



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 03:41 PM UTC

PDB ID : 1C4Z / pdb_00001c4z
Title : STRUCTURE OF AN E6AP-UBCH7 COMPLEX: INSIGHTS INTO THE UBIQUITINATION PATHWAY
Authors : Huang, L.; Kinnucan, E.; Wang, G.; Beaudenon, S.; Howley, P.M.; Huibregtse, J.M.; Pavletich, N.P.
Deposited on : 1999-10-14
Resolution : 2.60 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
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

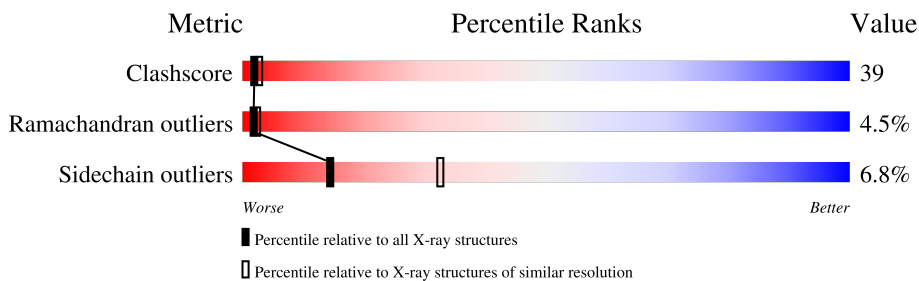
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)

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	358	
1	B	358	
1	C	358	
2	D	154	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 10040 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 UBIQUITIN-PROTEIN LIGASE E3A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	350	Total	C	N	O	S	0	0	0
			2861	1839	467	541	14			
1	B	350	Total	C	N	O	S	0	0	0
			2861	1839	467	541	14			
1	C	350	Total	C	N	O	S	0	0	0
			2861	1839	467	541	14			

- Molecule 2 is a protein called UBIQUITIN CONJUGATING ENZYME E2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	144	Total	C	N	O	S	0	0	0
			1098	715	189	190	4			

- Molecule 3 is water.

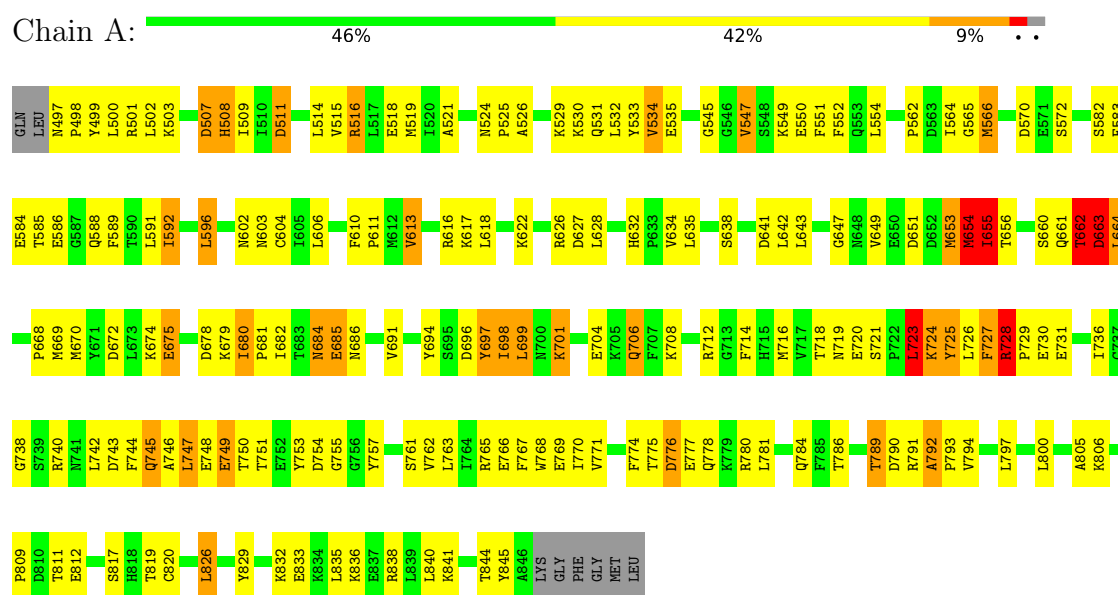
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	117	Total	O	0	0
			117	117		
3	B	99	Total	O	0	0
			99	99		
3	C	113	Total	O	0	0
			113	113		
3	D	30	Total	O	0	0
			30	30		

3 Residue-property plots

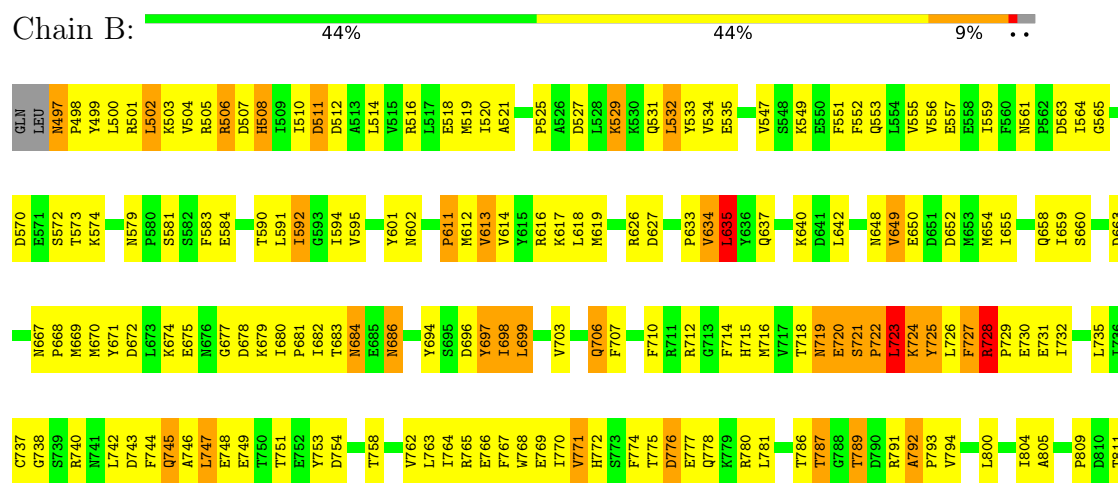
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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: UBIQUITIN-PROTEIN LIGASE E3A



