



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 18, 2026 – 12:22 PM UTC

PDB ID : 2DY3 / pdb_00002dy3
Title : Crystal Structure of alanine racemase from *Corynebacterium glutamicum*
Authors : Miyaguchi, I.; Sasaki, C.; Kato, R.; Oikawa, T.; Sugio, S.
Deposited on : 2006-09-05
Resolution : 2.10 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

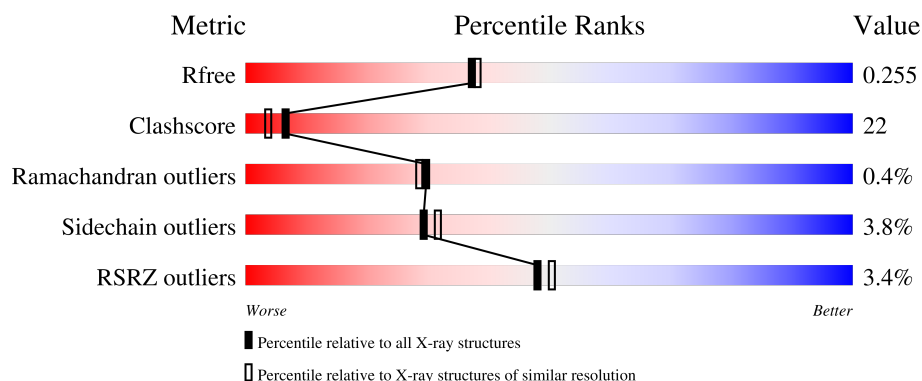
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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	361	2% 62% 28% • 6%
1	B	361	3% 63% 28% • 6%
1	C	361	2% 62% 29% • 5%
1	D	361	4% 59% 33% • 5%

2 Entry composition [i](#)

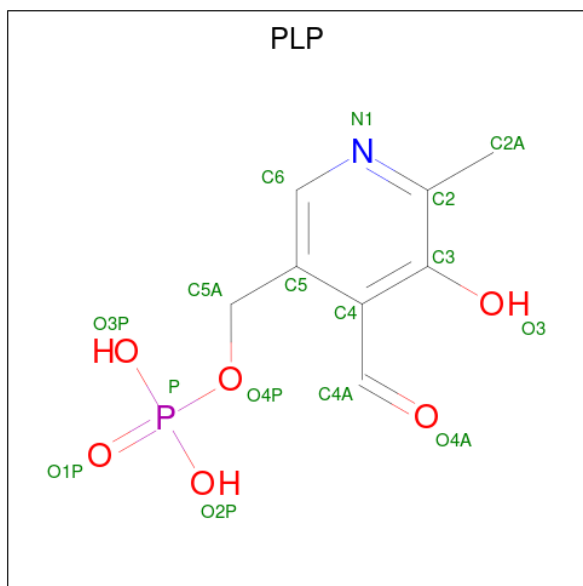
There are 3 unique types of molecules in this entry. The entry contains 11220 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Alanine racemase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	338	Total	C	N	O	S	0	0	0
			2581	1631	462	473	15			
1	B	340	Total	C	N	O	S	0	0	0
			2590	1637	464	473	16			
1	C	343	Total	C	N	O	S	0	0	0
			2614	1651	467	480	16			
1	D	344	Total	C	N	O	S	0	0	0
			2614	1650	466	482	16			

- 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		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
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		

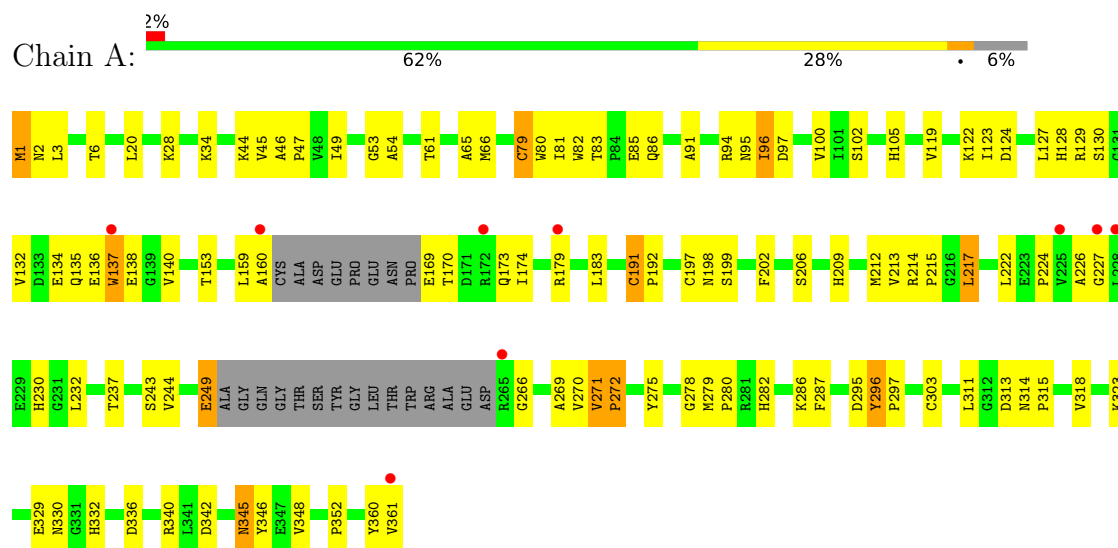
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	187	Total	O	0	0
			187	187		
3	B	195	Total	O	0	0
			195	195		
3	C	181	Total	O	0	0
			181	181		
3	D	198	Total	O	0	0
			198	198		

