



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 08:28 PM UTC

PDB ID : 1IWP / pdb_00001iwp
Title : Glycerol Dehydratase-cyanocobalamin Complex of Klebsiella pneumoniae
Authors : Yamanishi, M.; Yunoki, M.; Tobimatsu, T.; Toraya, T.
Deposited on : 2002-05-28
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)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
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

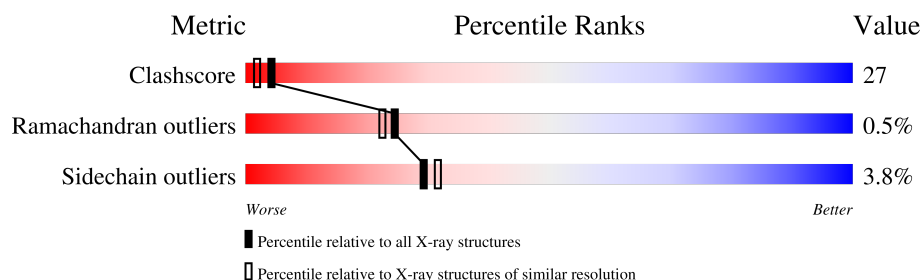
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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))
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	555	60% 37% .
1	L	555	65% 32% .
2	B	194	45% 47% . 5%
2	E	194	31% 59% 5% 5%
3	G	141	55% 39% ...
3	M	141	62% 32% . . .

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	PGO	A	1602	X	-	-	-
5	PGO	L	2602	X	-	-	-

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 14631 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 Glycerol Dehydratase Alpha subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	555	Total	C	N	O	S	0	0	0
			4244	2639	737	838	30			
1	L	555	Total	C	N	O	S	0	0	0
			4244	2639	737	838	30			

- Molecule 2 is a protein called Glycerol Dehydratase Beta subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	184	Total	C	N	O	S	0	0	0
			1424	899	257	264	4			
2	E	184	Total	C	N	O	S	0	0	0
			1424	899	257	264	4			

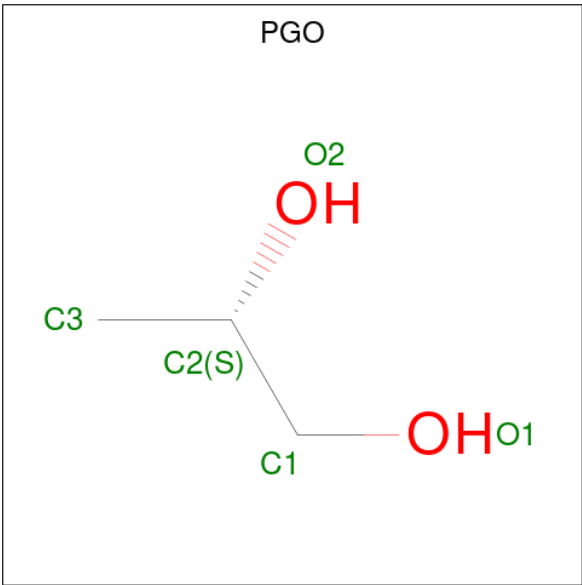
- Molecule 3 is a protein called Glycerol Dehydratase Gamma subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	G	138	Total	C	N	O	S	0	0	0
			1110	693	209	205	3			
3	M	138	Total	C	N	O	S	0	0	0
			1110	693	209	205	3			

- Molecule 4 is POTASSIUM ION (CCD ID: K) (formula: K).

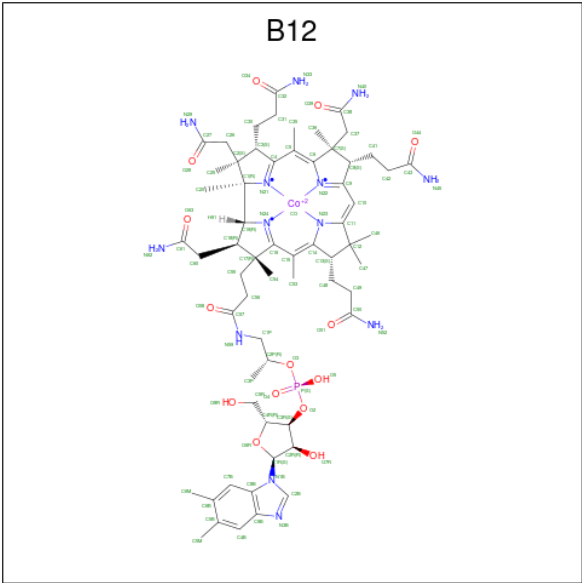
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total	0	0
			1 K		
4	L	1	Total	0	0
			1 K		

- Molecule 5 is S-1,2-PROPANEDIOL (CCD ID: PGO) (formula: C₃H₈O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			5	3	2		
5	L	1	Total	C	O	0	0
			5	3	2		

- Molecule 6 is COBALAMIN (CCD ID: B12) (formula: $C_{62}H_{89}CoN_{13}O_{14}P$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
6	B	1	Total	C	Co	N	O	P	0	0
			91	62	1	13	14	1		
6	E	1	Total	C	Co	N	O	P	0	0
			91	62	1	13	14	1		

- Molecule 7 is water.

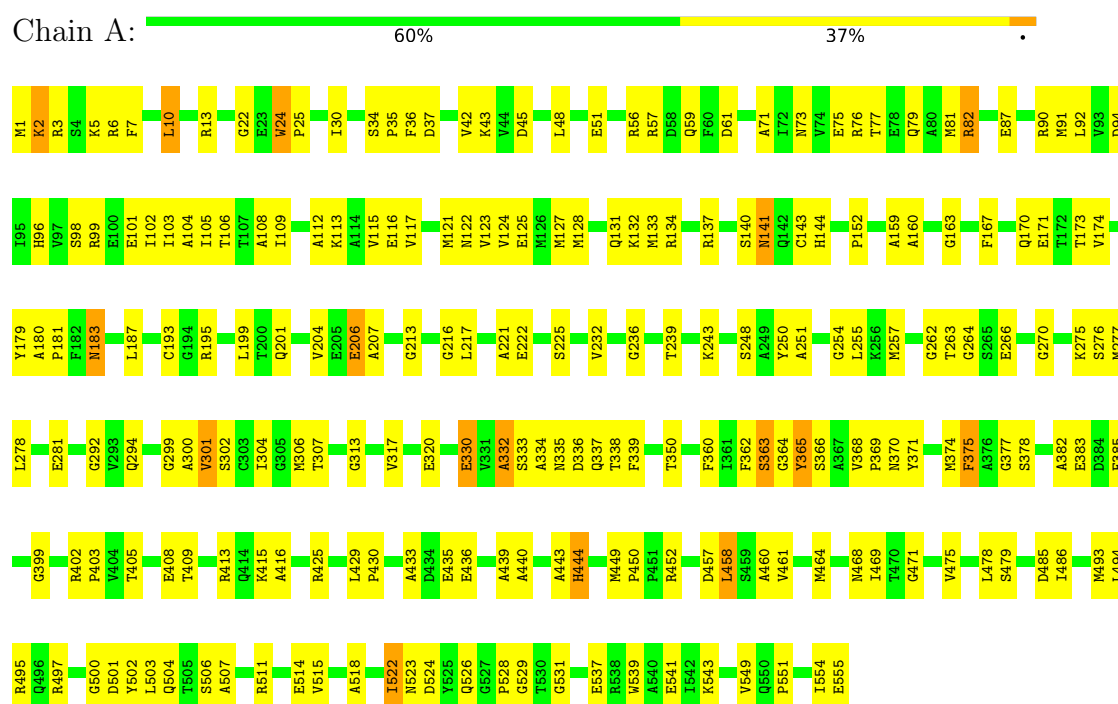
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	267	Total 267	O 267	0	0
7	B	98	Total 98	O 98	0	0
7	G	85	Total 85	O 85	0	0
7	L	254	Total 254	O 254	0	0
7	E	94	Total 94	O 94	0	0
7	M	83	Total 83	O 83	0	0

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.

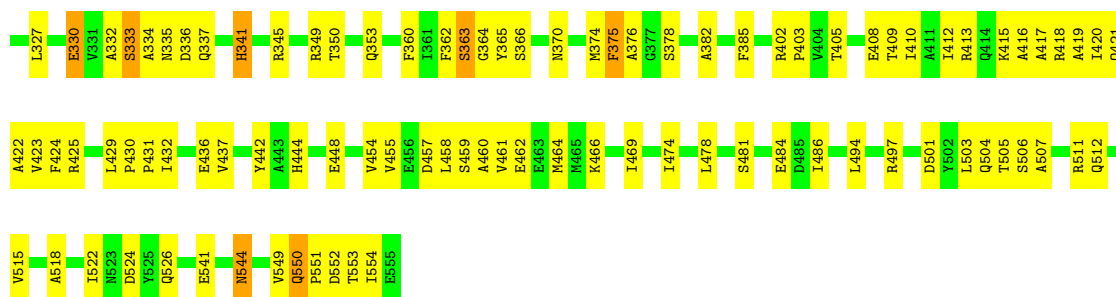
Note EDS was not executed.

• Molecule 1: Glycerol Dehydratase Alpha subunit



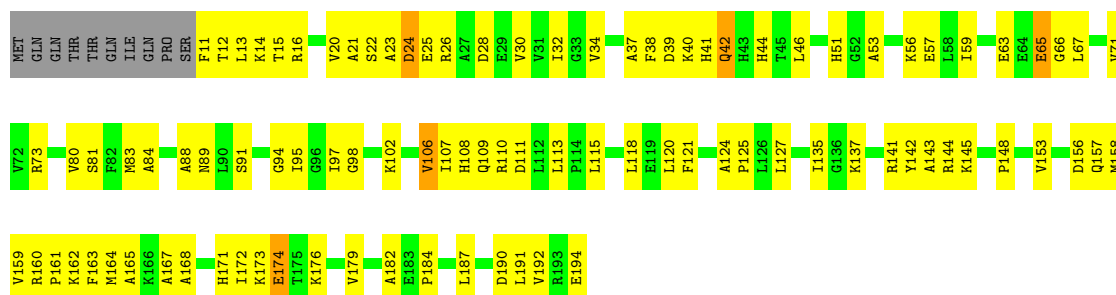
• Molecule 1: Glycerol Dehydratase Alpha subunit





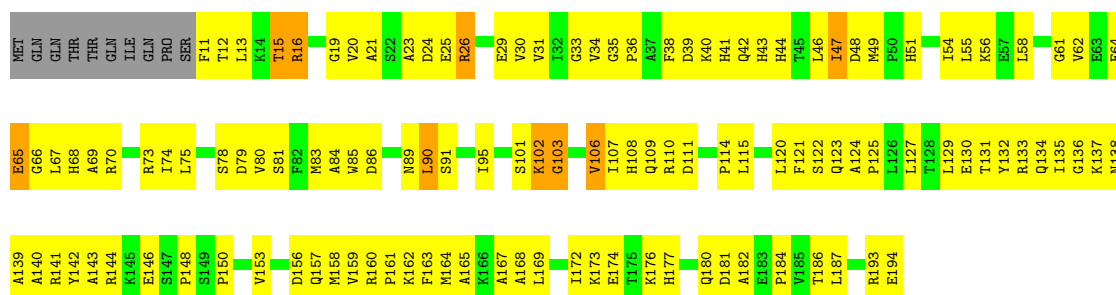
• Molecule 2: Glycerol Dehydratase Beta subunit

Chain B: 45% 47% 5%



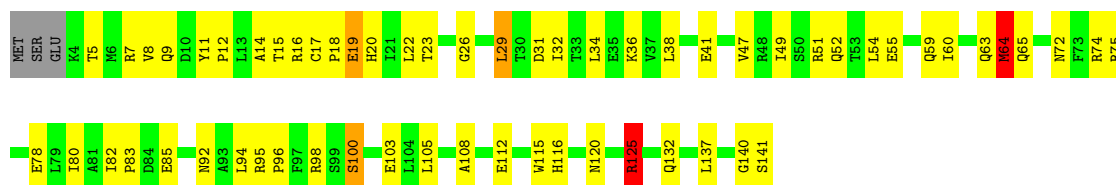
• Molecule 2: Glycerol Dehydratase Beta subunit

Chain E: 31% 59% 5% 5%



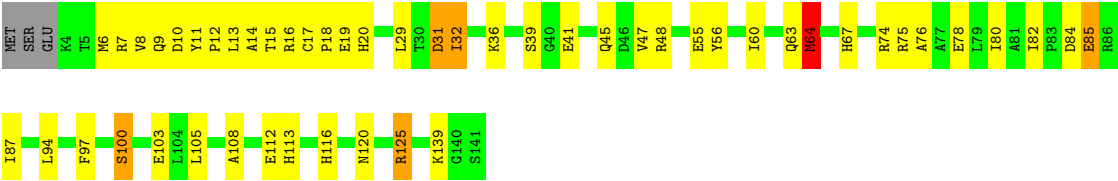
• Molecule 3: Glycerol Dehydratase Gamma subunit