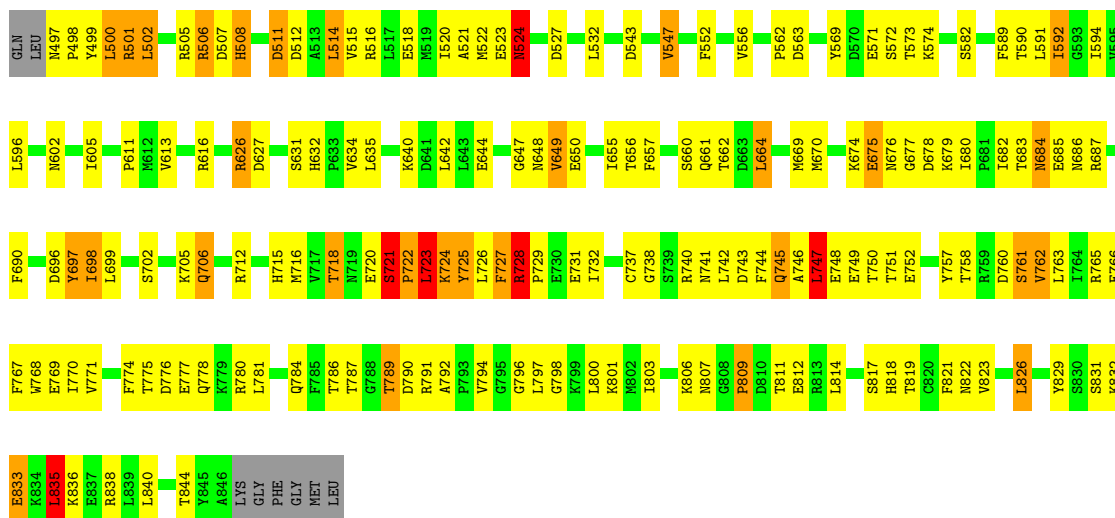
• Molecule 1: UBIQUITIN-PROTEIN LIGASE E3A





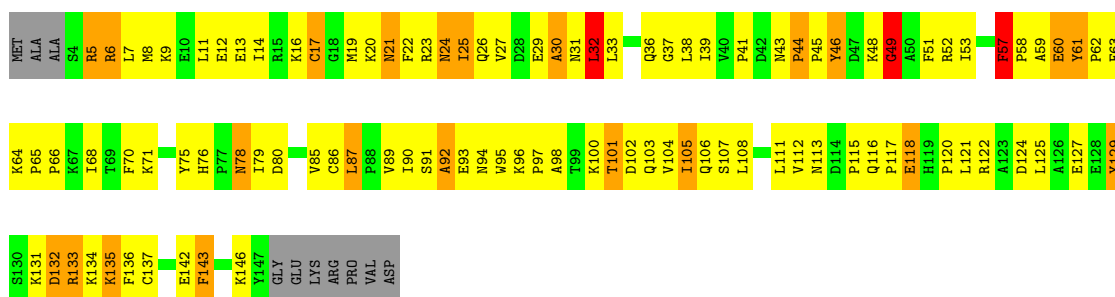
• Molecule 1: UBIQUITIN-PROTEIN LIGASE E3A

Chain C: 49% 39% 8% ..



• Molecule 2: UBIQUITIN CONJUGATING ENZYME E2

Chain D: 27% 51% 14% • 6%



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	103.40Å 112.70Å 123.80Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 2.60	Depositor
% Data completeness (in resolution range)	90.0 (15.00-2.60)	Depositor
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.237 , 0.290	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	10040	wwPDB-VP
Average B, all atoms (Å ²)	65.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

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	0.62	1/2923 (0.0%)	1.21	34/3943 (0.9%)
1	B	0.62	0/2923	1.20	31/3943 (0.8%)
1	C	0.65	1/2923 (0.0%)	1.24	28/3943 (0.7%)
2	D	0.53	0/1127	1.22	12/1536 (0.8%)
All	All	0.62	2/9896 (0.0%)	1.22	105/13365 (0.8%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	626	ARG	CD-NE	-6.76	1.36	1.46
1	A	653	MET	SD-CE	-5.22	1.66	1.79