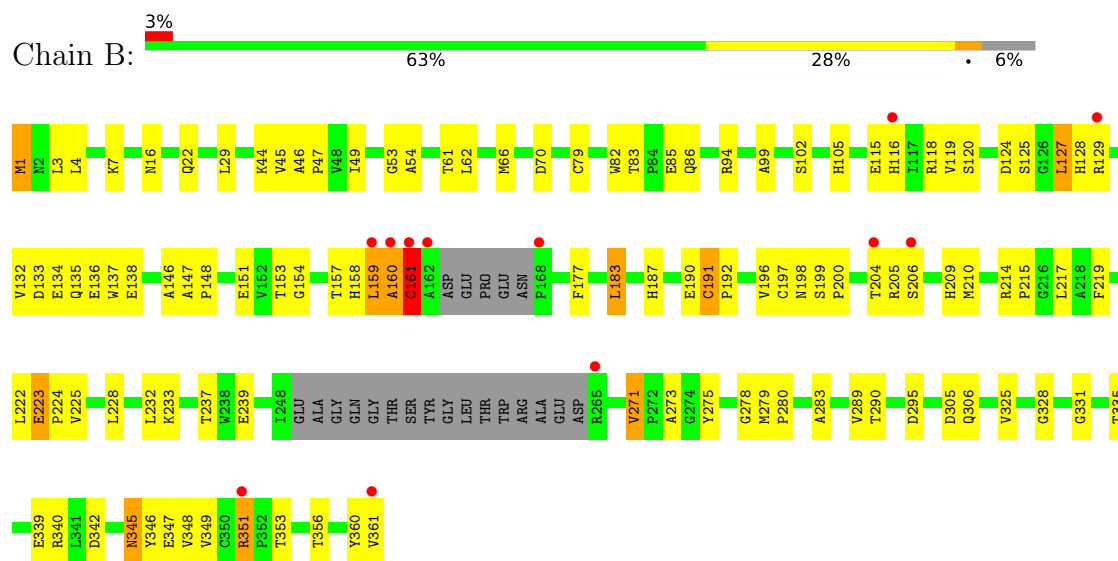
3 Residue-property plots

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: Alanine racemase

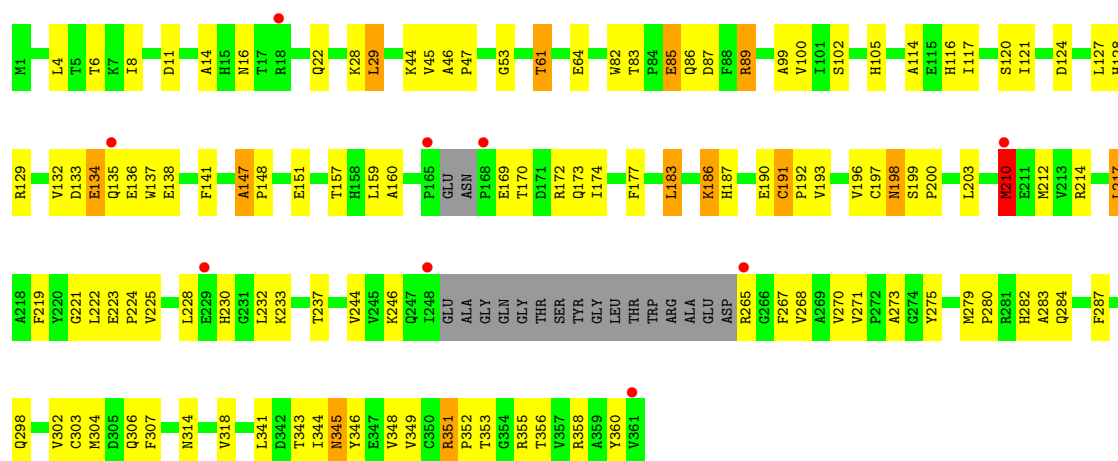


• Molecule 1: Alanine racemase

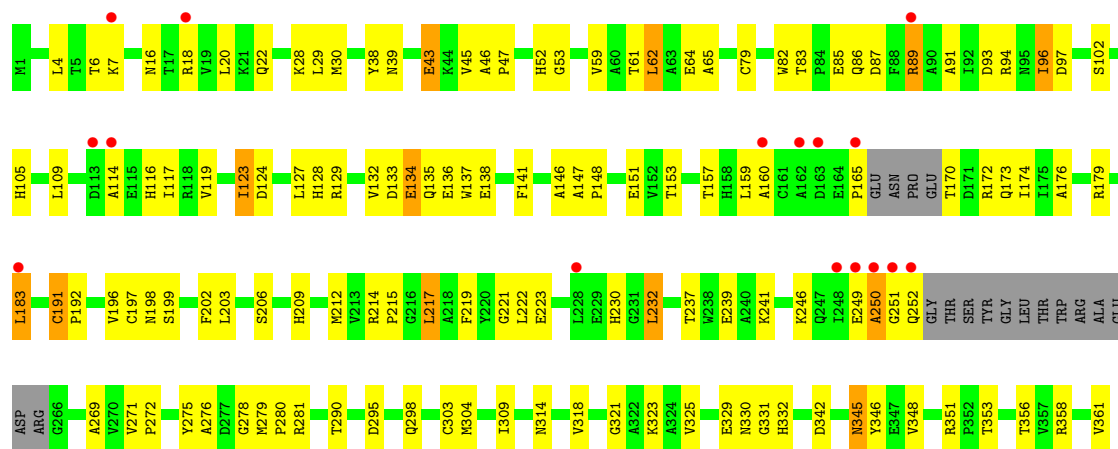


• Molecule 1: Alanine racemase





• Molecule 1: Alanine racemase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	78.38Å 113.61Å 88.10Å 90.00° 94.73° 90.00°	Depositor
Resolution (Å)	15.00 – 2.10 15.00 – 2.11	Depositor EDS
% Data completeness (in resolution range)	(Not available) (15.00-2.10) 90.5 (15.00-2.11)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.66 (at 2.12Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.227 , 0.269 0.214 , 0.255	Depositor DCC
R_{free} test set	4022 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	21.9	Xtriage
Anisotropy	0.533	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.45 , 58.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	11220	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 41.20 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.4464e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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	0.41	0/2634	0.98	12/3575 (0.3%)
1	B	0.39	0/2644	1.00	17/3589 (0.5%)
1	C	0.39	0/2669	0.98	14/3624 (0.4%)
1	D	0.39	0/2668	0.99	13/3623 (0.4%)
All	All	0.39	0/10615	0.99	56/14411 (0.4%)

There are no bond length outliers.

All (56) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	160	ALA	N-CA-C	-9.13	98.37	110.24
1	C	191	CYS	CA-C-N	8.84	128.43	119.24
1	C	191	CYS	C-N-CA	8.84	128.43	119.24
1	D	53	GLY	N-CA-C	8.37	124.43	114.48
1	B	197	CYS	N-CA-C	8.16	121.58	109.59
1	D	191	CYS	CA-C-N	7.91	127.20	118.97
1	D	191	CYS	C-N-CA	7.91	127.20	118.97
1	A	271	VAL	CA-C-N	7.71	129.47	119.84
1	A	271	VAL	C-N-CA	7.71	129.47	119.84
1	A	191	CYS	CA-C-N	7.53	126.81	118.97
1	A	191	CYS	C-N-CA	7.53	126.81	118.97
1	A	296	TYR	CA-C-N	7.29	127.70	119.83
1	A	296	TYR	C-N-CA	7.29	127.70	119.83
1	C	147	ALA	CA-C-N	7.27	127.12	119.05
1	C	147	ALA	C-N-CA	7.27	127.12	119.05
1	D	271	VAL	CA-C-N	7.19	128.83	119.84
1	D	271	VAL	C-N-CA	7.19	128.83	119.84
1	D	198	ASN	N-CA-C	-7.14	98.73	109.94
1	B	191	CYS	CA-C-N	7.03	126.85	119.05
1	B	191	CYS	C-N-CA	7.03	126.85	119.05

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	53	GLY	N-CA-C	6.87	122.66	114.48
1	C	197	CYS	N-CA-C	6.86	119.75	109.25
1	D	197	CYS	N-CA-C	6.78	119.62	109.25
1	A	198	ASN	N-CA-C	-6.69	99.44	109.94
1	C	53	GLY	N-CA-C	6.51	122.22	114.48
1	D	61	THR	N-CA-C	6.48	120.06	110.46
1	C	198	ASN	N-CA-C	-6.26	100.12	109.94
1	A	287	PHE	N-CA-C	6.15	118.12	108.96
1	A	197	CYS	N-CA-C	6.11	118.60	109.25
1	B	147	ALA	CA-C-N	6.04	125.25	118.97
1	B	147	ALA	C-N-CA	6.04	125.25	118.97
1	B	271	VAL	CA-C-N	5.99	127.33	119.84
1	B	271	VAL	C-N-CA	5.99	127.33	119.84
1	B	61	THR	N-CA-C	5.93	119.24	110.46
1	A	45	VAL	N-CA-C	5.92	116.09	110.53
1	B	45	VAL	N-CA-C	5.87	116.04	110.53
1	B	223	GLU	CA-C-N	5.85	125.39	119.19
1	B	223	GLU	C-N-CA	5.85	125.39	119.19
1	B	161	CYS	N-CA-C	5.83	118.95	108.17
1	D	298	GLN	N-CA-C	-5.70	102.46	110.50
1	A	61	THR	N-CA-C	5.69	119.24	110.42
1	D	147	ALA	CA-C-N	5.69	125.80	119.32
1	D	147	ALA	C-N-CA	5.69	125.80	119.32
1	B	198	ASN	N-CA-C	-5.68	101.59	110.17
1	C	210	MET	CB-CA-C	-5.65	108.43	115.89
1	C	61	THR	N-CA-C	5.59	118.73	110.46
1	C	287	PHE	N-CA-C	5.56	117.86	109.41
1	B	53	GLY	N-CA-C	5.53	121.06	114.48
1	B	351	ARG	N-CA-C	5.49	119.71	112.35
1	D	45	VAL	N-CA-C	5.48	115.68	110.53
1	D	134	GLU	N-CA-C	5.45	117.93	111.33
1	C	134	GLU	N-CA-C	5.15	117.56	111.33
1	C	45	VAL	N-CA-C	5.05	115.82	110.72
1	B	289	VAL	N-CA-C	-5.04	102.51	109.46
1	C	351	ARG	N-CA-C	5.04	119.10	112.35
1	C	14	ALA	N-CA-C	-5.00	105.83	111.28