Chain G: 55% 39% 5%



• Molecule 3: Glycerol Dehydratase Gamma subunit

Chain M: 62% 32% 5%



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	81.38Å 108.22Å 113.14Å 90.00° 96.75° 90.00°	Depositor
Resolution (Å)	45.00 – 2.10	Depositor
% Data completeness (in resolution range)	99.9 (45.00-2.10)	Depositor
R_{merge}	0.09	Depositor
R_{sym}	0.13	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.209 , 0.247	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	14631	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: K, PGO, B12

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.42	0/4307	0.97	19/5831 (0.3%)
1	L	0.42	1/4307 (0.0%)	0.97	23/5831 (0.4%)
2	B	0.38	0/1451	0.92	3/1964 (0.2%)
2	E	0.35	0/1451	0.92	5/1964 (0.3%)
3	G	0.36	0/1130	0.88	4/1529 (0.3%)
3	M	0.36	0/1130	0.88	3/1529 (0.2%)
All	All	0.40	1/13776 (0.0%)	0.94	57/18648 (0.3%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	L	133	MET	SD-CE	-5.70	1.65	1.79

All (57) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	444	HIS	N-CA-C	-8.21	101.77	112.68
1	A	225	SER	N-CA-C	7.88	121.61	110.50
1	L	375	PHE	N-CA-C	-7.64	103.28	112.59
1	L	363	SER	N-CA-C	-7.41	102.18	112.25
1	L	175	GLY	N-CA-C	-7.40	102.77	113.86
1	L	225	SER	N-CA-C	7.33	121.32	110.48
1	A	375	PHE	N-CA-C	-7.19	103.81	112.59
1	A	333	SER	N-CA-C	7.14	121.76	110.70
1	A	363	SER	N-CA-C	-6.89	102.89	112.25
2	E	163	PHE	N-CA-C	6.82	122.26	113.88
3	M	80	ILE	N-CA-C	6.73	117.43	110.36
2	B	163	PHE	N-CA-C	6.63	122.86	114.31
1	A	270	GLY	N-CA-C	6.62	124.17	115.36
3	G	100	SER	N-CA-C	-6.60	101.02	110.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L	330	GLU	N-CA-C	-6.39	100.83	110.28
1	L	444	HIS	N-CA-C	-6.35	104.48	112.93
1	L	203	SER	N-CA-C	6.22	118.58	108.63
1	A	365	TYR	N-CA-C	-6.15	100.94	110.10
1	A	332	ALA	N-CA-C	-6.14	96.32	107.75
3	M	64	MET	N-CA-C	-6.03	105.10	112.88
1	L	236	GLY	N-CA-C	-6.02	107.43	115.32
1	A	174	VAL	N-CA-C	5.99	118.62	108.86
3	M	100	SER	N-CA-C	-5.91	101.78	110.52
3	G	64	MET	N-CA-C	-5.90	105.26	112.88
1	L	121	MET	N-CA-C	5.80	118.86	109.40
1	L	224	VAL	N-CA-C	-5.79	98.29	107.15
1	A	61	ASP	N-CA-C	-5.78	101.44	110.17
1	L	22	GLY	N-CA-C	-5.77	103.68	112.51
1	A	24	TRP	CA-C-N	5.72	126.11	119.47
1	A	24	TRP	C-N-CA	5.72	126.11	119.47
1	L	71	ALA	N-CA-C	5.68	120.20	113.16
1	L	333	SER	N-CA-C	5.64	122.82	110.80
1	A	236	GLY	N-CA-C	-5.62	106.89	115.66
1	L	341	HIS	N-CA-C	-5.55	106.51	113.28
1	L	365	TYR	N-CA-C	-5.54	101.64	109.96
2	B	42	GLN	N-CA-C	-5.50	100.92	109.72
1	L	270	GLY	N-CA-C	5.50	122.67	115.36
2	E	90	LEU	N-CA-C	-5.45	105.64	114.09
2	E	103	GLY	N-CA-C	5.43	119.39	113.58
1	L	166	GLY	N-CA-C	5.42	122.17	114.85
1	A	71	ALA	N-CA-C	5.39	119.86	113.28
1	L	503	LEU	N-CA-C	-5.38	106.88	113.50
1	A	206	GLU	N-CA-C	5.37	117.58	111.02
1	A	22	GLY	N-CA-C	-5.37	105.67	112.54
1	A	330	GLU	N-CA-C	-5.37	102.33	110.28
2	E	35	GLY	CA-C-N	5.35	126.53	119.84
2	E	35	GLY	C-N-CA	5.35	126.53	119.84
2	B	118	LEU	N-CA-C	-5.34	104.34	112.04
1	L	507	ALA	N-CA-C	5.34	118.06	110.10
1	L	174	VAL	N-CA-C	5.31	117.03	108.85
1	A	294	GLN	N-CA-C	5.20	117.86	111.82
3	G	80	ILE	N-CA-C	5.20	115.82	110.36
1	L	550	GLN	CA-C-N	5.18	125.23	119.32
1	L	550	GLN	C-N-CA	5.18	125.23	119.32
1	L	61	ASP	N-CA-C	-5.15	102.39	110.17
3	G	125	ARG	N-CA-C	-5.13	105.68	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	507	ALA	N-CA-C	5.03	117.59	110.10

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	4244	0	4195	222	0
1	L	4244	0	4195	184	0
2	B	1424	0	1446	88	0
2	E	1424	0	1446	164	0
3	G	1110	0	1120	66	0
3	M	1110	0	1120	57	0
4	A	1	0	0	0	0
4	L	1	0	0	0	0
5	A	5	0	6	1	0
5	L	5	0	6	0	0
6	B	91	0	88	5	0
6	E	91	0	88	8	0
7	A	267	0	0	46	0
7	B	98	0	0	26	0
7	E	94	0	0	59	0
7	G	85	0	0	7	0
7	L	254	0	0	36	0
7	M	83	0	0	8	0
All	All	14631	0	13710	745	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 27.

All (745) 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:L:306:MET:HE3	2:E:164:MET:HG2	1.19	1.18