All (105) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	745	GLN	N-CA-C	-17.71	87.16	110.53
1	B	745	GLN	N-CA-C	-16.99	88.10	110.53
1	A	745	GLN	N-CA-C	-15.33	88.88	110.50
1	C	723	LEU	N-CA-C	-10.58	100.38	113.18
1	B	747	LEU	N-CA-C	-9.84	100.40	111.82
1	A	663	ASP	N-CA-C	9.73	124.32	108.55
1	B	724	LYS	N-CA-C	-9.61	97.84	110.53
1	A	697	TYR	N-CA-C	-9.10	97.97	110.35
1	C	724	LYS	N-CA-C	-9.09	98.53	110.53
1	A	724	LYS	N-CA-C	-8.82	98.88	110.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	728	ARG	CA-C-N	8.55	128.25	119.19
1	C	728	ARG	C-N-CA	8.55	128.25	119.19
1	B	697	TYR	N-CA-C	-8.52	97.18	109.96
1	C	697	TYR	N-CA-C	-8.26	98.85	110.50
1	B	723	LEU	N-CA-C	-8.25	102.66	112.89
1	C	747	LEU	N-CA-C	-8.15	102.48	111.36
1	B	506	ARG	N-CA-C	-8.11	99.70	110.24
1	A	723	LEU	N-CA-C	-8.09	102.67	112.54
1	B	579	ASN	CA-C-N	8.09	128.18	119.28
1	B	579	ASN	C-N-CA	8.09	128.18	119.28
1	C	718	THR	N-CA-C	7.88	121.99	112.38
1	A	728	ARG	CA-C-N	7.80	127.86	119.28
1	A	728	ARG	C-N-CA	7.80	127.86	119.28
1	A	747	LEU	N-CA-C	-7.65	102.94	111.82
2	D	57	PHE	CA-C-N	7.35	127.35	119.78
2	D	57	PHE	C-N-CA	7.35	127.35	119.78
1	A	749	GLU	N-CA-C	-7.31	101.12	110.19
1	C	722	PRO	N-CA-C	7.23	121.67	111.33
1	A	663	ASP	O-C-N	7.20	131.68	123.48
1	A	663	ASP	CA-C-N	7.16	135.21	121.54
1	A	663	ASP	C-N-CA	7.16	135.21	121.54
2	D	143	PHE	N-CA-C	-7.12	104.74	113.50
1	B	500	LEU	N-CA-C	-7.08	103.64	111.36
2	D	61	TYR	N-CA-C	-7.05	100.35	110.08
1	A	721	SER	CA-C-N	6.96	128.53	119.84
1	A	721	SER	C-N-CA	6.96	128.53	119.84
1	C	792	ALA	CA-C-N	6.89	127.06	120.31
1	C	792	ALA	C-N-CA	6.89	127.06	120.31
1	A	655	ILE	N-CA-C	-6.82	99.27	108.96
1	C	831	SER	N-CA-C	6.80	118.73	108.46
1	B	721	SER	CA-C-N	6.74	128.27	119.84
1	B	721	SER	C-N-CA	6.74	128.27	119.84
1	A	610	PHE	CA-C-N	-6.73	113.72	120.31
1	A	610	PHE	C-N-CA	-6.73	113.72	120.31
1	C	721	SER	CA-C-N	6.66	127.57	120.11
1	C	721	SER	C-N-CA	6.66	127.57	120.11
1	C	547	VAL	N-CA-C	-6.54	103.95	110.62
1	C	680	ILE	CA-C-N	6.54	126.51	120.03
1	C	680	ILE	C-N-CA	6.54	126.51	120.03
1	B	728	ARG	N-CA-C	6.49	119.05	110.36
1	C	506	ARG	N-CA-C	-6.41	101.20	110.24
1	B	749	GLU	N-CA-C	-6.24	102.73	110.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	680	ILE	CA-C-N	6.23	126.72	119.99
1	A	680	ILE	C-N-CA	6.23	126.72	119.99
1	C	592	ILE	CB-CA-C	-6.22	103.75	112.14
2	D	24	ASN	N-CA-C	6.19	116.41	108.24
1	B	497	ASN	CA-C-N	6.16	126.17	119.89
1	B	497	ASN	C-N-CA	6.16	126.17	119.89
1	B	611	PRO	N-CA-C	-6.15	101.41	111.68
2	D	93	GLU	N-CA-C	-6.06	105.19	112.58
1	B	498	PRO	N-CA-C	5.95	120.57	111.11
1	A	611	PRO	N-CA-C	-5.92	102.58	111.57
2	D	49	GLY	N-CA-C	-5.86	99.29	113.18
1	C	835	LEU	N-CA-C	-5.86	104.58	110.97
1	B	728	ARG	CA-C-N	5.83	125.51	119.56
1	B	728	ARG	C-N-CA	5.83	125.51	119.56
1	A	547	VAL	N-CA-C	-5.81	104.84	110.42
1	A	800	LEU	N-CA-C	5.80	118.54	111.82
1	B	792	ALA	CA-C-N	5.75	125.73	120.21
1	B	792	ALA	C-N-CA	5.75	125.73	120.21
1	A	817	SER	N-CA-C	5.72	117.55	108.79
1	B	703	VAL	N-CA-C	-5.65	107.23	112.43
1	B	771	VAL	N-CA-C	5.63	116.36	110.62
1	C	524	ASN	N-CA-C	5.60	122.18	109.81
1	C	725	TYR	N-CA-C	-5.58	102.14	113.29
1	B	565	GLY	N-CA-C	5.57	122.51	114.10
1	A	662	THR	CB-CA-C	-5.56	100.09	109.83
2	D	87	LEU	CA-C-N	5.56	125.03	119.24
2	D	87	LEU	C-N-CA	5.56	125.03	119.24
1	B	532	LEU	N-CA-C	5.53	117.11	109.15
2	D	46	TYR	N-CA-C	-5.52	102.15	110.70
1	C	721	SER	N-CA-C	-5.46	97.74	109.81
1	B	640	LYS	N-CA-C	-5.45	105.25	111.14
2	D	105	ILE	N-CA-C	-5.41	98.08	109.34
1	C	817	SER	N-CA-C	5.38	116.45	108.60
1	B	725	TYR	N-CA-C	-5.35	102.39	113.31
1	A	534	VAL	N-CA-C	5.34	116.67	108.71
1	A	792	ALA	CA-C-N	5.32	125.32	120.21
1	A	792	ALA	C-N-CA	5.32	125.32	120.21
1	A	511	ASP	N-CA-C	5.30	116.75	110.97
1	C	572	SER	N-CA-C	5.22	117.05	111.36
1	C	611	PRO	N-CA-C	-5.21	103.59	111.41
1	A	728	ARG	N-CA-C	5.18	117.30	110.36
1	B	731	GLU	N-CA-C	-5.18	106.12	112.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	32	LEU	N-CA-C	5.17	121.82	110.80
1	B	696	ASP	N-CA-C	-5.16	105.55	111.07
1	B	635	LEU	N-CA-C	-5.11	105.80	111.36
1	A	507	ASP	N-CA-C	-5.10	104.94	110.91
1	C	762	VAL	N-CA-C	5.08	116.41	110.62
1	A	669	MET	N-CA-C	-5.07	101.61	109.72
1	A	701	LYS	N-CA-C	5.06	116.49	111.07
1	A	566	MET	N-CA-C	-5.06	107.28	113.50
1	B	787	THR	N-CA-C	-5.05	103.27	110.59
1	A	725	TYR	N-CA-C	-5.02	103.07	113.31
1	C	696	ASP	N-CA-C	-5.01	105.10	111.11

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	671	TYR	Sidechain

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2861	0	2827	238	9
1	B	2861	0	2827	216	22
1	C	2861	0	2827	188	30
2	D	1098	0	1063	163	0
3	A	117	0	0	28	0
3	B	99	0	0	18	0
3	C	113	0	0	19	1
3	D	30	0	0	7	0
All	All	10040	0	9544	750	31

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 39.