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	2581	0	2564	110	0
1	B	2590	0	2576	105	0
1	C	2614	0	2594	124	0
1	D	2614	0	2589	124	0
2	A	15	0	7	1	0
2	B	15	0	7	0	0
2	C	15	0	7	2	0
2	D	15	0	7	0	0
3	A	187	0	0	8	0
3	B	195	0	0	6	0
3	C	181	0	0	1	0
3	D	198	0	0	6	0
All	All	11220	0	10351	451	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 (451) 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:91:ALA:HB1	1:A:96:ILE:HG21	1.32	1.09
1:A:160:ALA:H	1:A:173:GLN:HE22	1.12	0.96
1:D:29:LEU:HD11	1:D:219:PHE:HZ	1.29	0.96
1:D:89:ARG:HH11	1:D:89:ARG:HB2	1.30	0.94
1:B:1:MET:HE1	1:B:3:LEU:HD23	1.50	0.94
1:B:16:ASN:HD21	1:B:233:LYS:H	1.14	0.92
1:C:89:ARG:H	1:C:89:ARG:HD2	1.35	0.92
1:A:179:ARG:HE	1:A:179:ARG:HA	1.35	0.90
1:C:284:GLN:HA	1:C:298:GLN:HE22	1.36	0.90
1:B:279:MET:HE3	1:B:280:PRO:HD2	1.54	0.89
1:C:196:VAL:HG13	1:C:210:MET:HE1	1.54	0.88
1:D:28:LYS:HE2	1:D:212:MET:HE3	1.58	0.85
1:A:1:MET:HE3	1:A:2:ASN:C	2.02	0.84
1:D:91:ALA:O	1:D:96:ILE:HG22	1.77	0.84
1:A:249:GLU:HB2	1:A:266:GLY:H	1.43	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:28:LYS:HE2	1:C:212:MET:HE3	1.59	0.82
1:A:28:LYS:HE2	1:A:212:MET:HE3	1.61	0.81
1:A:314:ASN:HD21	1:A:318:VAL:H	1.27	0.81
1:C:186:LYS:HE3	1:C:186:LYS:HA	1.64	0.79
1:D:91:ALA:HB1	1:D:96:ILE:HG21	1.66	0.78
1:A:91:ALA:HB1	1:A:96:ILE:CG2	2.13	0.78
1:A:214:ARG:HD2	2:A:401:PLP:N1	1.98	0.78
1:D:133:ASP:OD1	1:D:135:GLN:HG2	1.84	0.77
1:C:271:VAL:HG11	1:C:307:PHE:CE2	2.20	0.77
1:C:279:MET:HE3	1:C:279:MET:HA	1.67	0.77
1:B:290:THR:HG22	1:B:295:ASP:OD1	1.84	0.76
1:C:314:ASN:HD21	1:C:318:VAL:H	1.33	0.76
1:A:102:SER:OG	1:A:105:HIS:HD2	1.68	0.75
1:A:100:VAL:HG23	1:A:119:VAL:CG1	2.17	0.75
1:D:29:LEU:HD11	1:D:219:PHE:CZ	2.19	0.75
1:A:160:ALA:N	1:A:173:GLN:HE22	1.85	0.75
1:D:65:ALA:HB1	1:D:96:ILE:HG13	1.69	0.75
1:D:102:SER:OG	1:D:105:HIS:HD2	1.70	0.74
1:A:65:ALA:HB1	1:A:96:ILE:HG13	1.70	0.74
1:A:132:VAL:O	1:A:137:TRP:HZ3	1.68	0.73
1:C:133:ASP:OD1	1:C:135:GLN:HG2	1.88	0.73
1:A:1:MET:HE1	1:A:3:LEU:HD23	1.71	0.73
1:C:196:VAL:CG1	1:C:210:MET:HE1	2.19	0.73
1:D:314:ASN:HD21	1:D:318:VAL:H	1.37	0.72
1:B:200:PRO:O	1:B:204:THR:HG22	1.89	0.72
1:B:278:GLY:O	1:B:280:PRO:HD3	1.90	0.72
1:C:100:VAL:CG1	1:C:121:ILE:HA	2.20	0.71
1:B:161:CYS:SG	1:B:200:PRO:HG3	2.31	0.71
1:C:100:VAL:HG12	1:C:121:ILE:HA	1.71	0.71
1:C:271:VAL:HG11	1:C:307:PHE:CZ	2.25	0.71
1:D:345:ASN:HD22	1:D:346:TYR:N	1.88	0.71
1:D:16:ASN:O	1:D:20:LEU:HD23	1.91	0.71
1:B:214:ARG:HG3	1:B:214:ARG:HH11	1.54	0.70
1:B:351:ARG:HA	1:B:351:ARG:NE	2.06	0.70
1:D:109:LEU:HD13	1:D:119:VAL:HG11	1.73	0.70
1:B:7:LYS:HE3	1:B:239:GLU:OE1	1.92	0.70
1:D:46:ALA:HB3	1:D:47:PRO:HD3	1.75	0.69
1:C:102:SER:OG	1:C:105:HIS:HD2	1.76	0.69
1:A:278:GLY:O	1:A:280:PRO:HD3	1.92	0.69
1:A:160:ALA:H	1:A:173:GLN:NE2	1.89	0.69
1:A:100:VAL:HG23	1:A:119:VAL:HG11	1.76	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:83:THR:H	1:A:86:GLN:HE21	1.41	0.68
1:C:279:MET:HE1	1:C:341:LEU:HD21	1.74	0.68
1:A:179:ARG:HA	1:A:179:ARG:NE	2.06	0.68
1:D:91:ALA:HB1	1:D:96:ILE:CG2	2.24	0.68
1:A:123:ILE:HG23	1:A:137:TRP:CH2	2.29	0.67
1:B:134:GLU:HA	1:B:137:TRP:CD2	2.30	0.67
1:C:353:THR:O	1:C:356:THR:HG23	1.95	0.67
1:C:230:HIS:HB2	1:C:232:LEU:HD21	1.77	0.67
1:C:129:ARG:NH1	1:D:303:CYS:SG	2.68	0.66
1:B:82:TRP:O	1:B:105:HIS:HE1	1.77	0.66
1:A:91:ALA:O	1:A:96:ILE:HG22	1.96	0.66
1:D:134:GLU:HA	1:D:137:TRP:CD2	2.30	0.65
1:D:28:LYS:HE2	1:D:212:MET:CE	2.26	0.65
1:A:217:LEU:HD22	1:A:222:LEU:HB2	1.79	0.65
1:D:241:LYS:HE3	1:D:321:GLY:O	1.96	0.65
1:B:217:LEU:CD1	1:B:222:LEU:HB2	2.26	0.64
1:B:353:THR:O	1:B:356:THR:HG23	1.97	0.64
1:D:82:TRP:O	1:D:105:HIS:HE1	1.79	0.64
1:D:114:ALA:HB3	1:D:117:ILE:HD11	1.79	0.64
1:A:82:TRP:O	1:A:105:HIS:HE1	1.80	0.64
1:D:222:LEU:HD13	1:D:345:ASN:HB2	1.79	0.64
1:A:122:LYS:HE2	1:A:130:SER:OG	1.97	0.64
1:B:279:MET:HE3	1:B:280:PRO:CD	2.24	0.64
1:B:345:ASN:HD22	1:B:346:TYR:N	1.95	0.64
1:A:345:ASN:HD22	1:A:346:TYR:N	1.96	0.64
1:C:190:GLU:CD	1:C:192:PRO:HG3	2.22	0.64
1:B:83:THR:H	1:B:86:GLN:HE21	1.45	0.63
1:A:209:HIS:HD2	3:A:425:HOH:O	1.81	0.63
1:B:279:MET:CE	1:B:280:PRO:HD2	2.26	0.63
1:B:190:GLU:CD	1:B:192:PRO:HG3	2.24	0.63
1:C:83:THR:H	1:C:86:GLN:HE21	1.46	0.63
1:C:127:LEU:HD21	1:C:160:ALA:HB2	1.81	0.63
1:D:199:SER:O	1:D:203:LEU:HD13	1.99	0.63
1:D:345:ASN:HD22	1:D:346:TYR:H	1.43	0.63
1:D:153:THR:O	1:D:192:PRO:HD2	1.98	0.63
1:C:345:ASN:HD22	1:C:346:TYR:N	1.96	0.62
1:D:230:HIS:HB2	1:D:232:LEU:HD22	1.82	0.62
1:B:290:THR:OG1	1:B:325:VAL:HB	1.99	0.62
1:A:153:THR:HG23	3:A:542:HOH:O	1.99	0.62
1:C:4:LEU:HG	1:C:356:THR:HG22	1.81	0.62
1:C:198:ASN:CG	1:C:200:PRO:HD2	2.25	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:190:GLU:OE1	1:C:192:PRO:HG3	2.00	0.61
1:C:196:VAL:HG22	1:C:210:MET:SD	2.40	0.61
1:D:345:ASN:HA	1:D:348:VAL:HG22	1.82	0.61
1:C:193:VAL:HG11	3:C:441:HOH:O	1.99	0.61
1:D:89:ARG:HB2	1:D:89:ARG:NH1	2.11	0.61
1:A:134:GLU:HA	1:A:137:TRP:CD2	2.34	0.61
1:D:29:LEU:C	1:D:29:LEU:HD13	2.25	0.61
1:D:353:THR:O	1:D:356:THR:HG23	2.01	0.61
1:B:158:HIS:HA	1:B:214:ARG:HH22	1.66	0.61