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:306:MET:HE1	2:E:165:ALA:HA	1.34	1.09
1:L:126:MET:HE1	1:L:315:ARG:HG3	1.36	1.08
1:A:306:MET:HE3	2:B:164:MET:HG2	1.08	1.07
1:A:306:MET:HE1	2:B:165:ALA:HA	1.40	1.02
1:A:522:ILE:H	1:A:522:ILE:HD12	1.22	1.01
1:A:137:ARG:HH11	1:A:524:ASP:H	1.06	0.97
3:M:11:TYR:HB2	3:M:60:ILE:HD13	1.45	0.97
1:L:141:ASN:HD21	1:L:362:PHE:HB2	1.31	0.95
2:B:156:ASP:HB3	2:B:159:VAL:HG23	1.50	0.93
1:A:554:ILE:HG21	2:E:169:LEU:HD13	1.50	0.92
3:G:7:ARG:HD2	3:G:8:VAL:H	1.35	0.92
2:E:127:LEU:HD12	7:E:2624:HOH:O	1.70	0.91
2:E:156:ASP:HB3	2:E:159:VAL:HG23	1.53	0.90
2:E:125:PRO:HD2	7:E:2662:HOH:O	1.71	0.90
2:E:86:ASP:HB2	7:E:2671:HOH:O	1.74	0.88
3:M:12:PRO:HG2	3:M:15:THR:HG22	1.53	0.88
2:E:85:TRP:HB2	7:E:2646:HOH:O	1.73	0.88
1:A:137:ARG:NH1	1:A:524:ASP:H	1.73	0.87
2:E:47:ILE:HD13	2:E:47:ILE:H	1.38	0.86
2:B:91:SER:HB3	7:B:1675:HOH:O	1.74	0.86
1:A:56:ARG:H	1:A:59:GLN:NE2	1.74	0.85
7:L:2849:HOH:O	3:M:75:ARG:HB3	1.76	0.85
1:A:306:MET:HA	1:A:306:MET:HE2	1.58	0.84
3:M:12:PRO:HG2	3:M:15:THR:CG2	2.07	0.84
3:G:12:PRO:HG2	3:G:15:THR:CG2	2.08	0.83
3:G:22:LEU:HB3	7:G:221:HOH:O	1.76	0.83
1:A:306:MET:CE	2:B:164:MET:HG2	2.03	0.82
2:E:83:MET:HA	7:E:2671:HOH:O	1.79	0.81
1:L:6:ARG:HD3	7:L:2697:HOH:O	1.81	0.81
1:L:226:VAL:HG13	7:L:2843:HOH:O	1.81	0.80
2:B:80:VAL:HG22	2:B:106:VAL:HG12	1.64	0.80
1:L:370:ASN:HD22	2:E:157:GLN:NE2	1.80	0.80
2:B:168:ALA:O	2:B:172:ILE:HG12	1.82	0.79
2:E:80:VAL:HG22	2:E:106:VAL:HG12	1.64	0.79
2:E:193:ARG:HB3	2:E:193:ARG:HH11	1.46	0.79
1:L:306:MET:HE3	2:E:164:MET:CG	2.08	0.79
1:L:306:MET:CE	2:E:164:MET:HG2	2.09	0.78
2:E:84:ALA:HB2	2:E:106:VAL:HG13	1.65	0.78
2:E:62:VAL:HG22	7:E:2610:HOH:O	1.83	0.78
2:E:134:GLN:HE22	2:E:137:LYS:HD3	1.47	0.78
2:E:129:LEU:HD23	7:E:2630:HOH:O	1.83	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:13:ARG:HH11	1:L:13:ARG:HB3	1.48	0.78
1:L:137:ARG:HH11	1:L:524:ASP:H	1.32	0.78
1:A:302:SER:HA	1:A:337:GLN:HG3	1.66	0.78
3:G:31:ASP:O	3:G:36:LYS:HD2	1.83	0.78
1:L:73:ASN:C	1:L:73:ASN:HD22	1.92	0.77
1:A:264:GLY:N	1:A:277:MET:HE3	1.99	0.77
1:L:137:ARG:HH12	1:L:524:ASP:HB3	1.49	0.77
2:B:84:ALA:HB2	2:B:106:VAL:HG13	1.66	0.77
2:E:134:GLN:HE21	2:E:134:GLN:HA	1.48	0.77
2:B:26:ARG:HB2	2:B:26:ARG:HH21	1.50	0.77
1:L:112:ALA:O	1:L:116:GLU:HG3	1.85	0.76
2:B:88:ALA:HA	7:B:1675:HOH:O	1.86	0.76
1:A:263:THR:HB	1:A:277:MET:HE2	1.67	0.76
1:A:264:GLY:CA	1:A:277:MET:HE3	2.16	0.76
2:E:124:ALA:HB3	2:E:125:PRO:HD3	1.67	0.76
2:E:90:LEU:HD11	2:E:184:PRO:HG2	1.68	0.76
1:L:174:VAL:HG12	7:L:2832:HOH:O	1.87	0.75
2:E:31:VAL:HA	7:E:2681:HOH:O	1.86	0.75
1:L:141:ASN:ND2	1:L:362:PHE:HB2	2.00	0.75
2:E:182:ALA:HB1	7:E:2661:HOH:O	1.86	0.74
3:G:12:PRO:HG2	3:G:15:THR:HG22	1.69	0.74
1:L:137:ARG:NH1	1:L:524:ASP:HB3	2.03	0.74
1:L:320:GLU:HB3	7:L:2819:HOH:O	1.86	0.74
1:A:306:MET:HE1	2:B:165:ALA:CA	2.18	0.74
1:A:1:MET:HE2	1:A:3:ARG:HG3	1.70	0.73
1:A:98:SER:OG	1:A:101:GLU:HG3	1.88	0.73
1:A:123:VAL:HB	7:A:1813:HOH:O	1.88	0.73
1:L:146:THR:HG21	7:L:2826:HOH:O	1.87	0.73
1:A:277:MET:HE1	1:A:307:THR:OG1	1.88	0.73
1:L:421:GLN:HA	7:L:2757:HOH:O	1.89	0.73
7:L:2621:HOH:O	2:E:172:ILE:HD11	1.86	0.73
1:L:294:GLN:HE21	1:L:505:THR:HA	1.53	0.72
1:L:306:MET:HE2	1:L:306:MET:HA	1.71	0.72
2:B:65:GLU:CG	2:B:144:ARG:HH12	2.02	0.72
2:E:58:LEU:O	2:E:62:VAL:HG23	1.89	0.72
2:E:75:LEU:HD12	7:E:2661:HOH:O	1.89	0.72
1:A:251:ALA:HA	7:A:1826:HOH:O	1.88	0.72
1:L:123:VAL:HA	1:L:126:MET:HE3	1.71	0.72
1:A:415:LYS:HE2	1:A:486:ILE:HD11	1.71	0.72
1:L:431:PRO:HA	7:L:2841:HOH:O	1.87	0.72
2:B:115:LEU:HD13	6:B:1601:B12:H411	1.70	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:424:PHE:HB2	7:L:2757:HOH:O	1.89	0.71
1:A:112:ALA:O	1:A:116:GLU:HG3	1.91	0.71
1:A:528:PRO:HG3	7:L:2824:HOH:O	1.90	0.71
1:A:195:ARG:HD3	1:A:511:ARG:HG2	1.72	0.71
2:B:65:GLU:HG3	2:B:144:ARG:HH12	1.55	0.71
1:A:554:ILE:CG2	2:E:169:LEU:HD13	2.21	0.70
2:E:137:LYS:HG2	7:E:2645:HOH:O	1.90	0.70
2:B:11:PHE:HB3	7:B:1694:HOH:O	1.92	0.70
3:M:7:ARG:HH11	3:M:63:GLN:NE2	1.89	0.70
3:G:11:TYR:HB2	3:G:60:ILE:HD13	1.72	0.70
2:E:193:ARG:HB3	2:E:193:ARG:NH1	2.05	0.70
1:A:539:TRP:O	1:A:543:LYS:HG2	1.91	0.70
1:L:126:MET:HE1	1:L:315:ARG:CG	2.20	0.70
1:L:159:ALA:HB1	1:L:170:GLN:HE22	1.57	0.70
2:E:156:ASP:HB3	2:E:159:VAL:CG2	2.20	0.70
1:L:253:ARG:HG3	3:M:48:ARG:NH2	2.06	0.69
2:E:157:GLN:HG2	7:E:2652:HOH:O	1.93	0.69
1:A:511:ARG:HB3	1:A:511:ARG:NH2	2.07	0.69
1:L:98:SER:HA	1:L:526:GLN:HE22	1.58	0.69
2:E:58:LEU:HD23	7:E:2654:HOH:O	1.92	0.69
1:L:193:CYS:SG	1:L:486:ILE:HD13	2.33	0.68
2:E:74:ILE:HG12	7:E:2668:HOH:O	1.93	0.68
1:A:163:GLY:HA3	7:A:1835:HOH:O	1.93	0.68
1:A:497:ARG:HD3	7:A:1720:HOH:O	1.93	0.68
2:B:127:LEU:HA	7:B:1683:HOH:O	1.93	0.68
2:E:36:PRO:HD3	2:E:83:MET:HE2	1.75	0.68
1:A:56:ARG:H	1:A:59:GLN:HE21	1.41	0.68
5:A:1602:PGO:H2	7:A:1840:HOH:O	1.92	0.68
1:L:306:MET:HE1	2:E:165:ALA:CA	2.19	0.68
3:M:56:TYR:HB3	7:M:217:HOH:O	1.94	0.68
3:G:12:PRO:HG2	3:G:15:THR:HG21	1.76	0.67
1:A:554:ILE:HG21	2:E:169:LEU:CD1	2.22	0.67
1:A:30:ILE:HD13	7:A:1868:HOH:O	1.94	0.67
2:E:159:VAL:HG11	7:E:2662:HOH:O	1.93	0.67
3:G:7:ARG:HA	3:G:63:GLN:HE22	1.60	0.67
2:B:21:ALA:HB3	2:B:184:PRO:HB2	1.76	0.66
2:E:153:VAL:HG12	7:E:2653:HOH:O	1.94	0.66
1:L:180:ALA:HB3	1:L:181:PRO:HD3	1.76	0.66
2:E:12:THR:HG23	2:E:194:GLU:OE1	1.95	0.66
1:A:522:ILE:H	1:A:522:ILE:CD1	1.98	0.66
1:A:239:THR:HG23	7:A:1863:HOH:O	1.94	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:M:125:ARG:HD2	7:M:148:HOH:O	1.95	0.65
2:E:78:SER:C	2:E:83:MET:HE3	2.22	0.65
3:M:55:GLU:CD	3:M:74:ARG:HH22	2.04	0.65
2:B:20:VAL:HG12	7:B:1674:HOH:O	1.96	0.65
3:G:7:ARG:HD2	3:G:8:VAL:N	2.08	0.65
3:G:19:GLU:HB2	7:G:224:HOH:O	1.96	0.65
1:L:332:ALA:HA	1:L:360:PHE:HB2	1.79	0.65
2:E:127:LEU:HD22	2:E:131:THR:HG21	1.79	0.65
2:B:30:VAL:HG22	7:B:1665:HOH:O	1.95	0.65
3:M:7:ARG:HA	3:M:63:GLN:HE22	1.61	0.65
2:E:46:LEU:HD12	2:E:125:PRO:HD3	1.79	0.65
1:A:217:LEU:HD21	7:A:1869:HOH:O	1.96	0.65
1:L:92:LEU:HD23	1:L:102:ILE:HD13	1.79	0.65
2:E:26:ARG:HD2	7:E:2683:HOH:O	1.97	0.64
1:A:159:ALA:HB1	1:A:170:GLN:HE22	1.62	0.64
3:M:32:ILE:N	3:M:32:ILE:HD12	2.13	0.64
2:B:156:ASP:HB3	2:B:159:VAL:CG2	2.24	0.63
1:L:549:VAL:HG21	1:L:554:ILE:HD11	1.81	0.63
1:A:73:ASN:OD1	1:A:75:GLU:HG2	1.98	0.63
1:L:462:GLU:HB3	7:L:2806:HOH:O	1.97	0.63
2:E:194:GLU:HB2	7:E:2680:HOH:O	1.98	0.63
1:L:6:ARG:NH1	7:L:2697:HOH:O	2.22	0.63
2:E:134:GLN:HA	2:E:134:GLN:NE2	2.13	0.63
1:A:152:PRO:HG3	7:A:1642:HOH:O	1.99	0.62
2:B:83:MET:HB2	7:B:1664:HOH:O	1.98	0.62
1:A:436:GLU:HG2	1:A:450:PRO:HG2	1.81	0.62
1:A:511:ARG:HB3	1:A:511:ARG:HH21	1.63	0.62
1:L:415:LYS:HE2	1:L:486:ILE:HD11	1.81	0.62
2:E:158:MET:C	2:E:161:PRO:HD2	2.25	0.62
1:A:75:GLU:HG3	1:A:76:ARG:HG3	1.80	0.62
2:E:67:LEU:HD13	7:E:2675:HOH:O	1.98	0.62
2:E:168:ALA:O	2:E:172:ILE:HG12	2.00	0.62
1:L:462:GLU:O	1:L:466:LYS:HG3	1.99	0.62
1:A:551:PRO:HD2	7:A:1834:HOH:O	1.99	0.62
2:E:43:HIS:HB3	7:E:2639:HOH:O	1.99	0.62
3:M:55:GLU:OE2	3:M:74:ARG:NH2	2.32	0.62
1:A:332:ALA:HA	1:A:360:PHE:HB2	1.81	0.62
1:L:148:LEU:HD13	1:L:148:LEU:O	1.99	0.62
2:E:120:LEU:HD12	2:E:121:PHE:H	1.64	0.61
3:G:14:ALA:O	3:G:18:PRO:HG3	1.99	0.61
2:E:16:ARG:CB	2:E:16:ARG:HH21	2.14	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:30:ILE:HG21	7:A:1868:HOH:O	2.01	0.60
2:E:107:ILE:HG23	7:E:2689:HOH:O	2.01	0.60
1:A:35:PRO:HD2	7:A:1868:HOH:O	2.01	0.60
1:A:141:ASN:OD1	1:A:362:PHE:HB2	2.00	0.60
6:B:1601:B12:H362	6:B:1601:B12:H351	1.84	0.60
1:L:170:GLN:HE21	1:L:187:LEU:HD11	1.67	0.60
1:A:5:LYS:HD3	1:L:448:GLU:OE2	2.02	0.60
1:A:464:MET:HG3	1:A:469:ILE:HG13	1.82	0.60
7:A:1801:HOH:O	3:G:49:ILE:HD12	2.02	0.60
2:E:172:ILE:O	2:E:176:LYS:HG2	2.02	0.60
3:M:7:ARG:HH11	3:M:63:GLN:HE21	1.50	0.60
1:A:122:ASN:OD1	1:A:125:GLU:HG3	2.01	0.60
1:A:555:GLU:O	2:E:44:HIS:HE1	1.84	0.60
2:B:98:GLY:HA3	7:B:1664:HOH:O	2.01	0.60
1:L:300:ALA:HB1	1:L:304:ILE:HA	1.83	0.60
2:E:131:THR:C	2:E:133:ARG:H	2.09	0.60
2:B:158:MET:C	2:B:161:PRO:HD2	2.27	0.60
2:E:66:GLY:C	2:E:67:LEU:HD12	2.27	0.60
1:A:124:VAL:HG12	7:A:1816:HOH:O	2.01	0.59
1:A:24:TRP:HB2	1:L:551:PRO:HG3	1.85	0.59
1:L:57:ARG:HD2	7:L:2842:HOH:O	2.02	0.59
6:E:2601:B12:H531	6:E:2601:B12:H552	1.85	0.59