All (750) 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:626:ARG:HD2	3:A:60:HOH:O	1.38	1.19
2:D:80:ASP:OD1	2:D:121:LEU:HG	1.44	1.14
1:A:531:GLN:NE2	1:B:626:ARG:NE	1.99	1.09
1:A:531:GLN:NE2	1:B:626:ARG:CZ	2.16	1.09
1:A:531:GLN:NE2	1:B:626:ARG:CD	2.17	1.06
1:A:531:GLN:HE22	1:B:626:ARG:CD	1.69	1.04
1:B:616:ARG:HG2	1:B:729:PRO:HG2	1.34	1.03
1:A:516:ARG:HH11	1:A:516:ARG:HG2	1.25	1.02
1:A:503:LYS:H	1:A:516:ARG:NH1	1.58	0.98
1:B:683:THR:H	1:B:686:ASN:ND2	1.63	0.96
1:A:740:ARG:NH1	1:C:746:ALA:HB2	1.80	0.95
1:C:649:VAL:H	1:C:684:ASN:HD21	1.14	0.95
1:A:531:GLN:HE21	1:B:626:ARG:CZ	1.79	0.95
1:B:532:LEU:H	1:B:602:ASN:HD21	1.09	0.95
1:C:770:ILE:HD13	1:C:836:LYS:HB2	1.50	0.92
1:A:531:GLN:NE2	1:B:626:ARG:HD2	1.84	0.91
2:D:143:PHE:HA	2:D:146:LYS:HE2	1.54	0.89
2:D:104:VAL:HG23	2:D:105:ILE:HD12	1.53	0.89
1:C:571:GLU:HG2	3:C:81:HOH:O	1.73	0.88
1:B:824:LEU:HD11	1:B:826:LEU:HG	1.53	0.88
1:A:684:ASN:N	1:A:684:ASN:HD22	1.71	0.88
2:D:23:ARG:HD2	2:D:24:ASN:N	1.90	0.87
1:A:766:GLU:OE2	1:A:832:LYS:HB2	1.75	0.86
1:A:748:GLU:HA	1:A:768:TRP:CH2	2.09	0.86
1:C:723:LEU:O	1:C:726:LEU:HB2	1.75	0.86
1:B:683:THR:H	1:B:686:ASN:HD21	0.89	0.86
1:B:683:THR:N	1:B:686:ASN:HD21	1.73	0.86
1:C:721:SER:H	1:C:722:PRO:CD	1.90	0.85
1:C:787:THR:HG22	1:C:822:ASN:OD1	1.77	0.85
1:B:613:VAL:HB	3:B:269:HOH:O	1.77	0.84
1:B:746:ALA:HB2	1:C:740:ARG:NH1	1.92	0.84
1:C:532:LEU:H	1:C:602:ASN:HD21	1.26	0.83
2:D:101:THR:HA	2:D:104:VAL:HG22	1.60	0.83
2:D:60:GLU:CG	2:D:64:LYS:HD2	2.09	0.82
1:B:771:VAL:HA	1:B:774:PHE:CD2	2.14	0.82
1:C:591:LEU:HD11	3:C:214:HOH:O	1.79	0.81
1:C:649:VAL:HG12	1:C:650:GLU:H	1.45	0.81
2:D:11:LEU:O	2:D:14:ILE:HG23	1.79	0.81
1:A:697:TYR:O	1:A:698:ILE:HB	1.81	0.81
1:B:718:THR:HG21	1:B:723:LEU:HD21	1.61	0.81
1:A:532:LEU:H	1:A:602:ASN:HD21	1.26	0.81
1:C:670:MET:HE2	1:C:670:MET:HA	1.62	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:60:GLU:HG2	2:D:64:LYS:HD2	1.63	0.80
1:A:531:GLN:HE22	1:B:626:ARG:CG	1.94	0.80
1:A:723:LEU:HD22	1:A:723:LEU:H	1.47	0.80
1:A:740:ARG:HH12	1:C:746:ALA:HB2	1.43	0.80
1:A:771:VAL:HA	1:A:774:PHE:CD2	2.17	0.79
1:C:664:LEU:HD12	1:C:664:LEU:H	1.46	0.79
2:D:117:PRO:O	2:D:120:PRO:HD3	1.82	0.79
2:D:44:PRO:HB2	2:D:45:PRO:HD2	1.64	0.79
1:C:697:TYR:O	1:C:698:ILE:HB	1.83	0.79
1:C:742:LEU:HD11	1:C:780:ARG:NH1	1.97	0.79
2:D:24:ASN:HB2	2:D:36:GLN:O	1.82	0.79
1:C:649:VAL:N	1:C:684:ASN:HD21	1.81	0.78
1:A:532:LEU:O	1:B:626:ARG:NH2	2.16	0.78
1:B:723:LEU:O	1:B:726:LEU:HB2	1.84	0.77
1:A:502:LEU:HA	1:A:516:ARG:NH1	1.98	0.77
1:B:743:ASP:OD2	1:C:740:ARG:HD3	1.84	0.77
2:D:52:ARG:HB3	2:D:71:LYS:HD2	1.66	0.77
1:C:520:ILE:HD11	3:C:38:HOH:O	1.85	0.77
1:A:668:PRO:HB3	2:D:59:ALA:HB2	1.67	0.77
1:C:626:ARG:HD3	3:C:15:HOH:O	1.85	0.76
2:D:36:GLN:CD	2:D:52:ARG:HD3	2.11	0.76
1:A:763:LEU:HD11	1:A:826:LEU:HD13	1.66	0.76
1:B:532:LEU:H	1:B:602:ASN:ND2	1.82	0.76
1:A:616:ARG:HG2	1:A:729:PRO:HG2	1.66	0.76
1:B:827:PRO:HD2	1:B:829:TYR:CE1	2.20	0.76
2:D:122:ARG:HH11	2:D:125:LEU:HD11	1.50	0.76
2:D:143:PHE:HA	2:D:146:LYS:CE	2.16	0.75
1:A:502:LEU:HA	1:A:516:ARG:HH12	1.49	0.75
1:B:827:PRO:HD2	1:B:829:TYR:HE1	1.50	0.75
1:B:787:THR:HG21	1:B:800:LEU:HD13	1.69	0.75
1:B:762:VAL:O	1:B:766:GLU:HG3	1.87	0.75
1:A:531:GLN:CD	1:B:626:ARG:HD2	2.11	0.74
2:D:36:GLN:NE2	2:D:52:ARG:HD3	2.04	0.73
1:A:516:ARG:HG2	1:A:516:ARG:NH1	1.98	0.73
1:A:745:GLN:O	1:A:746:ALA:HB3	1.88	0.73
1:B:742:LEU:HD11	1:B:780:ARG:NH1	2.03	0.73
1:C:497:ASN:ND2	1:C:499:TYR:H	1.87	0.73
1:C:718:THR:HG21	1:C:723:LEU:HD21	1.71	0.73
1:C:745:GLN:O	1:C:746:ALA:HB3	1.89	0.73