1:D:123:ILE:HD12	1:D:124:ASP:C	2.26	0.61
1:D:239:GLU:OE2	1:D:323:LYS:HD2	2.00	0.61
1:B:191:CYS:N	1:B:192:PRO:HD3	2.15	0.61
1:C:230:HIS:HB2	1:C:232:LEU:CD2	2.30	0.60
1:A:313:ASP:OD1	1:A:315:PRO:HG3	2.01	0.60
1:D:96:ILE:HD13	1:D:97:ASP:O	2.00	0.60
1:D:132:VAL:HG13	1:D:136:GLU:HB2	1.82	0.60
1:A:138:GLU:HG3	3:A:508:HOH:O	1.99	0.60
1:C:157:THR:HG22	1:C:196:VAL:HG12	1.82	0.60
1:C:223:GLU:OE2	1:C:232:LEU:HD23	2.01	0.60
1:D:281:ARG:NH1	3:D:456:HOH:O	2.34	0.60
1:C:28:LYS:HE2	1:C:212:MET:CE	2.31	0.60
1:B:345:ASN:HA	1:B:348:VAL:HG22	1.83	0.60
1:D:28:LYS:HB3	1:D:212:MET:HE3	1.83	0.60
1:A:217:LEU:CD2	1:A:222:LEU:HB2	2.32	0.59
1:B:335:THR:O	1:B:339:GLU:HG2	2.01	0.59
1:A:134:GLU:HA	1:A:137:TRP:CE2	2.37	0.59
1:B:217:LEU:HD11	1:B:222:LEU:HB2	1.83	0.59
1:C:345:ASN:HA	1:C:348:VAL:HG22	1.84	0.59
1:D:4:LEU:HG	1:D:356:THR:HG22	1.85	0.59
1:C:46:ALA:HB3	1:C:47:PRO:HD3	1.83	0.59
1:D:91:ALA:C	1:D:96:ILE:HG22	2.28	0.58
1:A:132:VAL:O	1:A:137:TRP:CZ3	2.54	0.58
1:C:351:ARG:HA	1:C:351:ARG:NE	2.18	0.58
1:A:91:ALA:C	1:A:96:ILE:HG22	2.28	0.58
1:D:250:ALA:O	1:D:252:GLN:HG3	2.03	0.58
1:C:8:ILE:HD13	1:C:358:ARG:HG3	1.84	0.58
1:C:16:ASN:HD21	1:C:233:LYS:H	1.52	0.58
1:C:159:LEU:HD13	1:C:196:VAL:O	2.04	0.58
1:B:206:SER:HA	1:B:209:HIS:CE1	2.38	0.58
1:D:62:LEU:HD13	1:D:82:TRP:HB3	1.85	0.58
1:C:134:GLU:HA	1:C:137:TRP:CD2	2.38	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:160:ALA:H	1:D:173:GLN:HE22	1.51	0.58
1:B:279:MET:HE2	1:B:283:ALA:HB3	1.85	0.58
1:A:94:ARG:NE	3:A:533:HOH:O	2.36	0.58
1:A:28:LYS:HE2	1:A:212:MET:CE	2.31	0.57
1:B:190:GLU:OE1	1:B:192:PRO:HG3	2.03	0.57
1:B:279:MET:HE2	1:B:283:ALA:CB	2.33	0.57
1:C:199:SER:O	1:C:203:LEU:HD13	2.04	0.57
1:B:85:GLU:N	1:B:85:GLU:OE1	2.37	0.57
1:B:225:VAL:HG11	1:B:228:LEU:HD12	1.85	0.57
1:C:265:ARG:N	1:C:265:ARG:HD2	2.19	0.57
1:C:279:MET:HE3	1:C:280:PRO:HD2	1.84	0.57
1:C:61:THR:OG1	1:C:64:GLU:HG3	2.03	0.57
1:A:137:TRP:HB3	1:A:183:LEU:HD23	1.86	0.57
1:B:159:LEU:O	1:B:160:ALA:C	2.48	0.57
1:C:217:LEU:HD13	1:C:222:LEU:O	2.04	0.57
1:C:303:CYS:SG	1:D:129:ARG:NH1	2.77	0.57
1:D:20:LEU:HD12	1:D:202:PHE:CE2	2.40	0.57
1:A:345:ASN:HD22	1:A:346:TYR:H	1.50	0.56
1:C:284:GLN:HA	1:C:298:GLN:NE2	2.13	0.56
1:B:345:ASN:HD22	1:B:346:TYR:H	1.52	0.56
1:C:345:ASN:HD22	1:C:346:TYR:H	1.52	0.56
1:A:44:LYS:HG3	1:A:360:TYR:CZ	2.40	0.56
1:A:100:VAL:CG2	1:A:119:VAL:HG11	2.36	0.56
1:A:243:SER:HB3	1:A:272:PRO:HG3	1.88	0.56
1:C:87:ASP:HA	1:C:89:ARG:NH1	2.20	0.56
1:B:127:LEU:CD2	1:B:160:ALA:HB2	2.36	0.56
1:B:159:LEU:C	1:B:160:ALA:O	2.45	0.56
1:B:222:LEU:HD11	1:B:349:VAL:HG11	1.88	0.55
1:C:4:LEU:CD2	1:C:356:THR:HG22	2.36	0.55
1:D:230:HIS:HB2	1:D:232:LEU:CD2	2.36	0.55
1:C:232:LEU:N	1:C:232:LEU:HD22	2.22	0.55
1:D:217:LEU:HG	1:D:346:TYR:CZ	2.41	0.55
1:B:115:GLU:HG2	3:B:449:HOH:O	2.06	0.54
1:A:345:ASN:HA	1:A:348:VAL:HG22	1.89	0.54
1:D:20:LEU:HD12	1:D:202:PHE:HE2	1.71	0.54
1:B:351:ARG:HA	1:B:351:ARG:CZ	2.36	0.54
1:C:116:HIS:NE2	1:C:151:GLU:OE2	2.37	0.54
1:A:206:SER:HA	1:A:209:HIS:CE1	2.43	0.54
1:D:290:THR:HG22	1:D:295:ASP:OD2	2.07	0.54
1:A:361:VAL:HG23	3:A:513:HOH:O	2.07	0.54
1:D:87:ASP:HA	1:D:89:ARG:HH12	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:82:TRP:O	1:C:105:HIS:HE1	1.90	0.53
1:B:102:SER:OG	1:B:105:HIS:HD2	1.90	0.53
1:C:6:THR:HA	1:C:237:THR:O	2.08	0.53
1:D:137:TRP:HB3	1:D:141:PHE:CE2	2.43	0.53
1:A:28:LYS:HB3	1:A:212:MET:HE3	1.89	0.53
1:A:340:ARG:HG3	1:A:340:ARG:HH11	1.74	0.53
1:C:89:ARG:H	1:C:89:ARG:CD	2.11	0.53
1:A:100:VAL:HG23	1:A:119:VAL:HG13	1.88	0.53
1:B:159:LEU:CD2	1:B:196:VAL:HB	2.38	0.53
1:D:85:GLU:N	1:D:85:GLU:OE2	2.41	0.53
1:D:209:HIS:HD2	3:D:489:HOH:O	1.92	0.53
1:C:137:TRP:HB3	1:C:141:PHE:CE2	2.44	0.53
1:D:217:LEU:HD13	1:D:222:LEU:O	2.09	0.53
1:B:127:LEU:HD21	1:B:160:ALA:H	1.74	0.53
1:C:279:MET:CE	1:C:280:PRO:HD2	2.39	0.52
1:A:1:MET:HE1	1:A:3:LEU:CD2	2.38	0.52
1:D:191:CYS:N	1:D:192:PRO:HD3	2.24	0.52
1:C:221:GLY:HA2	1:C:232:LEU:HB3	1.90	0.52
1:A:96:ILE:HD13	1:A:97:ASP:O	2.09	0.52
1:B:99:ALA:HA	1:B:120:SER:O	2.10	0.52
1:C:246:LYS:HG3	1:D:129:ARG:O	2.09	0.52
1:D:170:THR:O	1:D:174:ILE:HD13	2.09	0.52
1:A:96:ILE:HG23	1:A:96:ILE:O	2.09	0.51
1:A:314:ASN:N	1:A:315:PRO:HD3	2.24	0.51
1:C:199:SER:HB2	1:C:200:PRO:HD3	1.92	0.51
1:A:191:CYS:N	1:A:192:PRO:HD3	2.25	0.51
1:C:275:TYR:HA	1:C:279:MET:O	2.10	0.51
1:D:223:GLU:OE2	1:D:232:LEU:HD23	2.10	0.51
1:A:66:MET:SD	1:A:94:ARG:HD3	2.50	0.51
1:A:275:TYR:HA	1:A:279:MET:O	2.11	0.51
1:D:249:GLU:C	1:D:251:GLY:H	2.19	0.51
1:A:217:LEU:HD12	1:A:224:PRO:HG3	1.92	0.51
1:A:170:THR:O	1:A:174:ILE:HG12	2.11	0.51
1:A:96:ILE:HD13	1:A:96:ILE:C	2.35	0.50
1:C:172:ARG:HH11	1:C:172:ARG:HG3	1.75	0.50
1:D:43:GLU:HG3	3:D:446:HOH:O	2.11	0.50
1:D:278:GLY:O	1:D:280:PRO:HD3	2.10	0.50
1:A:303:CYS:SG	1:B:129:ARG:NH1	2.85	0.50
1:B:127:LEU:HD21	1:B:160:ALA:HB2	1.94	0.50
1:B:347:GLU:O	1:B:351:ARG:HG2	2.12	0.50
1:C:217:LEU:HG	1:C:346:TYR:CZ	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:133:ASP:OD1	1:D:136:GLU:HG3	2.12	0.50
1:A:96:ILE:HD13	1:A:97:ASP:N	2.27	0.50
1:B:16:ASN:ND2	1:B:233:LYS:H	1.96	0.50