2:B:80:VAL:HG22	2:B:106:VAL:CG1	2.31	0.59
1:L:13:ARG:HB3	1:L:13:ARG:NH1	2.16	0.59
2:E:84:ALA:CB	2:E:106:VAL:HG13	2.32	0.59
1:A:458:LEU:O	1:A:461:VAL:HG12	2.03	0.59
2:E:141:ARG:HD2	2:E:146:GLU:OE1	2.02	0.59
1:A:306:MET:HE2	1:A:306:MET:CA	2.31	0.59
2:E:134:GLN:NE2	2:E:137:LYS:HD3	2.17	0.59
3:M:17:CYS:HB3	3:M:20:HIS:HD2	1.66	0.59
1:L:504:GLN:HG3	3:M:11:TYR:CE2	2.38	0.59
1:A:137:ARG:HD3	1:A:523:ASN:HA	1.85	0.59
1:A:25:PRO:HB3	7:A:1868:HOH:O	2.01	0.59
1:A:335:ASN:OD1	1:A:350:THR:HA	2.02	0.59
1:A:504:GLN:HG3	3:G:11:TYR:CE2	2.38	0.59
2:B:94:GLY:C	7:B:1675:HOH:O	2.46	0.59
2:E:136:GLY:HA2	7:E:2610:HOH:O	2.03	0.58
1:L:222:GLU:HG3	1:L:258:ARG:HD2	1.85	0.58
1:A:500:GLY:HA2	7:A:1801:HOH:O	2.02	0.58
1:L:121:MET:HG2	7:L:2824:HOH:O	2.03	0.58
2:E:160:ARG:HB3	2:E:161:PRO:HD3	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:E:2601:B12:H351	6:E:2601:B12:H362	1.85	0.58
1:A:99:ARG:O	1:A:103:ILE:HG13	2.04	0.58
1:A:479:SER:OG	3:G:38:LEU:HD11	2.02	0.58
2:B:26:ARG:HB2	2:B:26:ARG:NH2	2.18	0.58
6:B:1601:B12:H552	6:B:1601:B12:H531	1.86	0.58
3:M:14:ALA:O	3:M:18:PRO:HG3	2.04	0.58
1:A:56:ARG:CB	1:A:59:GLN:HE21	2.17	0.58
1:L:458:LEU:HD23	7:L:2694:HOH:O	2.03	0.58
2:E:61:GLY:HA2	7:E:2645:HOH:O	2.04	0.58
2:E:95:ILE:HG23	7:E:2689:HOH:O	2.03	0.58
1:L:374:MET:HA	7:E:2651:HOH:O	2.03	0.57
2:E:173:LYS:NZ	2:E:177:HIS:HE1	2.01	0.57
3:M:7:ARG:NH1	3:M:63:GLN:HE21	2.02	0.57
2:B:153:VAL:HG23	7:B:1606:HOH:O	2.05	0.57
2:E:25:GLU:O	2:E:26:ARG:HB2	2.04	0.57
1:A:444:HIS:ND1	7:L:2697:HOH:O	2.33	0.57
3:G:55:GLU:OE2	3:G:74:ARG:NH2	2.38	0.57
3:G:100:SER:OG	3:G:103:GLU:HG3	2.04	0.57
1:A:34:SER:HB3	1:A:37:ASP:CG	2.29	0.57
3:G:7:ARG:HG3	3:G:9:GLN:HG3	1.85	0.57
1:L:430:PRO:HD3	1:L:460:ALA:CB	2.34	0.57
2:E:135:ILE:C	7:E:2647:HOH:O	2.47	0.57
1:A:137:ARG:NH1	1:A:524:ASP:N	2.48	0.57
2:B:89:ASN:HA	2:B:110:ARG:HG2	1.87	0.57
1:A:248:SER:HB2	3:G:75:ARG:NH2	2.20	0.57
2:B:160:ARG:HB3	2:B:161:PRO:HD3	1.85	0.57
3:G:26:GLY:C	7:G:221:HOH:O	2.48	0.57
1:L:211:GLU:O	1:L:215:ARG:HG3	2.05	0.56
2:E:54:ILE:C	2:E:56:LYS:H	2.13	0.56
2:E:55:LEU:C	7:E:2605:HOH:O	2.48	0.56
2:B:137:LYS:O	2:B:141:ARG:HG2	2.05	0.56
3:G:7:ARG:CG	3:G:9:GLN:HE21	2.19	0.56
1:L:121:MET:HA	7:L:2824:HOH:O	2.05	0.56
1:L:148:LEU:HD11	2:E:153:VAL:O	2.04	0.56
3:M:64:MET:HE3	3:M:64:MET:HA	1.87	0.56
2:E:66:GLY:O	2:E:67:LEU:HD12	2.06	0.56
1:A:132:LYS:HE3	1:A:133:MET:HE1	1.88	0.56
3:G:23:THR:N	7:G:221:HOH:O	2.39	0.56
2:B:109:GLN:OE1	2:B:110:ARG:O	2.24	0.56
1:L:302:SER:HA	1:L:337:GLN:HG3	1.88	0.56
2:E:144:ARG:CB	2:E:144:ARG:HH11	2.18	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:193:CYS:SG	1:A:486:ILE:HG12	2.46	0.56
1:L:402:ARG:HD3	1:L:541:GLU:OE2	2.05	0.56
2:E:141:ARG:HB2	2:E:148:PRO:HG3	1.88	0.56
3:G:7:ARG:HB3	3:G:9:GLN:HE21	1.70	0.56
2:E:143:ALA:HB1	7:E:2617:HOH:O	2.06	0.56
1:L:334:ALA:HA	1:L:363:SER:OG	2.06	0.56
1:A:263:THR:HA	7:A:1679:HOH:O	2.05	0.55
1:L:137:ARG:HH11	1:L:524:ASP:N	2.03	0.55
3:M:12:PRO:HG2	3:M:15:THR:HG21	1.88	0.55
1:A:232:VAL:HG21	1:A:266:GLU:HA	1.89	0.55
1:L:51:GLU:HG3	7:L:2740:HOH:O	2.06	0.55
1:A:501:ASP:HB3	1:A:515:VAL:HG11	1.89	0.55
1:L:132:LYS:HE3	1:L:133:MET:CE	2.36	0.55
2:E:29:GLU:HA	2:E:68:HIS:O	2.06	0.55
3:M:39:SER:OG	3:M:41:GLU:HG2	2.07	0.55
1:A:5:LYS:HD3	1:L:448:GLU:CD	2.32	0.55
2:E:73:ARG:HG3	2:E:73:ARG:HH11	1.71	0.55
3:M:85:GLU:CD	3:M:85:GLU:H	2.13	0.55
1:A:96:HIS:HE1	1:L:94:ASP:OD2	1.90	0.55
6:E:2601:B12:N62	7:E:2651:HOH:O	2.34	0.55
2:B:80:VAL:HG12	7:B:1623:HOH:O	2.07	0.54
1:A:144:HIS:CD2	7:A:1840:HOH:O	2.60	0.54
1:A:425:ARG:NH1	7:A:1851:HOH:O	2.40	0.54
1:A:515:VAL:CG1	3:G:12:PRO:HB3	2.37	0.54
1:A:96:HIS:CE1	1:L:94:ASP:OD2	2.61	0.54
1:L:464:MET:HG3	1:L:469:ILE:HG13	1.88	0.54
2:E:11:PHE:HA	2:E:194:GLU:HG2	1.89	0.54
1:A:277:MET:HE1	1:A:307:THR:CA	2.36	0.54
2:E:115:LEU:HD13	6:E:2601:B12:H411	1.90	0.54
1:A:485:ASP:CG	1:A:486:ILE:HD12	2.33	0.54
1:A:92:LEU:HD23	1:A:102:ILE:HD13	1.90	0.54
1:L:259:TYR:HB3	7:L:2843:HOH:O	2.08	0.54
1:A:334:ALA:HA	1:A:363:SER:OG	2.08	0.53
1:L:484:GLU:HB2	7:L:2699:HOH:O	2.08	0.53
3:M:7:ARG:HG3	3:M:9:GLN:HG2	1.90	0.53
1:A:137:ARG:HH12	1:A:524:ASP:HB3	1.72	0.53
1:A:478:LEU:HD13	1:A:486:ILE:HG22	1.89	0.53
1:A:518:ALA:O	1:A:522:ILE:HG13	2.08	0.53
1:L:141:ASN:HD22	1:L:142:GLN:H	1.57	0.53
2:B:124:ALA:HB3	2:B:125:PRO:HD3	1.91	0.53
1:L:73:ASN:C	1:L:73:ASN:ND2	2.64	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:M:7:ARG:CG	3:M:9:GLN:HG2	2.38	0.53
1:A:425:ARG:HG2	1:A:425:ARG:HH11	1.74	0.53
1:A:374:MET:HE3	7:A:1853:HOH:O	2.07	0.53
2:B:84:ALA:CB	2:B:106:VAL:HG13	2.38	0.53
2:E:95:ILE:HG21	7:E:2618:HOH:O	2.07	0.53
2:E:137:LYS:NZ	2:E:137:LYS:HB3	2.23	0.53
1:L:478:LEU:HD13	1:L:486:ILE:HG22	1.89	0.53
2:E:184:PRO:HG3	7:E:2635:HOH:O	2.08	0.53
1:A:277:MET:HE1	1:A:307:THR:CB	2.38	0.53
1:L:459:SER:HA	7:L:2806:HOH:O	2.08	0.53
2:E:58:LEU:N	7:E:2605:HOH:O	2.41	0.53
1:A:87:GLU:HG3	1:A:91:MET:HE3	1.90	0.53
1:A:495:ARG:NH1	3:G:29:LEU:HD22	2.24	0.53
7:L:2849:HOH:O	3:M:76:ALA:N	2.41	0.53
3:M:7:ARG:HD2	3:M:63:GLN:HE22	1.73	0.53
2:B:26:ARG:NH2	2:B:26:ARG:CB	2.73	0.52
1:L:185:LEU:HD13	1:L:474:ILE:HD12	1.91	0.52
3:M:108:ALA:CB	3:M:125:ARG:HD3	2.39	0.52
2:B:37:ALA:HB1	2:B:41:HIS:HB2	1.92	0.52
2:B:109:GLN:CD	2:B:110:ARG:O	2.52	0.52
1:L:494:LEU:HB3	3:M:47:VAL:HG11	1.92	0.52
1:A:133:MET:HE2	1:A:133:MET:N	2.25	0.52
1:A:300:ALA:HB1	1:A:304:ILE:HA	1.90	0.52
1:L:132:LYS:HG2	1:L:133:MET:HE2	1.92	0.52
1:L:552:ASP:OD2	1:L:553:THR:HG23	2.10	0.52
2:B:44:HIS:HD2	7:B:1639:HOH:O	1.91	0.52
1:L:182:PHE:CE2	1:L:461:VAL:HB	2.44	0.52
2:E:129:LEU:HA	7:E:2630:HOH:O	2.10	0.52
1:L:511:ARG:HB3	1:L:512:GLN:HE22	1.75	0.52
2:B:15:THR:HG22	7:B:1630:HOH:O	2.10	0.52
1:L:263:THR:HA	7:L:2633:HOH:O	2.09	0.52
1:A:458:LEU:HA	1:A:461:VAL:HG12	1.92	0.51
1:L:335:ASN:OD1	1:L:350:THR:HA	2.10	0.51
3:G:32:ILE:HD12	3:G:32:ILE:N	2.26	0.51
1:L:77:THR:HA	1:L:108:ALA:O	2.09	0.51
7:A:1863:HOH:O	3:G:95:ARG:HA	2.09	0.51
3:G:140:GLY:O	3:G:141:SER:O	2.29	0.51
1:L:263:THR:HG21	7:L:2819:HOH:O	2.08	0.51
1:L:403:PRO:HG2	7:L:2634:HOH:O	2.10	0.51
1:A:402:ARG:HD3	1:A:541:GLU:OE2	2.10	0.51
1:L:232:VAL:HG21	1:L:266:GLU:HA	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:137:LYS:O	2:E:141:ARG:HG2	2.10	0.51
1:A:36:PHE:O	1:A:275:LYS:HE2	2.10	0.51
1:A:160:ALA:HB2	1:A:416:ALA:HB2	1.93	0.51
1:L:174:VAL:HG21	1:L:177:ALA:HA	1.92	0.51
2:E:47:ILE:HD12	2:E:125:PRO:HA	1.91	0.51
2:E:81:SER:HB3	6:E:2601:B12:HM62	1.91	0.51
2:E:114:PRO:HA	7:E:2646:HOH:O	2.09	0.51
3:M:74:ARG:HD2	7:M:159:HOH:O	2.11	0.51
2:B:32:ILE:CD1	2:B:97:ILE:HD12	2.41	0.51
1:L:464:MET:CG	1:L:469:ILE:HG13	2.41	0.51
1:A:79:GLN:HG3	1:A:82:ARG:NH2	2.26	0.51
1:L:518:ALA:O	1:L:522:ILE:HG12	2.11	0.51
1:A:10:LEU:O	1:A:13:ARG:HB2	2.10	0.51
2:B:38:PHE:CE1	2:B:51:HIS:HB3	2.46	0.51
1:L:522:ILE:HG13	7:L:2838:HOH:O	2.11	0.51
1:A:56:ARG:HB2	1:A:59:GLN:HE21	1.76	0.51
2:B:25:GLU:O	2:B:26:ARG:HB2	2.11	0.51
1:L:132:LYS:HG2	1:L:133:MET:CE	2.41	0.51
2:E:110:ARG:O	2:E:111:ASP:HB2	2.10	0.51
2:B:191:LEU:HG	7:B:1694:HOH:O	2.11	0.50
3:M:45:GLN:H	3:M:45:GLN:CD	2.20	0.50
1:A:337:GLN:HE21	1:A:337:GLN:HA	1.75	0.50
2:B:173:LYS:O	2:B:176:LYS:HB2	2.10	0.50
1:L:143:CYS:HB3	1:L:167:PHE:CE1	2.45	0.50
1:A:125:GLU:HA	7:A:1816:HOH:O	2.11	0.50
1:A:181:PRO:HB2	1:A:461:VAL:HG23	1.92	0.50
2:E:67:LEU:HD11	2:E:144:ARG:CG	2.42	0.50
2:E:131:THR:C	2:E:133:ARG:N	2.68	0.50
1:A:383:GLU:HG2	1:L:9:VAL:HG11	1.94	0.50
1:A:430:PRO:HD3	1:A:460:ALA:CB	2.41	0.50
1:L:306:MET:CE	2:E:165:ALA:HA	2.24	0.50
2:E:31:VAL:HG23	2:E:91:SER:HB2	1.92	0.50
2:E:138:ASN:ND2	2:E:150:PRO:HA	2.26	0.50
2:E:139:ALA:C	7:E:2618:HOH:O	2.55	0.50
3:M:7:ARG:HG3	3:M:9:GLN:H	1.76	0.50
3:M:7:ARG:HD2	3:M:63:GLN:NE2	2.26	0.50
2:B:22:SER:HA	7:B:1698:HOH:O	2.10	0.50
2:B:171:HIS:HD2	7:B:1609:HOH:O	1.94	0.50
2:E:80:VAL:HG22	2:E:106:VAL:CG1	2.40	0.50
1:A:43:LYS:HB3	1:A:51:GLU:HB2	1.92	0.50
1:L:382:ALA:HA	1:L:385:PHE:CE2	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:67:LEU:HD11	2:E:144:ARG:CD	2.42	0.50
1:A:180:ALA:HB3	1:A:181:PRO:HD3	1.94	0.50
1:A:77:THR:HA	1:A:108:ALA:O	2.12	0.49
1:A:105:ILE:O	1:A:109:ILE:HG23	2.12	0.49
1:L:409:THR:O	1:L:413:ARG:HG3	2.12	0.49