2:D:127:GLU:O	2:D:131:LYS:HG2	1.89	0.73
1:A:521:ALA:O	1:A:525:PRO:HG3	1.89	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:80:ASP:CG	2:D:121:LEU:HG	2.12	0.73
2:D:76:HIS:CE1	2:D:115:PRO:HG3	2.25	0.72
1:A:653:MET:HE1	2:D:97:PRO:HB2	1.71	0.72
1:B:533:TYR:HA	1:C:626:ARG:NH2	2.05	0.72
2:D:105:ILE:HG22	2:D:106:GLN:H	1.55	0.71
2:D:105:ILE:O	2:D:106:GLN:HB3	1.89	0.71
1:A:728:ARG:CZ	1:C:794:VAL:HG21	2.20	0.71
1:B:766:GLU:O	1:B:770:ILE:HG13	1.91	0.71
1:A:634:VAL:HG12	3:A:8:HOH:O	1.89	0.70
1:B:618:LEU:HD21	3:B:293:HOH:O	1.91	0.70
2:D:105:ILE:HG22	2:D:106:GLN:N	2.06	0.70
1:C:655:ILE:HG13	1:C:682:ILE:HD12	1.74	0.70
1:B:839:LEU:HD23	1:B:839:LEU:O	1.92	0.70
1:C:613:VAL:HG22	1:C:627:ASP:HB3	1.72	0.70
2:D:134:LYS:C	2:D:136:PHE:H	1.99	0.70
1:B:745:GLN:O	1:B:746:ALA:HB3	1.91	0.70
1:C:723:LEU:H	1:C:723:LEU:HD22	1.56	0.70
1:A:794:VAL:HG21	1:B:728:ARG:NH2	2.06	0.70
2:D:143:PHE:CD2	2:D:146:LYS:HE3	2.27	0.70
1:A:589:PHE:O	1:A:592:ILE:HD12	1.91	0.70
1:A:618:LEU:HD13	3:A:320:HOH:O	1.92	0.70
1:C:748:GLU:HA	1:C:768:TRP:CH2	2.26	0.70
1:B:724:LYS:O	1:B:725:TYR:HB2	1.92	0.69
1:C:723:LEU:HA	1:C:726:LEU:HD12	1.74	0.69
1:A:586:GLU:HG2	3:A:275:HOH:O	1.91	0.69
1:A:661:GLN:OE1	3:A:225:HOH:O	2.09	0.69
1:B:723:LEU:HD22	1:B:723:LEU:H	1.54	0.69
1:C:762:VAL:O	1:C:766:GLU:HG3	1.94	0.68
2:D:5:ARG:O	2:D:8:MET:HG3	1.93	0.68
1:A:503:LYS:N	1:A:516:ARG:NH1	2.38	0.68
1:B:787:THR:HG22	1:B:822:ASN:OD1	1.92	0.68
1:A:777:GLU:HG3	3:A:303:HOH:O	1.94	0.68
1:A:697:TYR:O	1:A:698:ILE:CB	2.40	0.68
2:D:39:ILE:O	2:D:41:PRO:HD3	1.94	0.68
2:D:91:SER:O	2:D:92:ALA:O	2.11	0.68
1:C:626:ARG:CZ	3:C:15:HOH:O	2.41	0.68
1:B:718:THR:HG21	1:B:723:LEU:CD2	2.23	0.67
1:A:724:LYS:O	1:A:725:TYR:HB2	1.95	0.67
1:B:655:ILE:HG13	1:B:682:ILE:HD12	1.75	0.67
1:C:721:SER:H	1:C:722:PRO:HD3	1.59	0.67
1:B:794:VAL:HG21	1:C:728:ARG:CZ	2.24	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:679:LYS:HD3	1:C:679:LYS:C	2.20	0.67
1:C:613:VAL:CG2	1:C:627:ASP:HB3	2.23	0.67
2:D:133:ARG:HB2	2:D:133:ARG:NH1	2.08	0.67
1:C:684:ASN:N	1:C:684:ASN:HD22	1.92	0.67
1:C:763:LEU:HD11	1:C:826:LEU:HD13	1.77	0.67
1:A:829:TYR:CE2	1:A:838:ARG:HG3	2.30	0.66
1:A:770:ILE:HD12	1:A:835:LEU:HD22	1.78	0.66
2:D:131:LYS:O	2:D:132:ASP:HB2	1.95	0.66
1:A:723:LEU:O	1:A:726:LEU:HB2	1.95	0.66
1:B:775:THR:O	1:B:778:GLN:N	2.28	0.66
1:C:784:GLN:NE2	1:C:789:THR:HA	2.10	0.66
2:D:44:PRO:CB	2:D:45:PRO:HD2	2.24	0.66
1:A:514:LEU:HD21	1:A:591:LEU:HB2	1.78	0.66
1:A:744:PHE:HA	1:A:747:LEU:HB3	1.78	0.66
2:D:133:ARG:O	2:D:133:ARG:HG3	1.95	0.66
1:B:516:ARG:HD2	1:B:519:MET:HE3	1.77	0.65
2:D:133:ARG:HB2	2:D:133:ARG:HH11	1.60	0.65
1:B:719:ASN:O	1:B:720:GLU:HB2	1.96	0.65
1:B:754:ASP:O	1:B:805:ALA:HA	1.96	0.65
1:C:649:VAL:HG12	1:C:650:GLU:N	2.11	0.65
1:A:531:GLN:HE22	1:B:626:ARG:HG3	1.60	0.65
1:B:533:TYR:HA	1:C:626:ARG:HH22	1.60	0.65
1:C:766:GLU:OE2	1:C:832:LYS:HB2	1.96	0.65
1:A:748:GLU:HG3	1:A:768:TRP:CE2	2.31	0.65
1:B:516:ARG:O	1:B:520:ILE:HG13	1.96	0.65
1:C:505:ARG:HG2	1:C:512:ASP:OD1	1.96	0.65
1:C:511:ASP:O	1:C:515:VAL:HG23	1.97	0.65
1:C:724:LYS:O	1:C:725:TYR:HB2	1.95	0.65
1:A:684:ASN:HD22	1:A:684:ASN:H	1.43	0.64
1:C:771:VAL:HA	1:C:774:PHE:CD2	2.32	0.64
2:D:60:GLU:HG3	2:D:64:LYS:HD2	1.79	0.64
2:D:122:ARG:NH1	2:D:125:LEU:HD11	2.12	0.64
1:C:626:ARG:NH1	3:C:15:HOH:O	2.29	0.64
2:D:37:GLY:O	2:D:52:ARG:HA	1.96	0.64
1:A:524:ASN:OD1	1:A:526:ALA:HB3	1.97	0.63
1:A:728:ARG:NH1	1:C:794:VAL:HG21	2.14	0.63
1:C:497:ASN:HD22	1:C:498:PRO:CD	2.10	0.63
1:B:516:ARG:HG2	1:B:516:ARG:HH11	1.63	0.63