1:A:202:PHE:CD1	1:A:213:VAL:HG11	2.47	0.50
1:D:30:MET:O	1:D:214:ARG:HA	2.12	0.50
1:A:124:ASP:OD2	1:A:128:HIS:HA	2.12	0.49
1:A:132:VAL:HG12	1:A:136:GLU:HB2	1.92	0.49
1:B:49:ILE:HG22	1:B:54:ALA:HB2	1.94	0.49
1:C:314:ASN:ND2	1:C:318:VAL:H	2.04	0.49
1:D:295:ASP:OD1	1:D:332:HIS:CE1	2.65	0.49
1:A:249:GLU:CB	1:A:266:GLY:H	2.20	0.49
1:A:1:MET:HE2	1:A:1:MET:O	2.12	0.49
1:A:49:ILE:HG22	1:A:54:ALA:HB2	1.94	0.49
1:A:314:ASN:ND2	1:A:318:VAL:H	2.02	0.49
1:B:46:ALA:HB3	1:B:47:PRO:HD3	1.94	0.49
1:B:215:PRO:HG2	1:B:219:PHE:HE1	1.77	0.49
1:B:217:LEU:CD1	1:B:222:LEU:O	2.60	0.49
1:D:172:ARG:HB2	3:D:432:HOH:O	2.11	0.49
1:A:46:ALA:HB3	1:A:47:PRO:HD3	1.94	0.49
1:C:4:LEU:CG	1:C:356:THR:HG22	2.43	0.49
1:C:8:ILE:HD12	1:C:8:ILE:N	2.27	0.49
1:C:345:ASN:O	1:C:348:VAL:HG22	2.12	0.49
1:D:4:LEU:CD2	1:D:356:THR:HG22	2.43	0.49
1:C:85:GLU:N	1:C:85:GLU:OE1	2.45	0.49
1:D:134:GLU:HA	1:D:137:TRP:CE2	2.47	0.49
1:D:275:TYR:HA	1:D:279:MET:O	2.13	0.49
1:D:314:ASN:HD21	1:D:318:VAL:N	2.09	0.49
1:A:96:ILE:CG2	1:A:96:ILE:O	2.61	0.49
1:C:132:VAL:CG1	1:C:136:GLU:HB2	2.43	0.49
1:B:138:GLU:HB2	3:B:485:HOH:O	2.13	0.48
1:D:28:LYS:CB	1:D:212:MET:HE3	2.43	0.48
1:D:30:MET:HB3	1:D:214:ARG:HB3	1.95	0.48
1:D:295:ASP:OD1	1:D:332:HIS:HE1	1.97	0.48
1:B:361:VAL:HG21	3:B:577:HOH:O	2.13	0.48
1:D:241:LYS:O	1:D:272:PRO:HG2	2.13	0.48
1:B:134:GLU:HA	1:B:137:TRP:CE2	2.48	0.48
1:C:132:VAL:HG13	1:C:136:GLU:HB2	1.95	0.48
1:C:183:LEU:HD22	1:C:183:LEU:O	2.14	0.48
1:D:269:ALA:HB3	1:D:309:ILE:CG1	2.44	0.48
1:D:89:ARG:NH1	1:D:89:ARG:H	2.12	0.48
1:B:159:LEU:HD23	1:B:196:VAL:O	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:39:ASN:ND2	1:D:358:ARG:HH21	2.12	0.48
1:C:100:VAL:HG13	1:C:100:VAL:O	2.14	0.48
1:A:44:LYS:HG3	1:A:360:TYR:CE2	2.49	0.47
1:C:159:LEU:HD11	1:C:196:VAL:HB	1.95	0.47
1:D:124:ASP:OD2	1:D:128:HIS:HA	2.14	0.47
1:A:135:GLN:H	1:A:135:GLN:CD	2.21	0.47
1:B:214:ARG:HG3	1:B:214:ARG:NH1	2.26	0.47
1:C:222:LEU:HD11	1:C:349:VAL:HG11	1.96	0.47
1:A:28:LYS:CB	1:A:212:MET:HE3	2.44	0.47
1:B:127:LEU:HG	1:B:160:ALA:HB2	1.96	0.47
1:B:177:PHE:HE2	1:B:210:MET:HE1	1.80	0.47
1:B:279:MET:HE3	1:B:279:MET:HA	1.97	0.47
1:C:157:THR:O	1:C:214:ARG:NH2	2.47	0.47
1:D:16:ASN:O	1:D:20:LEU:CD2	2.59	0.47
1:A:222:LEU:HD23	1:A:345:ASN:HB2	1.96	0.47
1:B:215:PRO:HG2	1:B:219:PHE:CE1	2.50	0.47
1:C:196:VAL:HG13	1:C:210:MET:CE	2.37	0.47
1:B:4:LEU:HG	1:B:356:THR:HG22	1.95	0.47
1:B:237:THR:HA	1:B:328:GLY:HA3	1.96	0.47
1:C:343:THR:OG1	1:C:344:ILE:N	2.46	0.47
1:D:7:LYS:HD2	1:D:361:VAL:HG21	1.95	0.47
1:C:190:GLU:HG3	1:C:192:PRO:HD3	1.96	0.47
1:D:62:LEU:CD1	1:D:82:TRP:HB3	2.45	0.47
1:B:157:THR:HG22	1:B:196:VAL:HG12	1.96	0.47
1:D:114:ALA:HB3	1:D:117:ILE:CG1	2.45	0.47
1:B:135:GLN:HG2	3:B:552:HOH:O	2.14	0.47
1:C:279:MET:HE2	1:C:283:ALA:CB	2.45	0.47
1:B:158:HIS:O	1:B:160:ALA:N	2.48	0.46
1:D:18:ARG:HE	1:D:52:HIS:HD2	1.64	0.46
1:D:290:THR:HG23	3:D:442:HOH:O	2.14	0.46
1:A:85:GLU:OE2	1:A:85:GLU:N	2.46	0.46
1:B:217:LEU:HD13	1:B:222:LEU:HB2	1.94	0.46
1:C:191:CYS:N	1:C:192:PRO:HD3	2.30	0.46
1:B:225:VAL:CG1	1:B:228:LEU:HD12	2.45	0.46
1:D:176:ALA:O	1:D:179:ARG:HB3	2.15	0.46
1:B:82:TRP:HA	1:B:86:GLN:NE2	2.31	0.46
1:D:127:LEU:HD21	1:D:160:ALA:HB2	1.98	0.46
1:A:323:LYS:HE2	3:A:551:HOH:O	2.16	0.46
1:C:29:LEU:HD21	1:C:219:PHE:HZ	1.80	0.46
1:D:59:VAL:O	1:D:79:CYS:HA	2.15	0.46
1:D:132:VAL:CG1	1:D:136:GLU:HB2	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:16:ASN:HD21	1:C:233:LYS:N	2.14	0.46
1:A:244:VAL:HG12	1:A:270:VAL:HB	1.97	0.46
1:B:146:ALA:O	1:B:148:PRO:HD3	2.16	0.46
1:D:124:ASP:HB3	1:D:133:ASP:HA	1.98	0.46
1:D:239:GLU:CD	1:D:323:LYS:HD2	2.39	0.46
1:C:282:HIS:HE1	1:D:342:ASP:O	1.98	0.45
1:C:170:THR:O	1:C:174:ILE:HG12	2.16	0.45
1:C:279:MET:HE2	1:C:283:ALA:HB2	1.97	0.45
1:D:221:GLY:HA2	1:D:232:LEU:HB3	1.99	0.45
1:A:199:SER:HB3	1:A:224:PRO:HG2	1.99	0.45
1:D:96:ILE:HD13	1:D:96:ILE:C	2.41	0.45
1:A:295:ASP:OD2	1:A:332:HIS:CE1	2.69	0.45
1:D:290:THR:OG1	1:D:325:VAL:HB	2.15	0.45
1:A:213:VAL:C	1:A:215:PRO:HD3	2.42	0.45
1:D:87:ASP:OD2	1:D:89:ARG:NH1	2.50	0.45
1:A:169:GLU:O	1:A:173:GLN:HG3	2.17	0.45
1:A:342:ASP:OD1	1:D:93:ASP:OD2	2.35	0.45
1:C:134:GLU:HG3	1:C:137:TRP:CZ3	2.52	0.45
1:D:83:THR:H	1:D:86:GLN:HE21	1.65	0.45
1:A:6:THR:HA	1:A:237:THR:O	2.17	0.45
1:D:249:GLU:C	1:D:251:GLY:N	2.74	0.45
1:D:114:ALA:HB3	1:D:117:ILE:CD1	2.45	0.44
1:B:124:ASP:OD2	1:B:128:HIS:HA	2.17	0.44
1:B:127:LEU:HD22	3:B:465:HOH:O	2.17	0.44
1:B:154:GLY:HA2	1:B:191:CYS:HA	1.99	0.44
1:C:133:ASP:OD2	1:D:246:LYS:HD2	2.18	0.44
1:D:4:LEU:CG	1:D:356:THR:HG22	2.47	0.44
1:B:125:SER:N	3:B:445:HOH:O	2.50	0.44
1:B:133:ASP:OD1	1:B:136:GLU:HG3	2.18	0.44
1:B:116:HIS:HE1	1:B:118:ARG:HG3	1.81	0.44
1:C:82:TRP:HA	1:C:86:GLN:NE2	2.33	0.44
1:C:271:VAL:HG13	1:C:271:VAL:O	2.18	0.44
1:D:138:GLU:HG2	1:D:183:LEU:HD11	1.99	0.44
1:A:296:TYR:HA	1:A:297:PRO:HD3	1.73	0.44
1:B:22:GLN:HA	1:B:22:GLN:NE2	2.32	0.44
1:C:177:PHE:CE2	1:C:210:MET:CE	3.00	0.44
1:D:18:ARG:O	1:D:22:GLN:HG3	2.17	0.44
1:A:96:ILE:CD1	1:A:97:ASP:O	2.65	0.44
1:A:282:HIS:HE1	1:B:342:ASP:O	2.01	0.44
1:C:44:LYS:HG3	1:C:360:TYR:CE2	2.53	0.44