2:B:23:ALA:O	2:B:24:ASP:HB2	2.12	0.49
1:L:172:THR:HB	1:L:187:LEU:HD22	1.94	0.49
1:L:501:ASP:HB3	1:L:515:VAL:HG11	1.94	0.49
3:M:15:THR:HG23	3:M:16:ARG:HG2	1.94	0.49
3:M:100:SER:OG	3:M:103:GLU:HG3	2.12	0.49
1:L:419:ALA:O	1:L:423:VAL:HG23	2.12	0.49
1:A:375:PHE:CZ	7:A:1840:HOH:O	2.65	0.49
2:B:184:PRO:HG3	7:B:1653:HOH:O	2.11	0.49
1:L:1:MET:HA	1:L:3:ARG:NH1	2.28	0.49
1:L:418:ARG:O	1:L:421:GLN:HB3	2.12	0.49
1:A:494:LEU:HB3	3:G:47:VAL:HG11	1.95	0.49
2:B:81:SER:OG	6:B:1601:B12:HM62	2.13	0.49
1:L:425:ARG:HA	7:L:2803:HOH:O	2.11	0.49
2:E:44:HIS:HB2	2:E:48:ASP:HA	1.93	0.49
2:E:89:ASN:HA	7:E:2644:HOH:O	2.12	0.49
3:G:52:GLN:O	3:G:55:GLU:HB3	2.13	0.49
2:E:47:ILE:H	2:E:47:ILE:CD1	2.19	0.49
3:M:82:ILE:HB	3:M:87:ILE:HD11	1.94	0.49
1:A:42:VAL:CG1	1:A:81:MET:HG3	2.43	0.49
3:M:13:LEU:HD11	7:M:217:HOH:O	2.13	0.49
7:A:1815:HOH:O	3:G:34:LEU:HD13	2.12	0.49
3:G:17:CYS:HB3	3:G:20:HIS:HD2	1.78	0.49
1:L:43:LYS:HB3	1:L:51:GLU:HB2	1.95	0.49
1:L:181:PRO:HB2	1:L:461:VAL:HG23	1.94	0.49
1:A:128:MET:O	1:A:131:GLN:HG2	2.13	0.49
3:G:49:ILE:HD13	3:G:54:LEU:CD2	2.43	0.49
1:A:3:ARG:HG3	1:A:3:ARG:HH11	1.78	0.49
1:L:196:PRO:HD2	1:L:511:ARG:NH2	2.28	0.49
2:E:132:TYR:HD2	7:E:2630:HOH:O	1.94	0.49
3:M:97:PHE:CE1	3:M:139:LYS:HE2	2.48	0.49
1:A:336:ASP:O	1:A:378:SER:HA	2.13	0.48
1:L:409:THR:O	1:L:412:ILE:HG22	2.13	0.48
1:A:171:GLU:CD	7:A:1840:HOH:O	2.55	0.48
2:B:53:ALA:O	2:B:57:GLU:HG2	2.12	0.48
1:L:141:ASN:HD21	1:L:362:PHE:CB	2.16	0.48
1:L:294:GLN:NE2	1:L:505:THR:HA	2.26	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:44:HIS:HA	2:E:49:MET:O	2.13	0.48
2:E:67:LEU:CD2	2:E:143:ALA:HB3	2.43	0.48
1:L:374:MET:HE3	7:E:2651:HOH:O	2.13	0.48
1:A:56:ARG:HG3	1:A:59:GLN:NE2	2.28	0.48
1:L:330:GLU:OE2	1:L:506:SER:HA	2.13	0.48
1:A:143:CYS:HB3	1:A:167:PHE:CE1	2.49	0.48
1:A:503:LEU:HD21	7:A:1826:HOH:O	2.14	0.48
3:G:19:GLU:H	3:G:19:GLU:CD	2.20	0.48
1:L:143:CYS:HB3	1:L:167:PHE:CD1	2.48	0.48
1:L:299:GLY:HA2	1:L:320:GLU:CD	2.38	0.48
1:A:24:TRP:HB2	1:L:551:PRO:CG	2.44	0.48
1:A:106:THR:O	1:A:109:ILE:HG12	2.13	0.48
1:L:154:GLN:HG2	1:L:158:ASP:OD2	2.14	0.48
1:L:417:ALA:CB	1:L:437:VAL:HG13	2.44	0.48
3:G:64:MET:O	3:G:65:GLN:HB2	2.13	0.48
1:L:550:GLN:HA	1:L:550:GLN:OE1	2.13	0.48
2:E:109:GLN:CD	2:E:110:ARG:O	2.57	0.48
1:A:56:ARG:HG3	1:A:59:GLN:HE21	1.79	0.48
1:A:301:VAL:HG12	1:A:302:SER:H	1.79	0.48
1:L:464:MET:O	1:L:469:ILE:HG12	2.14	0.48
2:E:16:ARG:HH21	2:E:16:ARG:HB3	1.78	0.48
2:E:121:PHE:HB3	2:E:127:LEU:HD11	1.96	0.48
3:M:113:HIS:HE1	7:M:196:HOH:O	1.96	0.48
2:B:192:VAL:N	7:B:1694:HOH:O	2.46	0.47
1:A:497:ARG:O	3:G:49:ILE:HB	2.14	0.47
2:E:58:LEU:HA	7:E:2654:HOH:O	2.14	0.47
1:A:433:ALA:HB1	1:A:435:GLU:OE1	2.15	0.47
2:B:15:THR:HB	2:B:39:ASP:OD1	2.15	0.47
2:B:15:THR:CG2	2:B:187:LEU:HD22	2.45	0.47
3:G:82:ILE:HG12	3:G:115:TRP:CD2	2.49	0.47
1:A:143:CYS:HB3	1:A:167:PHE:CD1	2.49	0.47
1:L:160:ALA:HB2	1:L:416:ALA:HB2	1.96	0.47
2:E:127:LEU:CD2	2:E:131:THR:HG21	2.43	0.47
1:A:436:GLU:HG2	1:A:450:PRO:CG	2.44	0.47
3:G:7:ARG:HB3	3:G:9:GLN:NE2	2.29	0.47
1:A:430:PRO:HG2	1:A:457:ASP:HA	1.97	0.47
1:L:224:VAL:HG21	1:L:257:MET:HE2	1.96	0.47
1:A:1:MET:O	1:A:3:ARG:N	2.44	0.47
1:A:206:GLU:HG2	7:B:1602:HOH:O	2.14	0.47
1:A:216:GLY:HA2	1:A:497:ARG:NH1	2.29	0.47
1:A:307:THR:O	1:A:313:GLY:HA3	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:108:ALA:CB	3:G:125:ARG:HD3	2.45	0.47
1:L:308:GLY:O	1:L:345:ARG:NH2	2.48	0.47
1:L:455:VAL:HG22	7:E:2650:HOH:O	2.14	0.47
2:E:42:GLN:OE1	2:E:101:SER:HB2	2.14	0.47
3:M:67:HIS:HD2	7:M:168:HOH:O	1.98	0.47
2:B:107:ILE:HD11	2:B:135:ILE:HG23	1.97	0.47
2:B:110:ARG:HD3	7:B:1648:HOH:O	2.14	0.47
3:M:48:ARG:NH1	3:M:84:ASP:OD1	2.48	0.47
1:A:262:GLY:N	1:A:281:GLU:OE1	2.44	0.47
1:A:277:MET:CE	1:A:307:THR:OG1	2.62	0.47
1:A:292:GLY:HA3	3:G:72:ASN:HB2	1.96	0.47
2:E:38:PHE:CE1	2:E:51:HIS:HB3	2.50	0.47
1:A:317:VAL:O	1:A:320:GLU:HG2	2.15	0.47
2:B:40:LYS:HE2	2:B:41:HIS:CE1	2.50	0.47
3:G:18:PRO:HD2	3:G:19:GLU:OE2	2.15	0.47
2:E:138:ASN:HB2	7:E:2647:HOH:O	2.14	0.47
1:A:382:ALA:HA	1:A:385:PHE:CE2	2.50	0.46
1:A:405:THR:OG1	1:A:408:GLU:HG2	2.15	0.46
1:A:549:VAL:HG12	7:L:2737:HOH:O	2.15	0.46
7:A:1856:HOH:O	3:G:15:THR:HB	2.15	0.46
3:G:112:GLU:O	3:G:116:HIS:HA	2.14	0.46
1:A:98:SER:HA	1:A:526:GLN:NE2	2.30	0.46
1:A:383:GLU:HG2	1:L:9:VAL:CG1	2.45	0.46
3:G:7:ARG:CD	3:G:8:VAL:H	2.17	0.46
3:G:11:TYR:HA	3:G:12:PRO:C	2.40	0.46
2:E:33:GLY:HA2	7:E:2668:HOH:O	2.14	0.46
2:B:59:ILE:O	2:B:63:GLU:HG3	2.16	0.46
2:B:179:VAL:HB	2:B:182:ALA:CB	2.45	0.46
1:L:174:VAL:HG11	1:L:180:ALA:N	2.30	0.46
2:E:58:LEU:HB2	7:E:2605:HOH:O	2.14	0.46
3:M:74:ARG:HH21	3:M:74:ARG:HG2	1.80	0.46
1:A:48:LEU:HD11	1:A:57:ARG:NH2	2.30	0.46
1:A:439:ALA:O	1:A:443:ALA:HB2	2.14	0.46
2:E:16:ARG:HB3	2:E:16:ARG:NH2	2.30	0.46
2:E:25:GLU:O	2:E:26:ARG:CB	2.63	0.46
2:E:135:ILE:HG22	2:E:135:ILE:O	2.15	0.46
3:M:31:ASP:O	3:M:36:LYS:HD2	2.15	0.46
1:A:486:ILE:HD12	1:A:486:ILE:N	2.31	0.46
2:E:137:LYS:HB3	2:E:137:LYS:HZ3	1.80	0.46
1:A:132:LYS:HE3	1:A:133:MET:CE	2.45	0.46
1:A:370:ASN:HD22	2:B:157:GLN:NE2	2.13	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:45:ASP:HB3	1:L:50:VAL:HG11	1.98	0.46
1:L:174:VAL:HA	7:L:2832:HOH:O	2.15	0.46
1:L:253:ARG:HG3	3:M:48:ARG:HH22	1.77	0.46
1:A:254:GLY:O	1:A:497:ARG:HA	2.16	0.46
1:L:161:GLU:HG3	1:L:409:THR:HG23	1.98	0.46
2:E:30:VAL:C	7:E:2681:HOH:O	2.58	0.46
2:E:47:ILE:HD13	2:E:47:ILE:N	2.18	0.46
2:E:54:ILE:C	2:E:56:LYS:N	2.71	0.46
2:E:120:LEU:HD12	2:E:121:PHE:N	2.30	0.46
1:A:121:MET:HA	1:A:125:GLU:OE1	2.16	0.46
1:L:366:SER:HB2	1:L:378:SER:HB3	1.98	0.46
2:E:21:ALA:HB2	2:E:186:THR:HG23	1.98	0.46
2:E:73:ARG:HB2	2:E:187:LEU:HD11	1.98	0.46
2:E:84:ALA:HB1	2:E:108:HIS:HB2	1.98	0.46
2:E:162:LYS:HE2	7:E:2625:HOH:O	2.16	0.46
6:E:2601:B12:H473	6:E:2601:B12:H491	1.98	0.46
1:A:137:ARG:NH1	1:A:524:ASP:HB3	2.30	0.46
1:A:263:THR:HB	1:A:277:MET:CE	2.42	0.46
1:A:522:ILE:HD12	1:A:522:ILE:N	2.07	0.46
2:B:67:LEU:N	2:B:67:LEU:HD12	2.31	0.46
1:L:106:THR:O	1:L:109:ILE:HG12	2.15	0.46
1:A:199:LEU:HD23	1:A:493:MET:HE1	1.98	0.45
2:B:95:ILE:C	7:B:1675:HOH:O	2.59	0.45
1:L:195:ARG:O	1:L:198:VAL:HG23	2.16	0.45
1:L:183:ASN:CG	7:L:2832:HOH:O	2.59	0.45
2:B:191:LEU:C	7:B:1694:HOH:O	2.60	0.45
3:G:7:ARG:CB	3:G:9:GLN:HE21	2.29	0.45
3:G:59:GLN:O	3:G:63:GLN:HG3	2.16	0.45
2:E:130:GLU:O	2:E:134:GLN:HG2	2.17	0.45
1:A:436:GLU:OE2	1:A:452:ARG:HG2	2.16	0.45
2:B:42:GLN:OE1	2:B:174:GLU:HB2	2.17	0.45
3:G:7:ARG:CD	3:G:8:VAL:N	2.79	0.45
2:E:67:LEU:HD11	2:E:144:ARG:HG3	1.98	0.45
1:A:440:ALA:HB2	1:A:449:MET:HE1	1.98	0.45
2:B:66:GLY:C	2:B:67:LEU:HD12	2.42	0.45
3:G:17:CYS:N	3:G:18:PRO:HD3	2.31	0.45
3:G:51:ARG:HG3	7:G:162:HOH:O	2.14	0.45
3:G:132:GLN:HB2	3:G:137:LEU:HD11	1.98	0.45
1:L:185:LEU:HD13	1:L:474:ILE:CD1	2.46	0.45
1:L:458:LEU:HA	1:L:461:VAL:HG12	1.99	0.45
2:E:62:VAL:HG21	2:E:69:ALA:HB2	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:485:ASP:OD1	1:A:486:ILE:HD12	2.17	0.45
7:A:1815:HOH:O	3:G:34:LEU:HD22	2.16	0.45
2:B:179:VAL:HB	2:B:182:ALA:HB2	1.99	0.45
1:L:141:ASN:HD22	1:L:142:GLN:N	2.13	0.45
1:L:422:ALA:HB1	1:L:481:SER:CB	2.46	0.45
3:M:6:MET:HG2	3:M:56:TYR:CD2	2.51	0.45
1:A:1:MET:HE2	1:A:3:ARG:CG	2.45	0.45
1:A:34:SER:HA	7:A:1868:HOH:O	2.17	0.45
1:A:371:TYR:CD1	1:A:371:TYR:C	2.94	0.45
2:B:16:ARG:HD3	2:B:190:ASP:OD1	2.17	0.45
1:L:24:TRP:HB3	1:L:29:LEU:HB2	1.98	0.45
2:E:79:ASP:O	2:E:83:MET:HG3	2.16	0.45
3:M:10:ASP:O	3:M:16:ARG:HB2	2.17	0.45
1:A:140:SER:O	1:A:360:PHE:HA	2.17	0.45
1:A:301:VAL:HG12	1:A:302:SER:N	2.31	0.45
2:B:56:LYS:NZ	7:B:1644:HOH:O	2.48	0.45
1:L:40:SER:HB2	1:L:81:MET:HE1	1.99	0.45
3:M:11:TYR:CG	3:M:12:PRO:HA	2.52	0.45
3:M:45:GLN:OE1	3:M:45:GLN:N	2.48	0.45
1:L:333:SER:HB2	1:L:353:GLN:HG2	1.98	0.45
1:L:432:ILE:HB	7:L:2757:HOH:O	2.16	0.45
1:L:462:GLU:HG2	1:L:466:LYS:HE2	1.98	0.45
1:A:201:GLN:OE1	1:A:222:GLU:HB3	2.17	0.44
1:L:422:ALA:HB1	1:L:481:SER:HB2	1.99	0.44
2:E:40:LYS:HE2	2:E:41:HIS:CE1	2.53	0.44
2:E:103:GLY:C	7:E:2624:HOH:O	2.60	0.44
1:A:7:PHE:HE1	1:L:409:THR:HG21	1.83	0.44
1:A:503:LEU:CD2	7:A:1826:HOH:O	2.64	0.44
3:G:55:GLU:CD	3:G:74:ARG:NH2	2.74	0.44
1:L:281:GLU:O	1:L:285:ILE:HG13	2.17	0.44
2:E:102:LYS:HE2	2:E:167:ALA:HB1	1.99	0.44