1:C:506:ARG:O	1:C:507:ASP:HB2	1.99	0.63
1:A:531:GLN:NE2	1:B:626:ARG:NH1	2.45	0.63
1:A:755:GLY:O	1:A:806:LYS:HE2	1.97	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:22:PHE:HA	2:D:38:LEU:O	1.98	0.63
1:B:763:LEU:HD11	1:B:826:LEU:HD13	1.80	0.63
1:B:684:ASN:HD22	1:B:684:ASN:H	1.46	0.63
1:A:507:ASP:O	1:A:508:HIS:ND1	2.32	0.63
1:A:531:GLN:HE22	1:B:626:ARG:NE	1.80	0.63
2:D:115:PRO:O	2:D:117:PRO:HD3	1.99	0.63
1:B:728:ARG:HB2	1:B:730:GLU:OE1	1.99	0.62
1:B:809:PRO:O	1:B:811:THR:HG23	2.00	0.62
1:C:655:ILE:CG1	1:C:682:ILE:HD12	2.28	0.62
2:D:23:ARG:NH1	2:D:25:ILE:HG22	2.14	0.62
1:A:503:LYS:H	1:A:516:ARG:HH12	1.43	0.62
1:A:511:ASP:O	1:A:515:VAL:HG23	2.00	0.62
1:B:684:ASN:HD22	1:B:684:ASN:N	1.97	0.62
1:B:590:THR:O	1:B:594:ILE:HG13	1.98	0.62
1:B:669:MET:C	1:B:670:MET:HE2	2.24	0.62
1:A:613:VAL:HG22	1:A:627:ASP:HB3	1.80	0.62
1:B:721:SER:N	1:B:722:PRO:CD	2.62	0.62
1:A:533:TYR:HA	1:B:626:ARG:NH2	2.14	0.62
1:C:626:ARG:CD	3:C:15:HOH:O	2.47	0.62
1:C:683:THR:N	1:C:686:ASN:OD1	2.30	0.62
2:D:59:ALA:HA	3:D:172:HOH:O	2.00	0.61
1:B:497:ASN:N	3:B:210:HOH:O	2.33	0.61
1:C:661:GLN:HG3	1:C:697:TYR:OH	2.01	0.61
1:A:589:PHE:HA	1:A:592:ILE:HD11	1.83	0.61
1:A:696:ASP:OD2	1:A:701:LYS:HE2	2.00	0.61
1:A:706:GLN:CD	1:A:706:GLN:H	2.02	0.61
1:A:835:LEU:C	1:A:835:LEU:HD23	2.26	0.61
1:B:529:LYS:HG3	1:B:601:TYR:CE2	2.35	0.61
1:C:590:THR:O	1:C:594:ILE:HG13	2.00	0.61
1:A:749:GLU:C	1:A:751:THR:H	2.09	0.61
2:D:57:PHE:HB3	2:D:66:PRO:HG3	1.82	0.61
2:D:101:THR:CA	2:D:104:VAL:HG22	2.29	0.61
1:A:718:THR:HA	3:A:178:HOH:O	2.00	0.60
1:B:697:TYR:O	1:B:698:ILE:HB	2.01	0.60
1:C:516:ARG:NE	3:C:38:HOH:O	2.33	0.60
1:C:605:ILE:HB	3:C:70:HOH:O	2.01	0.60
1:C:697:TYR:O	1:C:698:ILE:CB	2.49	0.60
1:A:502:LEU:CA	1:A:516:ARG:HH12	2.14	0.60
1:C:497:ASN:HD21	1:C:499:TYR:H	1.50	0.60
1:C:591:LEU:HD21	3:C:214:HOH:O	2.02	0.60
1:C:505:ARG:NH1	1:C:508:HIS:CG	2.69	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:684:ASN:HB2	1:A:685:GLU:OE1	2.01	0.60
1:A:728:ARG:H	1:A:728:ARG:HD3	1.67	0.60
2:D:7:LEU:HD13	2:D:32:LEU:O	2.02	0.60
1:B:764:ILE:O	1:B:767:PHE:HB3	2.02	0.59
1:C:660:SER:HB3	1:C:670:MET:HE1	1.83	0.59
2:D:78:ASN:HD21	2:D:116:GLN:H	1.50	0.59
1:A:719:ASN:OD1	1:A:720:GLU:HG3	2.01	0.59
1:A:746:ALA:HB2	1:B:740:ARG:HH12	1.67	0.59
1:B:771:VAL:O	1:B:774:PHE:HB2	2.01	0.59
1:C:675:GLU:HB3	3:C:341:HOH:O	2.01	0.59
1:A:570:ASP:OD2	1:A:572:SER:HB3	2.03	0.59
1:B:723:LEU:HD22	1:B:723:LEU:N	2.17	0.59
1:A:534:VAL:HB	1:A:547:VAL:HG12	1.85	0.59
1:A:723:LEU:HD22	1:A:723:LEU:N	2.16	0.59
1:A:770:ILE:HD13	1:A:836:LYS:HB2	1.84	0.59
1:A:778:GLN:HA	1:A:781:LEU:HD12	1.85	0.59
1:A:675:GLU:HB3	3:A:163:HOH:O	2.02	0.59
1:C:741:ASN:HB2	3:C:23:HOH:O	2.02	0.59
1:B:837:GLU:OE1	1:B:838:ARG:NH2	2.36	0.59
1:C:505:ARG:HH12	1:C:508:HIS:CG	2.21	0.59
1:A:649:VAL:HB	1:A:684:ASN:ND2	2.18	0.59
1:B:775:THR:OG1	1:B:778:GLN:HG3	2.03	0.59
1:C:706:GLN:CD	1:C:706:GLN:H	2.11	0.58
1:A:516:ARG:HH11	1:A:516:ARG:CG	2.08	0.58
1:B:766:GLU:OE2	1:B:832:LYS:HB2	2.03	0.58
1:A:754:ASP:O	1:A:805:ALA:HA	2.03	0.58
2:D:14:ILE:C	2:D:16:LYS:H	2.12	0.58
1:A:503:LYS:HD3	3:A:146:HOH:O	2.04	0.58
1:B:502:LEU:CD2	1:B:504:VAL:HG13	2.33	0.58
2:D:36:GLN:NE2	2:D:52:ARG:HH11	2.02	0.58
1:B:649:VAL:H	1:B:684:ASN:HD21	1.52	0.58
1:B:841:LYS:HA	1:B:844:THR:HG22	1.85	0.58
1:A:532:LEU:H	1:A:602:ASN:ND2	2.00	0.58
1:A:712:ARG:O	1:A:716:MET:HG3	2.04	0.58
1:A:730:GLU:HG2	3:A:179:HOH:O	2.04	0.58
1:A:531:GLN:CD	1:B:626:ARG:NH1	2.62	0.57
1:A:653:MET:HE3	2:D:98:ALA:CA	2.34	0.57
1:B:506:ARG:O	1:B:507:ASP:HB2	2.04	0.57