1:C:124:ASP:OD2	1:C:128:HIS:HA	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:314:ASN:ND2	1:D:318:VAL:H	2.11	0.44
1:A:1:MET:HE2	1:A:1:MET:C	2.42	0.44
1:C:100:VAL:HG13	1:C:121:ILE:HG23	2.00	0.44
1:B:119:VAL:O	1:B:153:THR:HG22	2.18	0.43
1:B:273:ALA:O	1:B:306:GLN:HA	2.18	0.43
1:C:100:VAL:HG11	1:C:121:ILE:HG12	2.00	0.43
1:C:159:LEU:HD12	1:C:159:LEU:N	2.32	0.43
1:D:6:THR:HA	1:D:237:THR:O	2.18	0.43
1:D:146:ALA:O	1:D:148:PRO:HD3	2.17	0.43
1:B:183:LEU:HD22	1:B:187:HIS:HD2	1.83	0.43
1:C:44:LYS:HG3	1:C:360:TYR:CZ	2.54	0.43
1:B:44:LYS:HG3	1:B:360:TYR:CE2	2.54	0.43
1:B:116:HIS:CE1	1:B:118:ARG:HG3	2.53	0.43
1:A:230:HIS:HB2	1:A:232:LEU:HD13	2.00	0.43
1:A:286:LYS:O	1:A:340:ARG:HD3	2.18	0.43
1:B:159:LEU:HD21	1:B:196:VAL:HB	2.00	0.43
1:B:199:SER:HB3	1:B:224:PRO:HG2	2.01	0.43
1:B:275:TYR:HA	1:B:279:MET:O	2.19	0.43
1:C:8:ILE:CD1	1:C:358:ARG:HG3	2.48	0.43
1:D:7:LYS:HG3	1:D:361:VAL:CG1	2.48	0.43
1:B:82:TRP:O	1:B:105:HIS:CE1	2.66	0.42
1:B:116:HIS:NE2	1:B:151:GLU:OE2	2.52	0.42
1:A:34:LYS:HE3	1:B:305:ASP:OD2	2.19	0.42
1:A:132:VAL:CG1	1:A:136:GLU:HB2	2.48	0.42
1:A:271:VAL:HA	1:A:272:PRO:HD3	1.66	0.42
1:B:115:GLU:HG3	1:B:116:HIS:H	1.84	0.42
1:B:290:THR:HG21	1:B:331:GLY:HA2	2.01	0.42
1:C:198:ASN:OD1	1:C:200:PRO:HD2	2.19	0.42
1:D:249:GLU:O	1:D:251:GLY:N	2.52	0.42
1:C:355:ARG:HD2	1:D:64:GLU:OE2	2.19	0.42
1:C:246:LYS:HB2	1:C:268:VAL:HG23	2.00	0.42
1:A:269:ALA:HB2	1:A:311:LEU:HD11	2.02	0.42
1:B:66:MET:O	1:B:94:ARG:NH2	2.52	0.42
1:B:214:ARG:HH11	1:B:214:ARG:CG	2.27	0.42
1:D:127:LEU:HB2	3:D:494:HOH:O	2.19	0.42
1:D:203:LEU:HD23	1:D:230:HIS:CE1	2.54	0.42
1:D:278:GLY:HA2	1:D:351:ARG:HH21	1.84	0.42
1:C:138:GLU:OE2	1:C:187:HIS:NE2	2.46	0.42
1:D:157:THR:HG22	1:D:196:VAL:HG12	2.00	0.42
1:D:281:ARG:HG2	1:D:281:ARG:HH11	1.84	0.42
1:A:1:MET:HE2	1:B:86:GLN:HG2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:82:TRP:HA	1:A:86:GLN:NE2	2.35	0.42
1:B:70:ASP:OD1	1:B:94:ARG:NH2	2.44	0.42
1:B:159:LEU:HD13	1:B:159:LEU:HA	1.86	0.42
1:C:244:VAL:HG13	1:C:270:VAL:CG2	2.50	0.42
1:C:304:MET:HE1	1:D:38:TYR:CE2	2.54	0.42
1:D:116:HIS:NE2	1:D:151:GLU:OE2	2.52	0.42
1:A:1:MET:HG2	1:A:2:ASN:N	2.34	0.42
1:B:232:LEU:C	1:B:233:LYS:HD2	2.44	0.42
1:D:6:THR:OG1	1:D:358:ARG:HG2	2.20	0.42
1:C:114:ALA:HB3	1:C:117:ILE:HD11	2.02	0.42
1:C:214:ARG:NH1	2:C:401:PLP:N1	2.67	0.42
1:C:29:LEU:HD21	1:C:219:PHE:CZ	2.55	0.42
1:C:134:GLU:HG3	1:C:137:TRP:CE3	2.55	0.42
1:C:199:SER:N	1:C:200:PRO:CD	2.82	0.42
1:C:271:VAL:HG12	1:C:307:PHE:O	2.20	0.42
1:D:18:ARG:NE	1:D:52:HIS:HD2	2.18	0.42
1:A:80:TRP:HD1	1:A:81:ILE:HG13	1.84	0.41
1:A:132:VAL:HG11	1:A:140:VAL:HG21	2.01	0.41
1:B:340:ARG:HG3	1:B:340:ARG:HH11	1.85	0.41
1:C:177:PHE:HE2	1:C:210:MET:HE2	1.85	0.41
1:C:223:GLU:HA	1:C:224:PRO:HD3	1.79	0.41
1:D:29:LEU:C	1:D:29:LEU:CD1	2.93	0.41
1:C:29:LEU:CD2	1:C:219:PHE:HZ	2.33	0.41
1:C:273:ALA:O	1:C:306:GLN:HA	2.20	0.41
1:A:135:GLN:CD	1:A:135:GLN:N	2.78	0.41
1:C:89:ARG:HD2	1:C:89:ARG:N	2.18	0.41
1:A:82:TRP:HA	1:A:86:GLN:HE22	1.86	0.41
1:C:177:PHE:HE2	1:C:210:MET:CE	2.33	0.41
1:C:351:ARG:O	1:C:352:PRO:C	2.64	0.41
1:D:276:ALA:HB2	1:D:304:MET:HG3	2.03	0.41
1:C:177:PHE:CE2	1:C:210:MET:HE1	2.55	0.41
1:A:79:CYS:HB3	1:A:96:ILE:CD1	2.50	0.41
1:B:190:GLU:CG	1:B:192:PRO:HG3	2.50	0.41
1:D:290:THR:HG21	1:D:331:GLY:HA2	2.03	0.41
1:A:65:ALA:CB	1:A:96:ILE:HG13	2.46	0.41
1:A:79:CYS:HB3	1:A:96:ILE:HD11	2.02	0.41
1:A:329:GLU:O	1:A:330:ASN:HB2	2.20	0.41
1:A:348:VAL:O	1:A:352:PRO:HD3	2.21	0.41
1:C:127:LEU:HD13	1:C:173:GLN:NE2	2.35	0.41
1:B:204:THR:HG23	1:B:205:ARG:HG2	2.03	0.41
1:B:223:GLU:HA	1:B:224:PRO:HD3	1.77	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:147:ALA:HA	1:C:148:PRO:HD2	1.80	0.41
1:C:225:VAL:HB	1:C:228:LEU:HD12	2.03	0.41
1:D:82:TRP:HA	1:D:86:GLN:NE2	2.36	0.41
1:D:215:PRO:HG2	1:D:219:PHE:CE1	2.56	0.41
1:B:127:LEU:CG	1:B:160:ALA:HB2	2.51	0.41
1:B:214:ARG:NH1	1:B:214:ARG:CG	2.84	0.41
1:C:183:LEU:HD22	1:C:187:HIS:HD2	1.86	0.41
1:D:7:LYS:HB3	1:D:237:THR:HB	2.03	0.41
1:A:136:GLU:O	1:A:137:TRP:C	2.64	0.40
1:B:158:HIS:HA	1:B:214:ARG:NH2	2.33	0.40
1:C:232:LEU:CD2	1:C:232:LEU:N	2.84	0.40
1:C:298:GLN:HE21	1:C:302:VAL:HG22	1.86	0.40
1:A:127:LEU:HB2	3:A:432:HOH:O	2.21	0.40
1:B:345:ASN:O	1:B:348:VAL:HG22	2.20	0.40
1:C:214:ARG:HD2	2:C:401:PLP:N1	2.36	0.40
1:D:206:SER:HA	1:D:209:HIS:CE1	2.56	0.40
1:A:95:ASN:ND2	3:A:413:HOH:O	2.54	0.40
1:A:340:ARG:HG3	1:A:340:ARG:NH1	2.36	0.40
1:B:132:VAL:CG1	1:B:136:GLU:HB2	2.51	0.40
1:C:246:LYS:O	1:C:267:PHE:HA	2.21	0.40
1:A:65:ALA:HB1	1:A:96:ILE:CG1	2.48	0.40
1:A:336:ASP:OD2	1:A:340:ARG:NH1	2.52	0.40
1:B:347:GLU:O	1:B:351:ARG:NH1	2.54	0.40
1:C:99:ALA:HA	1:C:120:SER:O	2.22	0.40
1:D:134:GLU:OE2	1:D:179:ARG:NH1	2.52	0.40
1:D:329:GLU:O	1:D:330:ASN:HB2	2.21	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	332/361 (92%)	316 (95%)	13 (4%)	3 (1%)	14	10
1	B	334/361 (92%)	316 (95%)	17 (5%)	1 (0%)	36	36
1	C	337/361 (93%)	319 (95%)	17 (5%)	1 (0%)	36	36
1	D	338/361 (94%)	325 (96%)	12 (4%)	1 (0%)	36	36
All	All	1341/1444 (93%)	1276 (95%)	59 (4%)	6 (0%)	30	28