2:E:144:ARG:NH1	7:E:2641:HOH:O	2.50	0.44
1:A:127:MET:HG3	7:A:1813:HOH:O	2.18	0.44
1:A:468:ASN:HB3	7:A:1845:HOH:O	2.17	0.44
3:G:32:ILE:HD12	3:G:32:ILE:H	1.81	0.44
1:L:317:VAL:O	1:L:320:GLU:HG2	2.18	0.44
1:L:128:MET:O	1:L:131:GLN:HG2	2.16	0.44
1:L:232:VAL:HG23	1:L:271:TYR:HB2	1.99	0.44
2:E:139:ALA:O	2:E:142:TYR:N	2.50	0.44
1:A:299:GLY:O	1:A:300:ALA:HB3	2.18	0.44
3:G:41:GLU:HG2	7:G:212:HOH:O	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:11:PHE:CD2	2:E:193:ARG:HA	2.51	0.44
3:M:32:ILE:HD12	3:M:32:ILE:H	1.81	0.44
1:A:183:ASN:N	1:A:183:ASN:HD22	2.16	0.44
1:L:193:CYS:O	1:L:412:ILE:HD11	2.16	0.44
2:E:13:LEU:HD13	7:E:2623:HOH:O	2.18	0.44
2:E:64:GLU:CD	7:E:2645:HOH:O	2.61	0.44
1:A:45:ASP:HB2	7:A:1788:HOH:O	2.17	0.44
1:A:79:GLN:O	1:A:82:ARG:HB2	2.18	0.44
3:G:85:GLU:H	3:G:85:GLU:CD	2.25	0.44
2:E:19:GLY:O	2:E:20:VAL:C	2.60	0.44
1:A:106:THR:C	1:A:108:ALA:H	2.25	0.44
1:A:207:ALA:HB3	2:B:113:LEU:CD1	2.47	0.44
1:A:113:LYS:O	1:A:117:VAL:HG23	2.18	0.44
2:B:120:LEU:HD12	2:B:121:PHE:H	1.82	0.44
3:G:51:ARG:HG2	7:G:166:HOH:O	2.17	0.44
2:E:65:GLU:HG3	2:E:144:ARG:NH2	2.33	0.44
1:A:6:ARG:NH1	1:L:161:GLU:OE2	2.51	0.43
1:A:43:LYS:HB3	1:A:51:GLU:CB	2.48	0.43
1:A:127:MET:HE2	7:A:1813:HOH:O	2.17	0.43
1:A:307:THR:HA	7:A:1770:HOH:O	2.18	0.43
1:A:511:ARG:HH21	1:A:511:ARG:CB	2.29	0.43
2:E:46:LEU:HD21	2:E:167:ALA:HA	2.00	0.43
1:A:34:SER:HB2	1:A:276:SER:HB3	2.00	0.43
2:B:109:GLN:C	2:B:110:ARG:O	2.59	0.43
2:B:110:ARG:O	2:B:111:ASP:HB2	2.18	0.43
1:L:132:LYS:HE3	1:L:133:MET:HE1	2.00	0.43
1:A:471:GLY:O	1:A:475:VAL:HG23	2.18	0.43
1:A:551:PRO:O	1:A:554:ILE:HG22	2.19	0.43
2:B:73:ARG:HG3	2:B:73:ARG:HH11	1.82	0.43
3:G:55:GLU:CD	3:G:74:ARG:HH22	2.26	0.43
1:L:461:VAL:HG13	1:L:462:GLU:N	2.33	0.43
2:E:67:LEU:HD23	7:E:2617:HOH:O	2.18	0.43
2:E:70:ARG:HB3	7:E:2681:HOH:O	2.17	0.43
2:E:122:SER:HB2	6:E:2601:B12:O7R	2.19	0.43
1:A:537:GLU:HB2	7:A:1729:HOH:O	2.19	0.43
1:L:35:PRO:HD3	7:L:2853:HOH:O	2.18	0.43
1:L:306:MET:HE2	1:L:306:MET:CA	2.45	0.43
2:E:34:VAL:HB	2:E:38:PHE:HB3	1.99	0.43
1:A:137:ARG:NH1	1:A:531:GLY:HA2	2.33	0.43
1:L:73:ASN:HD21	1:L:75:GLU:HB2	1.83	0.43
1:L:222:GLU:HG3	1:L:258:ARG:CG	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:78:SER:HA	2:E:83:MET:CE	2.48	0.43
2:E:110:ARG:HD2	7:E:2644:HOH:O	2.18	0.43
3:M:17:CYS:HB3	3:M:20:HIS:CD2	2.49	0.43
2:B:143:ALA:C	2:B:145:LYS:H	2.26	0.43
3:G:83:PRO:HD3	3:G:115:TRP:CH2	2.54	0.43
1:L:1:MET:HA	1:L:3:ARG:HH11	1.84	0.43
1:L:137:ARG:NH1	1:L:524:ASP:CB	2.79	0.43
1:A:42:VAL:HG11	1:A:81:MET:HG3	2.00	0.43
1:A:56:ARG:N	1:A:59:GLN:HE21	2.13	0.43
1:A:94:ASP:OD2	1:L:96:HIS:NE2	2.43	0.43
1:L:43:LYS:HD2	1:L:43:LYS:HA	1.78	0.43
1:L:160:ALA:HB1	1:L:412:ILE:HG13	2.00	0.43
1:L:375:PHE:O	1:L:376:ALA:HB3	2.18	0.43
1:A:137:ARG:HD3	1:A:522:ILE:O	2.19	0.43
1:A:458:LEU:O	1:A:461:VAL:CG1	2.65	0.43
2:B:71:VAL:HG12	2:B:187:LEU:HD12	2.01	0.43
1:L:294:GLN:NE2	1:L:506:SER:H	2.17	0.43
1:L:410:ILE:HD13	1:L:442:TYR:HE1	1.84	0.43
1:A:173:THR:HB	1:A:375:PHE:CZ	2.53	0.43
2:E:80:VAL:HG12	7:E:2634:HOH:O	2.17	0.43
2:E:139:ALA:O	2:E:142:TYR:HB2	2.17	0.43
1:A:204:VAL:HB	7:A:1767:HOH:O	2.18	0.43
2:B:63:GLU:HA	2:B:67:LEU:O	2.19	0.43
2:B:95:ILE:N	7:B:1675:HOH:O	2.51	0.43
1:A:56:ARG:CG	1:A:59:GLN:HE21	2.32	0.42
1:L:349:ARG:C	1:L:349:ARG:HD3	2.44	0.42
1:L:511:ARG:HB3	1:L:512:GLN:NE2	2.34	0.42
1:A:132:LYS:C	1:A:133:MET:HE2	2.44	0.42
1:A:141:ASN:ND2	1:A:399:GLY:O	2.51	0.42
1:A:181:PRO:HD2	1:A:461:VAL:HG21	1.99	0.42
7:A:1816:HOH:O	1:L:128:MET:SD	2.62	0.42
2:B:12:THR:C	7:B:1644:HOH:O	2.63	0.42
2:B:26:ARG:NH1	2:B:28:ASP:OD1	2.52	0.42
1:L:424:PHE:HA	1:L:429:LEU:HD12	2.01	0.42
1:L:497:ARG:HD3	7:L:2852:HOH:O	2.18	0.42
3:M:7:ARG:HD2	3:M:8:VAL:H	1.84	0.42
1:A:187:LEU:HD11	7:A:1825:HOH:O	2.19	0.42
1:A:338:THR:HG23	1:A:377:GLY:C	2.44	0.42
2:B:141:ARG:HB2	2:B:148:PRO:HG3	2.01	0.42
1:L:432:ILE:HA	1:L:436:GLU:OE2	2.20	0.42
2:E:64:GLU:HB2	7:E:2645:HOH:O	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:76:ARG:NH2	1:A:104:ALA:HB1	2.34	0.42
1:A:98:SER:HA	1:A:526:GLN:HE22	1.84	0.42
1:A:430:PRO:HD3	1:A:460:ALA:HB1	2.02	0.42
2:B:46:LEU:HD21	2:B:167:ALA:HA	2.01	0.42
2:E:110:ARG:O	2:E:111:ASP:CB	2.68	0.42
1:A:115:VAL:HG12	1:A:278:LEU:HG	2.02	0.42
1:L:454:VAL:O	1:L:457:ASP:HB2	2.20	0.42
1:A:2:LYS:HD3	7:L:2786:HOH:O	2.20	0.42
1:A:90:ARG:HD2	7:A:1663:HOH:O	2.20	0.42
1:A:133:MET:O	1:A:134:ARG:C	2.62	0.42
1:A:299:GLY:C	1:A:301:VAL:H	2.27	0.42
1:A:409:THR:O	1:A:413:ARG:HG3	2.19	0.42
6:B:1601:B12:H491	6:B:1601:B12:H473	2.02	0.42
1:L:301:VAL:HG12	1:L:302:SER:H	1.84	0.42
1:L:334:ALA:C	1:L:336:ASP:N	2.75	0.42
2:E:15:THR:HB	2:E:39:ASP:OD2	2.19	0.42
2:E:95:ILE:N	2:E:95:ILE:HD12	2.34	0.42
3:G:16:ARG:C	3:G:18:PRO:HD3	2.44	0.42
1:L:63:ILE:HG23	1:L:287:ILE:HD11	2.02	0.42
1:L:341:HIS:NE2	2:E:162:LYS:HG3	2.34	0.42
1:L:416:ALA:O	1:L:420:ILE:HG22	2.19	0.42
2:E:123:GLN:HA	7:E:2662:HOH:O	2.19	0.42
3:M:78:GLU:HB2	3:M:120:ASN:HD22	1.85	0.42
1:A:366:SER:HB2	1:A:378:SER:HB3	2.01	0.42
1:A:429:LEU:O	1:A:430:PRO:C	2.62	0.42
7:A:1815:HOH:O	3:G:34:LEU:HB3	2.20	0.42
2:E:140:ALA:HB1	7:E:2675:HOH:O	2.19	0.42
1:A:42:VAL:HA	1:A:51:GLU:O	2.20	0.41
1:A:248:SER:HB2	3:G:75:ARG:HH22	1.84	0.41
3:G:11:TYR:HB2	3:G:60:ILE:CD1	2.47	0.41
2:E:21:ALA:CB	2:E:186:THR:HG23	2.50	0.41
1:A:330:GLU:OE2	1:A:506:SER:HA	2.20	0.41
1:L:13:ARG:HH11	1:L:13:ARG:CB	2.26	0.41
1:A:167:PHE:CE1	1:A:365:TYR:HB3	2.55	0.41
7:A:1863:HOH:O	3:G:96:PRO:HD3	2.20	0.41
1:L:155:ILE:CD1	1:L:183:ASN:OD1	2.68	0.41
1:A:403:PRO:HG2	7:A:1605:HOH:O	2.20	0.41
1:A:529:GLY:N	7:A:1781:HOH:O	2.41	0.41
2:B:121:PHE:HB3	2:B:127:LEU:HD21	2.02	0.41
1:L:224:VAL:HG13	1:L:246:LEU:HD23	2.02	0.41
1:L:405:THR:OG1	1:L:408:GLU:HG2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:M:139:LYS:HG2	7:M:166:HOH:O	2.19	0.41
1:L:61:ASP:HB2	1:L:230:GLU:CD	2.45	0.41
3:M:108:ALA:HB1	3:M:125:ARG:HD3	2.02	0.41
1:L:143:CYS:SG	1:L:170:GLN:HG2	2.60	0.41
2:B:110:ARG:O	2:B:111:ASP:CB	2.68	0.41
1:L:137:ARG:HD3	1:L:522:ILE:O	2.20	0.41
1:L:336:ASP:C	1:L:337:GLN:HG2	2.46	0.41
2:E:173:LYS:HZ3	2:E:177:HIS:HE1	1.67	0.41
2:B:65:GLU:CB	2:B:144:ARG:HH12	2.33	0.41
1:L:132:LYS:HE3	1:L:133:MET:HE3	2.03	0.41
1:L:544:ASN:HB3	7:L:2775:HOH:O	2.20	0.41
2:E:23:ALA:HA	2:E:90:LEU:HD23	2.03	0.41
1:A:171:GLU:N	7:A:1825:HOH:O	2.54	0.41
1:A:195:ARG:HD2	1:A:195:ARG:C	2.46	0.41
1:A:213:GLY:HA3	1:A:255:LEU:HD21	2.03	0.41
1:A:254:GLY:HA2	7:A:1826:HOH:O	2.19	0.41
1:A:368:VAL:HB	1:A:369:PRO:HD2	2.03	0.41
2:B:95:ILE:CD1	2:B:142:TYR:HB3	2.51	0.41
1:L:174:VAL:HG12	1:L:183:ASN:ND2	2.35	0.41
2:E:110:ARG:HD3	7:E:2674:HOH:O	2.20	0.41
3:M:12:PRO:O	3:M:15:THR:HG22	2.21	0.41
3:M:17:CYS:N	3:M:18:PRO:HD3	2.36	0.41
3:M:112:GLU:O	3:M:116:HIS:HA	2.20	0.41
3:G:78:GLU:HB2	3:G:120:ASN:ND2	2.36	0.41
1:L:302:SER:HB3	6:E:2601:B12:H532	2.03	0.41
2:E:46:LEU:HB2	2:E:125:PRO:HG3	2.03	0.41
2:E:194:GLU:HG3	7:E:2691:HOH:O	2.21	0.41
3:M:13:LEU:HD21	7:M:217:HOH:O	2.20	0.41
1:A:515:VAL:HG12	3:G:12:PRO:HB3	2.02	0.40
2:B:179:VAL:CG1	2:B:182:ALA:HB2	2.51	0.40
3:G:92:ASN:O	3:G:98:ARG:HG2	2.21	0.40
3:M:32:ILE:N	3:M:32:ILE:CD1	2.81	0.40
2:B:34:VAL:HB	2:B:38:PHE:CG	2.56	0.40
2:B:162:LYS:HD3	7:B:1655:HOH:O	2.20	0.40
2:E:36:PRO:HD3	2:E:83:MET:CE	2.48	0.40
2:E:73:ARG:HG3	2:E:73:ARG:NH1	2.34	0.40
1:A:334:ALA:C	1:A:336:ASP:N	2.79	0.40
1:A:435:GLU:CD	1:A:435:GLU:H	2.29	0.40
2:E:139:ALA:N	7:E:2647:HOH:O	2.29	0.40
1:A:132:LYS:HG2	1:A:133:MET:CE	2.51	0.40
1:A:143:CYS:HA	1:A:365:TYR:O	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:180:GLN:O	2:E:181:ASP:HB2	2.20	0.40
1:A:221:ALA:O	1:A:257:MET:HA	2.21	0.40
1:A:250:TYR:CB	1:A:257:MET:HG2	2.52	0.40
1:A:304:ILE:HG23	1:A:339:PHE:HB3	2.03	0.40
2:B:12:THR:OG1	2:B:194:GLU:HG2	2.20	0.40
1:L:327:LEU:HD13	1:L:327:LEU:HA	1.93	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	553/555 (100%)	527 (95%)	23 (4%)	3 (0%)	24	22
1	L	553/555 (100%)	520 (94%)	30 (5%)	3 (0%)	24	22
2	B	182/194 (94%)	171 (94%)	10 (6%)	1 (0%)	24	22
2	E	182/194 (94%)	153 (84%)	27 (15%)	2 (1%)	11	8
3	G	136/141 (96%)	133 (98%)	3 (2%)	0	100	100
3	M	136/141 (96%)	133 (98%)	3 (2%)	0	100	100
All	All	1742/1780 (98%)	1637 (94%)	96 (6%)	9 (0%)	24	22