1:B:670:MET:HE2	1:B:670:MET:N	2.18	0.57
1:B:697:TYR:O	1:B:698:ILE:CB	2.52	0.57
1:C:786:THR:O	1:C:819:THR:HA	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:507:ASP:O	1:B:508:HIS:HB2	2.03	0.57
1:B:518:GLU:OE1	1:B:518:GLU:HA	2.04	0.57
1:B:658:GLN:HG3	1:B:672:ASP:OD2	2.04	0.57
1:B:748:GLU:HA	1:B:768:TRP:CH2	2.40	0.57
2:D:25:ILE:HG13	2:D:26:GLN:N	2.19	0.57
2:D:105:ILE:O	2:D:107:SER:N	2.36	0.57
1:A:835:LEU:HD23	1:A:835:LEU:O	2.05	0.57
1:B:649:VAL:HG12	1:B:650:GLU:H	1.68	0.57
2:D:120:PRO:C	2:D:122:ARG:H	2.12	0.57
1:A:745:GLN:O	1:A:746:ALA:CB	2.53	0.57
2:D:27:VAL:HB	2:D:36:GLN:HB2	1.85	0.57
1:A:728:ARG:HD3	1:A:728:ARG:N	2.20	0.57
1:A:653:MET:HE3	2:D:98:ALA:HA	1.87	0.56
1:C:520:ILE:O	1:C:523:GLU:O	2.22	0.56
2:D:129:TYR:CD1	2:D:129:TYR:C	2.83	0.56
1:A:584:GLU:N	3:A:258:HOH:O	2.38	0.56
1:A:674:LYS:HD3	1:A:680:ILE:HD13	1.88	0.56
1:C:648:ASN:HB2	3:C:94:HOH:O	2.04	0.56
1:B:655:ILE:CG1	1:B:682:ILE:HD12	2.36	0.56
1:A:583:PHE:CE1	1:A:584:GLU:HG2	2.40	0.56
1:C:770:ILE:CD1	1:C:836:LYS:HB2	2.31	0.56
2:D:25:ILE:O	2:D:36:GLN:HB3	2.05	0.56
1:A:653:MET:HE1	2:D:97:PRO:CB	2.34	0.56
1:C:748:GLU:HG3	1:C:768:TRP:CE2	2.40	0.56
1:A:740:ARG:HD3	1:C:743:ASP:OD2	2.05	0.56
1:C:655:ILE:CD1	1:C:682:ILE:HD12	2.36	0.56
2:D:122:ARG:HD2	2:D:125:LEU:HG	1.86	0.56
1:A:626:ARG:CZ	3:A:124:HOH:O	2.54	0.56
1:B:724:LYS:O	1:B:725:TYR:CB	2.54	0.56
1:A:499:TYR:HA	1:A:531:GLN:O	2.05	0.55
1:B:619:MET:HE1	1:B:727:PHE:O	2.06	0.55
1:B:748:GLU:OE1	1:B:772:HIS:HE1	1.88	0.55
1:A:499:TYR:OH	1:B:626:ARG:HG3	2.06	0.55
1:A:714:PHE:CZ	3:A:320:HOH:O	2.59	0.55
2:D:70:PHE:CE2	2:D:79:ILE:HD13	2.41	0.55
2:D:135:LYS:O	2:D:135:LYS:HD3	2.07	0.55
1:B:521:ALA:O	1:B:525:PRO:HG3	2.06	0.55
1:C:670:MET:HE2	1:C:670:MET:CA	2.34	0.55
1:A:748:GLU:HA	1:A:768:TRP:CZ2	2.40	0.55
1:B:507:ASP:O	1:B:508:HIS:CB	2.54	0.55
1:A:806:LYS:HE2	3:A:111:HOH:O	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:789:THR:OG1	1:C:790:ASP:N	2.39	0.55
2:D:76:HIS:HE1	2:D:115:PRO:HG3	1.70	0.55
2:D:101:THR:O	2:D:104:VAL:HG22	2.08	0.54
1:A:718:THR:O	1:A:718:THR:HG22	2.06	0.54
2:D:108:LEU:C	2:D:108:LEU:HD23	2.33	0.54
1:C:723:LEU:O	1:C:726:LEU:CB	2.52	0.54
1:A:643:LEU:HD21	1:A:691:VAL:HG21	1.90	0.54
1:A:743:ASP:O	1:A:745:GLN:N	2.35	0.54
2:D:23:ARG:HH12	2:D:25:ILE:HG22	1.72	0.54
2:D:44:PRO:HB2	2:D:45:PRO:CD	2.37	0.54
1:C:724:LYS:O	1:C:725:TYR:CB	2.55	0.54
1:A:724:LYS:O	1:A:725:TYR:CB	2.56	0.54
1:B:745:GLN:O	1:B:746:ALA:CB	2.56	0.54
1:C:569:TYR:CZ	1:C:574:LYS:HA	2.43	0.54
1:C:631:SER:C	1:C:632:HIS:ND1	2.66	0.54
1:B:507:ASP:O	1:B:508:HIS:ND1	2.41	0.54
1:C:506:ARG:O	1:C:507:ASP:CB	2.56	0.54
1:B:722:PRO:C	3:B:174:HOH:O	2.52	0.53
2:D:104:VAL:C	2:D:105:ILE:O	2.45	0.53
1:A:503:LYS:N	1:A:516:ARG:HH12	2.03	0.53
2:D:38:LEU:HD23	2:D:51:PHE:C	2.33	0.53
1:B:502:LEU:HD23	1:B:503:LYS:N	2.23	0.53
1:A:840:LEU:O	1:A:844:THR:HG22	2.09	0.53
1:C:770:ILE:HD13	1:C:836:LYS:CB	2.32	0.53
1:C:616:ARG:HG2	1:C:729:PRO:HG2	1.91	0.53
1:C:723:LEU:HB3	1:C:732:ILE:HD11	1.91	0.53
2:D:24:ASN:O	2:D:25:ILE:HB	2.08	0.53
1:B:612:MET:SD	1:B:730:GLU:HG3	2.49	0.53
1:C:774:PHE:HE1	1:C:840:LEU:HD21	1.73	0.53
2:D:116:GLN:O	2:D:116:GLN:HG3	2.08	0.53
2:D:134:LYS:C	2:D:136:PHE:N	2.65	0.53
1:B:770:ILE:HD12	1:B:835:LEU:HD13	1.91	0.53
1:B:774:PHE:HD1	1:B:778:GLN:OE1	1.91	0.53
1:B:723:LEU:HD13	3:B:174:HOH:O	2.09	0.53
1:B:789:THR:HG23	3:B:306:HOH:O	2.09	0.53
2:D:39:ILE:HD13	2:D:53:ILE:HD11	1.90	0.53
1:B:648:ASN:OD1	1:B:649:VAL:O	2.27	0.52
1:C:505:ARG:NH1	1:C:508:HIS:ND1	2.57	0.52