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	227	GLY
1	A	226	ALA
1	C	169	GLU
1	D	250	ALA
1	B	159	LEU
1	A	272	PRO

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	266/283 (94%)	256 (96%)	10 (4%)	29	32
1	B	267/283 (94%)	258 (97%)	9 (3%)	32	35
1	C	270/283 (95%)	260 (96%)	10 (4%)	30	33
1	D	269/283 (95%)	257 (96%)	12 (4%)	24	25
All	All	1072/1132 (95%)	1031 (96%)	41 (4%)	29	32

All (41) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	20	LEU
1	A	79	CYS
1	A	96	ILE
1	A	129	ARG

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Mol	Chain	Res	Type
1	A	137	TRP
1	A	159	LEU
1	A	217	LEU
1	A	249	GLU
1	A	345	ASN
1	B	1	MET
1	B	29	LEU
1	B	62	LEU
1	B	79	CYS
1	B	127	LEU
1	B	161	CYS
1	B	183	LEU
1	B	271	VAL
1	B	345	ASN
1	C	11	ASP
1	C	22	GLN
1	C	29	LEU
1	C	85	GLU
1	C	89	ARG
1	C	183	LEU
1	C	186	LYS
1	C	210	MET
1	C	217	LEU
1	C	345	ASN
1	D	43	GLU
1	D	62	LEU
1	D	89	ARG
1	D	94	ARG
1	D	96	ILE
1	D	123	ILE
1	D	159	LEU
1	D	165	PRO
1	D	183	LEU
1	D	217	LEU
1	D	232	LEU
1	D	345	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (48) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	39	ASN
1	A	86	GLN