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	E	24	ASP
1	A	2	LYS
2	B	24	ASP
1	A	364	GLY
1	L	544	ASN
1	A	301	VAL

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Mol	Chain	Res	Type
1	L	301	VAL
1	L	364	GLY
2	E	26	ARG

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	453/453 (100%)	443 (98%)	10 (2%)	45	53
1	L	223/453 (49%)	217 (97%)	6 (3%)	39	45
2	B	153/163 (94%)	146 (95%)	7 (5%)	24	25
2	E	149/163 (91%)	142 (95%)	7 (5%)	23	24
3	G	117/120 (98%)	110 (94%)	7 (6%)	17	15
3	M	117/120 (98%)	108 (92%)	9 (8%)	12	9
All	All	1212/1472 (82%)	1166 (96%)	46 (4%)	29	32

All (46) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	LEU
1	A	82	ARG
1	A	141	ASN
1	A	179	TYR
1	A	183	ASN
1	A	243	LYS
1	A	458	LEU
1	A	502	TYR
1	A	514	GLU
1	A	522	ILE
2	B	13	LEU
2	B	14	LYS
2	B	65	GLU
2	B	102	LYS
2	B	106	VAL

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Mol	Chain	Res	Type
2	B	108	HIS
2	B	174	GLU
3	G	5	THR
3	G	19	GLU
3	G	29	LEU
3	G	64	MET
3	G	94	LEU
3	G	105	LEU
3	G	125	ARG
1	L	6	ARG
1	L	13	ARG
1	L	51	GLU
1	L	73	ASN
1	L	179	TYR
1	L	255	LEU
2	E	15	THR
2	E	16	ARG
2	E	47	ILE
2	E	65	GLU
2	E	102	LYS
2	E	106	VAL
2	E	174	GLU
3	M	19	GLU
3	M	29	LEU
3	M	31	ASP
3	M	32	ILE
3	M	64	MET
3	M	85	GLU
3	M	94	LEU
3	M	105	LEU
3	M	125	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (44) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	17	GLN
1	A	59	GLN
1	A	79	GLN
1	A	96	HIS
1	A	120	GLN
1	A	170	GLN
1	A	183	ASN

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Mol	Chain	Res	Type
1	A	447	ASN
1	A	468	ASN
1	A	496	GLN
1	A	504	GLN
1	A	526	GLN
2	B	41	HIS
2	B	89	ASN
2	B	134	GLN
2	B	157	GLN
2	B	171	HIS
2	B	188	HIS
3	G	9	GLN
3	G	52	GLN
3	G	63	GLN
3	G	65	GLN
3	G	101	GLN
3	G	133	GLN
1	L	17	GLN
1	L	46	ASN
1	L	73	ASN
1	L	120	GLN
1	L	141	ASN
1	L	170	GLN
2	E	41	HIS
2	E	43	HIS
2	E	44	HIS
2	E	89	ASN
2	E	134	GLN
2	E	138	ASN
2	E	157	GLN
2	E	177	HIS
3	M	20	HIS
3	M	63	GLN
3	M	65	GLN
3	M	67	HIS
3	M	101	GLN
3	M	133	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 6 ligands modelled in this entry, 2 are monoatomic - leaving 4 for Mogul analysis.

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	$\# Z > 2$
5	PGO	L	2602	4	4,4,4	0.61	0	4,4,4	0.80	0
6	B12	B	1601	-	94,101,101	1.52	17 (18%)	149,166,166	1.82	35 (23%)
6	B12	E	2601	-	94,101,101	1.60	18 (19%)	149,166,166	1.84	34 (22%)
5	PGO	A	1602	4	4,4,4	0.60	0	4,4,4	0.85	0

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
5	PGO	L	2602	4	1/1/1/1	0/2/2/2	-
6	B12	B	1601	-	-	9/56/223/223	0/3/11/11
6	B12	E	2601	-	-	10/56/223/223	0/3/11/11
5	PGO	A	1602	4	1/1/1/1	0/2/2/2	-

All (35) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	E	2601	B12	C14-N23	5.42	1.42	1.35
6	B	1601	B12	C14-N23	5.40	1.42	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	E	2601	B12	O58-C57	4.21	1.31	1.23
6	B	1601	B12	O58-C57	4.16	1.31	1.23
6	E	2601	B12	C19-N24	3.33	1.53	1.49
6	E	2601	B12	C41-C8	3.26	1.61	1.54
6	B	1601	B12	C41-C8	3.19	1.61	1.54
6	E	2601	B12	C9-N22	3.11	1.38	1.30
6	B	1601	B12	C46-C12	3.06	1.60	1.54
6	B	1601	B12	C19-N24	3.06	1.53	1.49
6	E	2601	B12	C4B-C9B	2.97	1.44	1.40
6	B	1601	B12	C12-C11	2.92	1.57	1.52
6	E	2601	B12	C12-C11	2.86	1.57	1.52
6	E	2601	B12	C46-C12	2.82	1.59	1.54
6	B	1601	B12	C4B-C9B	2.77	1.44	1.40
6	B	1601	B12	C9-N22	2.69	1.37	1.30
6	B	1601	B12	C17-C18	2.64	1.59	1.54
6	E	2601	B12	C48-C49	2.61	1.60	1.52
6	B	1601	B12	C48-C49	2.51	1.60	1.52
6	B	1601	B12	C6B-C5B	2.41	1.46	1.40
6	E	2601	B12	C6B-C5B	2.39	1.46	1.40
6	E	2601	B12	C7B-C6B	2.38	1.42	1.39
6	B	1601	B12	C54-C17	2.35	1.58	1.54
6	E	2601	B12	C53-C15	2.33	1.55	1.50
6	E	2601	B12	C17-C18	2.30	1.59	1.54
6	E	2601	B12	P-O5	-2.27	1.44	1.55
6	E	2601	B12	C11-N23	2.26	1.41	1.36
6	E	2601	B12	C30-C3	2.16	1.59	1.54
6	B	1601	B12	C7B-C6B	2.16	1.42	1.39
6	E	2601	B12	C54-C17	2.15	1.58	1.54
6	B	1601	B12	C8B-N1B	-2.15	1.35	1.39
6	B	1601	B12	C30-C3	2.13	1.59	1.54
6	B	1601	B12	C11-N23	2.11	1.40	1.36
6	B	1601	B12	P-O5	-2.09	1.45	1.55
6	E	2601	B12	C8B-N1B	-2.03	1.35	1.39

All (69) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	E	2601	B12	O58-C57-C56	-6.34	110.53	122.02
6	B	1601	B12	O58-C57-C56	-6.19	110.80	122.02
6	B	1601	B12	C7B-C8B-C9B	-5.04	116.43	122.47
6	E	2601	B12	C7B-C8B-C9B	-5.03	116.44	122.47
6	E	2601	B12	C8B-N1B-C2B	4.76	110.58	106.26

