG:NH1	2.83	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	519/544 (95%)	402 (78%)	95 (18%)	22 (4%)	2 14

All (22) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	377	VAL
1	A	179	ALA
1	A	289	TYR
1	A	378	ALA
1	A	380	ASN
1	A	404	GLU
1	A	142	THR
1	A	172	GLU
1	A	341	GLN
1	A	381	HIS
1	A	95	ARG
1	A	212	GLU
1	A	330	HIS
1	A	335	PHE
1	A	359	PRO
1	A	447	GLN
1	A	459	SER
1	A	182	PHE
1	A	263	ASP
1	A	429	MET
1	A	457	ALA
1	A	205	THR

5.3.2 Protein sidechains ⓘ

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	434/453 (96%)	395 (91%)	39 (9%)	9 31

All (39) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	18	ASP
1	A	41	ASN
1	A	53	ARG
1	A	63	GLU
1	A	67	SER

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Mol	Chain	Res	Type
1	A	74	VAL
1	A	80	LEU
1	A	88	GLU
1	A	100	VAL
1	A	106	SER
1	A	149	ARG
1	A	184	SER
1	A	186	ARG
1	A	204	PHE
1	A	215	GLN
1	A	232	GLN
1	A	235	ASP
1	A	268	ASP
1	A	277	GLN
1	A	279	PRO
1	A	307	THR
1	A	342	LEU
1	A	352	HIS
1	A	358	LEU
1	A	368	ASP
1	A	387	THR
1	A	388	PRO
1	A	433	GLU
1	A	438	VAL
1	A	443	LEU
1	A	446	LEU
1	A	468	THR
1	A	472	LEU
1	A	477	ASP
1	A	497	ARG
1	A	503	LEU
1	A	515	LEU
1	A	518	LEU
1	A	525	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	41	ASN
1	A	133	ASN
1	A	215	GLN
1	A	229	ASN

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Mol	Chain	Res	Type
1	A	341	GLN
1	A	380	ASN
1	A	392	GLN
1	A	447	GLN
1	A	448	ASN
1	A	460	GLN
1	A	464	GLN
1	A	504	ASN
1	A	525	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](#)

1 ligand is 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	A	900	1	15,15,16	2.39	6 (40%)	21,22,23	2.86	8 (38%)

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	A	900	1	-	0/6/6/8	0/1/1/1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	900	PLP	C5A-C5	5.93	1.66	1.50
2	A	900	PLP	P-O3P	-3.06	1.43	1.54
2	A	900	PLP	C6-N1	2.95	1.40	1.34
2	A	900	PLP	C6-C5	2.87	1.43	1.37
2	A	900	PLP	C2-N1	2.49	1.38	1.33
2	A	900	PLP	O4P-C5A	2.32	1.53	1.44

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	900	PLP	O2P-P-O4P	10.00	132.75	106.67
2	A	900	PLP	O4P-C5A-C5	4.02	116.89	109.36
2	A	900	PLP	O3P-P-O1P	3.90	126.03	110.83
2	A	900	PLP	O3P-P-O4P	-3.33	97.99	106.67
2	A	900	PLP	C6-C5-C4	-2.66	115.91	118.10
2	A	900	PLP	O3P-P-O2P	-2.35	99.00	107.80
2	A	900	PLP	O2P-P-O1P	-2.32	101.81	110.83
2	A	900	PLP	C4A-C4-C3	-2.14	116.96	120.52

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	900	PLP	1	0

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data [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	521/544 (95%)	-0.08	12 (2%) 61 42	27, 74, 130, 163	0

All (12) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	16	LEU	3.0
1	A	13	PRO	2.8
1	A	487	ARG	2.3
1	A	215	GLN	2.3
1	A	529	LEU	2.3
1	A	414	GLN	2.2
1	A	27	LYS	2.2
1	A	219	LYS	2.2
1	A	470	ASP	2.2
1	A	341	GLN	2.1
1	A	24	ALA	2.1
1	A	160	ALA	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	PLP	A	900	15/16	0.98	0.05	52,63,66,66	0

6.5 Other polymers [i](#)

There are no such residues in this entry.