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Mol	Chain	Res	Type
1	A	95	ASN
1	A	105	HIS
1	A	173	GLN
1	A	209	HIS
1	A	247	GLN
1	A	282	HIS
1	A	284	GLN
1	A	314	ASN
1	A	316	HIS
1	A	332	HIS
1	A	345	ASN
1	B	16	ASN
1	B	22	GLN
1	B	39	ASN
1	B	86	GLN
1	B	105	HIS
1	B	209	HIS
1	B	247	GLN
1	B	284	GLN
1	B	306	GLN
1	B	345	ASN
1	C	16	ASN
1	C	39	ASN
1	C	86	GLN
1	C	95	ASN
1	C	105	HIS
1	C	135	GLN
1	C	247	GLN
1	C	282	HIS
1	C	284	GLN
1	C	306	GLN
1	C	314	ASN
1	C	316	HIS
1	C	345	ASN
1	D	22	GLN
1	D	39	ASN
1	D	52	HIS
1	D	86	GLN
1	D	105	HIS
1	D	173	GLN
1	D	209	HIS
1	D	284	GLN

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Mol	Chain	Res	Type
1	D	306	GLN
1	D	314	ASN
1	D	332	HIS
1	D	345	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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	401	1	15,15,16	1.83	4 (26%)	21,22,23	1.32	4 (19%)
2	PLP	D	401	1	15,15,16	1.71	4 (26%)	21,22,23	1.25	2 (9%)
2	PLP	C	401	1	15,15,16	1.77	4 (26%)	21,22,23	1.29	2 (9%)
2	PLP	A	401	1	15,15,16	1.78	4 (26%)	21,22,23	1.45	4 (19%)

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	401	1	-	0/6/6/8	0/1/1/1
2	PLP	D	401	1	-	1/6/6/8	0/1/1/1
2	PLP	C	401	1	-	2/6/6/8	0/1/1/1
2	PLP	A	401	1	-	2/6/6/8	0/1/1/1

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	401	PLP	C2-N1	3.60	1.40	1.33
2	C	401	PLP	C5-C4	3.37	1.44	1.40
2	B	401	PLP	C5-C4	3.36	1.44	1.40
2	C	401	PLP	C2-N1	3.32	1.39	1.33
2	A	401	PLP	C5-C4	3.30	1.44	1.40
2	A	401	PLP	C2-N1	3.25	1.39	1.33
2	D	401	PLP	C2-N1	3.24	1.39	1.33
2	D	401	PLP	C5-C4	3.16	1.44	1.40
2	C	401	PLP	C6-N1	2.43	1.39	1.34
2	D	401	PLP	C6-N1	2.43	1.39	1.34
2	A	401	PLP	P-O2P	-2.32	1.46	1.54
2	A	401	PLP	C6-N1	2.28	1.39	1.34
2	B	401	PLP	C6-N1	2.27	1.39	1.34
2	D	401	PLP	P-O2P	-2.21	1.46	1.54
2	B	401	PLP	P-O2P	-2.16	1.46	1.54
2	C	401	PLP	P-O2P	-2.10	1.47	1.54

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	PLP	C4A-C4-C5	-2.73	118.13	120.94
2	D	401	PLP	C5-C6-N1	-2.39	119.94	123.83
2	A	401	PLP	C5-C6-N1	-2.37	119.97	123.83
2	C	401	PLP	C5-C6-N1	-2.25	120.17	123.83
2	A	401	PLP	C6-C5-C4	2.22	119.92	118.10
2	B	401	PLP	C5-C6-N1	-2.22	120.22	123.83
2	A	401	PLP	O3P-P-O2P	2.19	116.01	107.80
2	B	401	PLP	C6-C5-C4	2.10	119.81	118.10
2	C	401	PLP	O3P-P-O2P	2.08	115.61	107.80
2	D	401	PLP	O3P-P-O2P	2.04	115.46	107.80
2	B	401	PLP	O3P-P-O2P	2.03	115.41	107.80
2	B	401	PLP	C4A-C4-C5	-2.02	118.86	120.94

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	401	PLP	C4-C5-C5A-O4P
2	C	401	PLP	C4-C5-C5A-O4P
2	D	401	PLP	C4-C5-C5A-O4P
2	A	401	PLP	C6-C5-C5A-O4P
2	C	401	PLP	C6-C5-C5A-O4P

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	401	PLP	2	0
2	A	401	PLP	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	338/361 (93%)	-0.04	9 (2%) 56 59	9, 19, 37, 57	0
1	B	340/361 (94%)	0.08	12 (3%) 47 49	11, 21, 41, 65	0
1	C	343/361 (95%)	0.03	9 (2%) 57 60	12, 21, 40, 57	0
1	D	344/361 (95%)	0.07	16 (4%) 36 38	11, 20, 41, 67	0
All	All	1365/1444 (94%)	0.03	46 (3%) 48 50	9, 20, 40, 67	0

All (46) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	161	CYS	7.4
1	D	162	ALA	5.3
1	B	160	ALA	5.0
1	B	159	LEU	4.6
1	D	165	PRO	4.4
1	C	168	PRO	4.2
1	D	251	GLY	4.1
1	A	160	ALA	3.9
1	D	250	ALA	3.9
1	A	228	LEU	3.7
1	B	265	ARG	3.7
1	A	265	ARG	3.6
1	A	227	GLY	3.5
1	A	137	TRP	3.4
1	D	163	ASP	3.3
1	A	361	VAL	3.3
1	D	114	ALA	3.2
1	C	210	MET	3.2
1	C	265	ARG	3.1
1	D	113	ASP	3.0
1	D	252	GLN	3.0

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Mol	Chain	Res	Type	RSRZ
1	D	18	ARG	2.9
1	C	165	PRO	2.9
1	B	168	PRO	2.8
1	B	204	THR	2.7
1	A	225	VAL	2.7
1	B	129	ARG	2.7
1	D	248	ILE	2.7
1	B	361	VAL	2.6
1	A	179	ARG	2.6
1	B	162	ALA	2.5
1	C	361	VAL	2.5
1	D	89	ARG	2.5
1	D	249	GLU	2.4
1	B	351	ARG	2.3
1	C	18	ARG	2.2
1	D	228	LEU	2.1
1	D	160	ALA	2.1
1	C	135	GLN	2.1
1	B	116	HIS	2.1
1	D	7	LYS	2.1
1	C	229	GLU	2.0
1	C	248	ILE	2.0
1	B	206	SER	2.0
1	D	183	LEU	2.0
1	A	172	ARG	2.0

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

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

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

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	C	401	15/16	0.96	0.08	18,30,35,35	0
2	PLP	B	401	15/16	0.97	0.06	19,26,28,30	0
2	PLP	A	401	15/16	0.97	0.06	19,25,27,30	0
2	PLP	D	401	15/16	0.97	0.07	15,26,27,28	0

6.5 Other polymers [i](#)

There are no such residues in this entry.