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	1601	B12	C8B-N1B-C2B	4.72	110.55	106.26
6	E	2601	B12	C1R-N1B-C2B	-4.42	117.28	127.09
6	B	1601	B12	C1R-N1B-C2B	-4.37	117.41	127.09
6	B	1601	B12	C4B-C9B-C8B	4.33	124.14	120.16
6	B	1601	B12	C47-C12-C46	-4.31	102.26	109.41
6	E	2601	B12	C4B-C9B-C8B	4.20	124.02	120.16
6	E	2601	B12	C47-C12-C46	-4.15	102.52	109.41
6	B	1601	B12	O5-P-O2	4.12	123.47	106.70
6	E	2601	B12	C26-C2-C1	4.04	116.25	110.00
6	E	2601	B12	O5-P-O2	4.00	122.98	106.70
6	E	2601	B12	C8B-N1B-C1R	3.98	132.14	125.41
6	B	1601	B12	C26-C2-C1	3.98	116.15	110.00
6	B	1601	B12	C8B-N1B-C1R	3.93	132.05	125.41
6	E	2601	B12	C9-N22-C6	3.78	109.83	105.28
6	B	1601	B12	C9-N22-C6	3.60	109.61	105.28
6	B	1601	B12	C7B-C8B-N1B	3.44	138.19	131.39
6	E	2601	B12	C7B-C8B-N1B	3.42	138.15	131.39
6	B	1601	B12	C3P-C2P-C1P	3.25	117.70	111.42
6	E	2601	B12	C3P-C2P-C1P	3.25	117.70	111.42
6	E	2601	B12	C56-C57-N59	3.21	122.19	116.34
6	B	1601	B12	N1B-C2B-N3B	-3.18	109.42	113.94
6	E	2601	B12	C2-C26-C27	3.18	124.03	115.19
6	E	2601	B12	O2-P-O3	-3.17	94.02	102.87
6	E	2601	B12	N1B-C2B-N3B	-3.00	109.68	113.94
6	B	1601	B12	O2-P-O3	-2.95	94.62	102.87
6	B	1601	B12	C8B-C9B-N3B	-2.74	107.03	110.00
6	E	2601	B12	C8B-C9B-N3B	-2.74	107.04	110.00
6	B	1601	B12	C25-C2-C1	-2.73	109.68	113.75
6	B	1601	B12	C20-C1-C19	-2.71	106.74	109.35
6	B	1601	B12	O58-C57-N59	2.65	128.23	123.03
6	B	1601	B12	C9B-N3B-C2B	2.63	107.63	104.40
6	E	2601	B12	C49-C48-C13	2.60	122.02	114.65
6	B	1601	B12	C2-C26-C27	2.55	122.29	115.19
6	B	1601	B12	C56-C57-N59	2.54	120.97	116.34
6	E	2601	B12	C25-C2-C1	-2.53	109.97	113.75
6	B	1601	B12	C15-C16-N24	-2.46	118.91	122.42
6	B	1601	B12	O44-C43-C42	-2.41	113.76	121.04
6	E	2601	B12	C36-C7-C37	2.38	114.78	110.74
6	E	2601	B12	C9B-N3B-C2B	2.35	107.29	104.40
6	E	2601	B12	C8-C9-C10	-2.33	118.36	123.33
6	E	2601	B12	O44-C43-C42	-2.32	114.04	121.04
6	E	2601	B12	C20-C1-C19	-2.32	107.12	109.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	E	2601	B12	C15-C16-N24	-2.29	119.17	122.42
6	B	1601	B12	C2-C1-C19	2.28	122.16	118.61
6	E	2601	B12	C2P-C1P-N59	2.27	116.27	112.92
6	B	1601	B12	C8-C9-C10	-2.26	118.52	123.33
6	B	1601	B12	C17-C18-C19	-2.25	98.96	102.36
6	E	2601	B12	C47-C12-C13	2.24	121.81	112.74
6	E	2601	B12	C20-C1-N21	-2.24	106.56	110.26
6	B	1601	B12	C37-C7-C8	-2.23	102.49	108.37
6	B	1601	B12	C36-C7-C37	2.22	114.50	110.74
6	E	2601	B12	C37-C7-C8	-2.18	102.61	108.37
6	B	1601	B12	C13-C12-C11	-2.18	98.54	100.97
6	B	1601	B12	C47-C12-C13	2.17	121.55	112.74
6	E	2601	B12	O58-C57-N59	2.17	127.28	123.03
6	E	2601	B12	C17-C18-C19	-2.17	99.08	102.36
6	B	1601	B12	C54-C17-C55	-2.15	105.69	109.27
6	B	1601	B12	C48-C49-C50	2.12	119.76	112.55
6	B	1601	B12	C47-C12-C11	2.12	117.64	110.08
6	E	2601	B12	C42-C41-C8	2.10	120.61	114.65
6	E	2601	B12	C47-C12-C11	2.09	117.54	110.08
6	B	1601	B12	C55-C17-C16	2.07	120.64	116.59
6	E	2601	B12	C53-C15-C14	-2.04	114.37	118.42
6	B	1601	B12	C31-C32-N33	2.01	122.93	116.49

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
5	A	1602	PGO	C2
5	L	2602	PGO	C2

All (19) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	E	2601	B12	C12-C13-C48-C49
6	B	1601	B12	C12-C13-C48-C49
6	B	1601	B12	C1-C2-C26-C27
6	E	2601	B12	C30-C31-C32-O34
6	B	1601	B12	C30-C31-C32-O34
6	B	1601	B12	C30-C31-C32-N33
6	B	1601	B12	C25-C2-C26-C27
6	E	2601	B12	C1-C2-C26-C27
6	E	2601	B12	C25-C2-C26-C27
6	E	2601	B12	C8-C41-C42-C43

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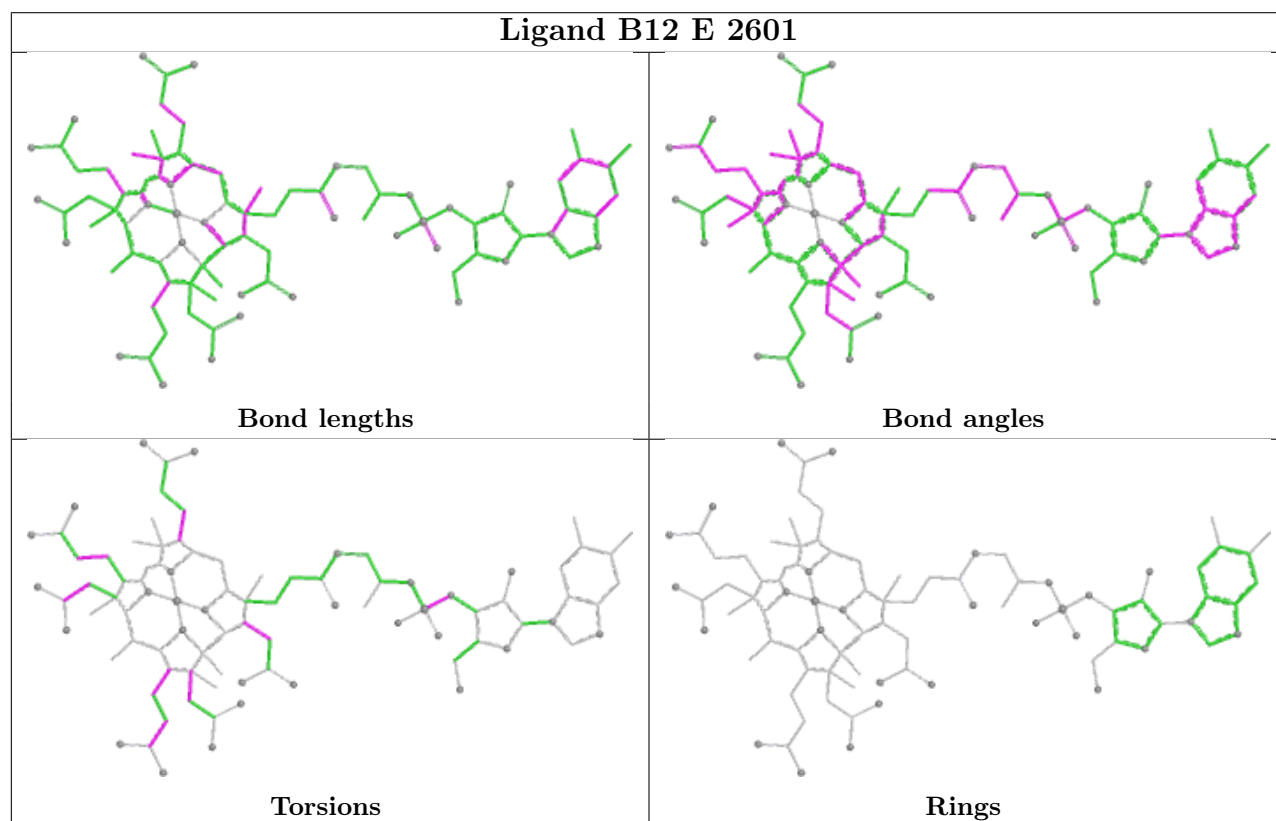
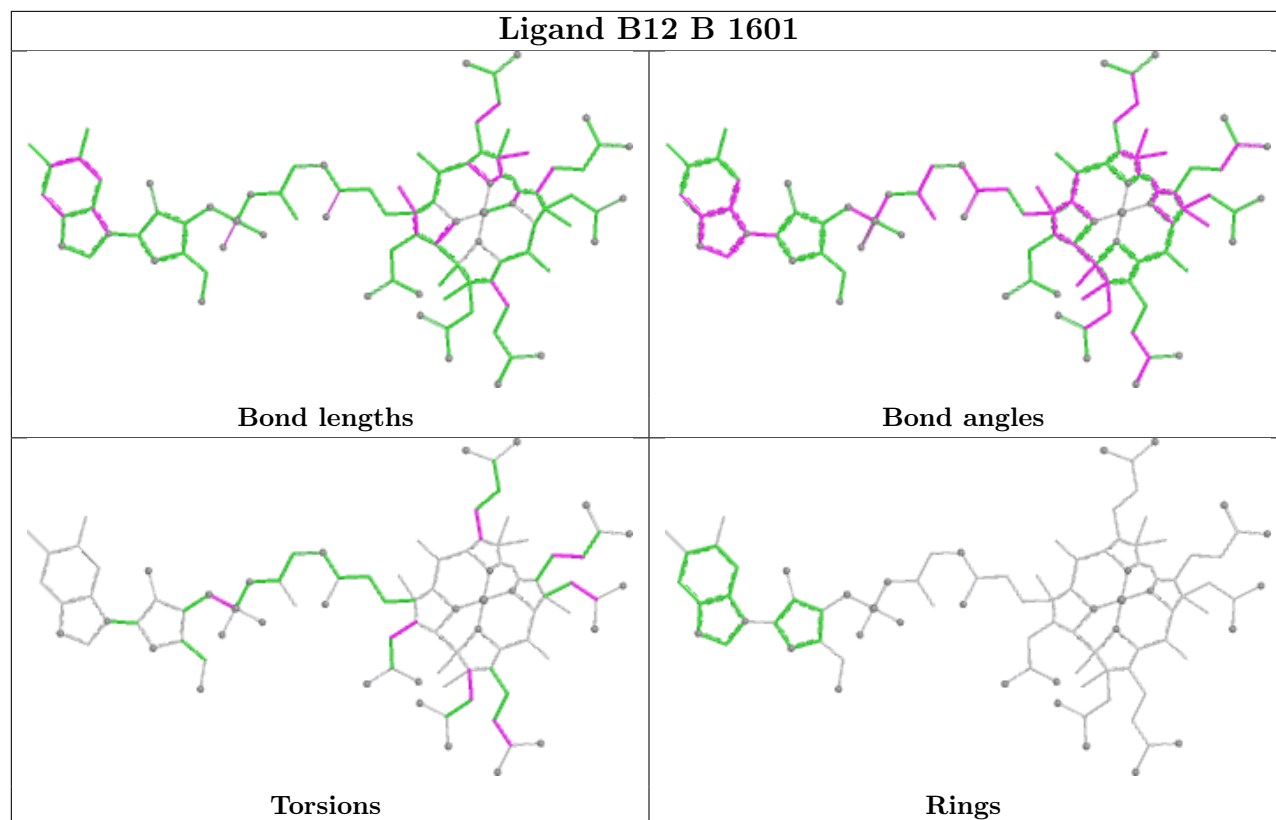
Mol	Chain	Res	Type	Atoms
6	E	2601	B12	C30-C31-C32-N33
6	B	1601	B12	C8-C41-C42-C43
6	B	1601	B12	C19-C18-C60-C61
6	E	2601	B12	C4-C3-C30-C31
6	B	1601	B12	C7-C37-C38-N40
6	E	2601	B12	C7-C37-C38-N40
6	B	1601	B12	C3R-O2-P-O4
6	E	2601	B12	C3R-O2-P-O4
6	E	2601	B12	C19-C18-C60-C61

There are no ring outliers.

3 monomers are involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	B	1601	B12	5	0
6	E	2601	B12	8	0
5	A	1602	PGO	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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.