2:D:78:ASN:HD21	2:D:116:GLN:N	2.07	0.52
1:B:535:GLU:HA	3:B:317:HOH:O	2.09	0.52
2:D:103:GLN:HB3	3:D:160:HOH:O	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:589:PHE:O	1:A:592:ILE:CD1	2.58	0.52
1:A:746:ALA:HB2	1:B:740:ARG:NH1	2.23	0.52
1:A:766:GLU:O	1:A:770:ILE:HG13	2.08	0.52
1:A:766:GLU:CD	1:A:832:LYS:HB2	2.34	0.52
2:D:80:ASP:OD1	2:D:121:LEU:CG	2.37	0.52
1:A:529:LYS:HE2	1:A:720:GLU:OE2	2.09	0.52
1:B:516:ARG:HD2	1:B:519:MET:CE	2.39	0.52
1:B:744:PHE:HA	1:B:747:LEU:HB3	1.92	0.52
1:A:570:ASP:OD2	1:A:570:ASP:C	2.52	0.52
1:A:728:ARG:NH2	1:C:794:VAL:HG21	2.24	0.52
1:A:740:ARG:NH1	1:C:746:ALA:CB	2.64	0.52
2:D:48:LYS:HA	3:D:159:HOH:O	2.09	0.52
2:D:89:VAL:HG13	2:D:90:ILE:HG23	1.91	0.52
1:A:663:ASP:HB3	1:A:664:LEU:HD12	1.92	0.52
1:A:694:TYR:O	1:A:697:TYR:O	2.28	0.52
1:B:824:LEU:C	1:B:824:LEU:HD13	2.34	0.52
1:B:837:GLU:OE2	1:B:838:ARG:NE	2.43	0.52
1:A:684:ASN:N	1:A:684:ASN:ND2	2.45	0.52
1:C:840:LEU:O	1:C:844:THR:HG22	2.10	0.52
1:A:763:LEU:HD13	1:A:763:LEU:O	2.10	0.52
1:C:721:SER:N	1:C:722:PRO:CD	2.61	0.52
1:C:760:ASP:O	1:C:761:SER:HB2	2.09	0.52
1:B:738:GLY:O	1:B:791:ARG:HD3	2.10	0.51
1:C:728:ARG:H	1:C:728:ARG:HD3	1.75	0.51
1:B:839:LEU:HD23	1:B:839:LEU:C	2.35	0.51
1:C:745:GLN:HB3	3:C:263:HOH:O	2.11	0.51
1:B:663:ASP:OD2	1:B:667:ASN:OD1	2.28	0.51
2:D:97:PRO:HG2	3:D:155:HOH:O	2.10	0.51
1:A:660:SER:OG	2:D:59:ALA:HB1	2.10	0.51
1:B:827:PRO:O	1:B:829:TYR:CD1	2.64	0.51
1:C:749:GLU:C	1:C:751:THR:H	2.18	0.51
1:C:500:LEU:HG	1:C:527:ASP:O	2.11	0.51
1:B:681:PRO:HD2	3:B:290:HOH:O	2.11	0.51
1:B:827:PRO:HB2	1:B:829:TYR:CE1	2.46	0.51
1:B:840:LEU:O	1:B:844:THR:HG22	2.11	0.51
1:C:720:GLU:O	1:C:721:SER:HB3	2.11	0.51
1:A:838:ARG:HE	1:A:838:ARG:HA	1.75	0.51
1:A:841:LYS:HA	1:A:844:THR:HG22	1.93	0.51
1:B:694:TYR:HD2	1:B:694:TYR:O	1.94	0.51
1:A:549:LYS:HD3	1:A:820:CYS:HA	1.93	0.50
1:B:614:VAL:N	3:B:269:HOH:O	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:748:GLU:OE1	1:B:772:HIS:CE1	2.64	0.50
1:B:613:VAL:HG22	1:B:627:ASP:HB3	1.93	0.50
1:B:634:VAL:HG22	3:B:53:HOH:O	2.11	0.50
1:B:735:LEU:HD23	1:C:728:ARG:HH22	1.75	0.50
2:D:14:ILE:C	2:D:16:LYS:N	2.67	0.50
1:C:649:VAL:HG23	1:C:684:ASN:ND2	2.27	0.50
2:D:7:LEU:CD1	2:D:33:LEU:HD23	2.42	0.50
1:B:743:ASP:O	1:B:744:PHE:HB2	2.11	0.50
1:C:687:ARG:O	1:C:690:PHE:HB3	2.11	0.50
1:C:723:LEU:HD22	1:C:723:LEU:N	2.23	0.50
2:D:71:LYS:HD3	2:D:71:LYS:C	2.36	0.50
1:A:833:GLU:OE2	1:A:833:GLU:N	2.43	0.50
1:A:838:ARG:NH2	1:A:841:LYS:HD2	2.26	0.50
2:D:87:LEU:H	2:D:87:LEU:HD23	1.77	0.50
1:A:653:MET:CE	2:D:97:PRO:HB2	2.40	0.50
1:A:654:MET:HE3	1:A:681:PRO:HB3	1.93	0.50
1:A:681:PRO:HD2	3:A:326:HOH:O	2.11	0.50
1:B:505:ARG:O	1:B:506:ARG:C	2.55	0.50
1:C:655:ILE:HD12	1:C:682:ILE:HD12	1.93	0.50
1:C:767:PHE:HB2	1:C:835:LEU:HD11	1.94	0.50
2:D:25:ILE:CG1	2:D:26:GLN:N	2.75	0.50
1:A:749:GLU:O	1:A:751:THR:N	2.45	0.50
1:B:774:PHE:HE1	1:B:840:LEU:HD21	1.77	0.50
2:D:57:PHE:HB3	2:D:66:PRO:CB	2.42	0.50
1:A:662:THR:O	1:A:663:ASP:OD1	2.30	0.49
1:B:561:ASN:O	1:B:564:ILE:HG22	2.12	0.49
2:D:75:TYR:CD2	2:D:143:PHE:HD1	2.30	0.49
1:B:617:LYS:HB3	1:B:707:PHE:CZ	2.46	0.49
1:A:662:THR:HG23	2:D:59:ALA:HB2	1.94	0.49
1:A:763:LEU:CD1	1:A:826:LEU:HD13	2.41	0.49
1:A:794:VAL:HG21	1:B:728:ARG:CZ	2.42	0.49
2:D:6:ARG:HD3	2:D:62:PRO:HG3	1.94	0.49
2:D:31:ASN:O	2:D:33:LEU:N	2.43	0.49
1:A:775:THR:O	1:A:778:GLN:N	2.41	0.49
2:D:104:VAL:HG23	2:D:105:ILE:N	2.28	0.49
1:A:738:GLY:O	1:A:791:ARG:HD3	2.12	0.49
1:A:771:VAL:O	1:A:774:PHE:HB2	2.13	0.49
2:D:11:LEU:HD11	2:D:26:GLN:NE2	2.27	0.49
2:D:101:THR:HA	2:D:104:VAL:CG2	2.38	0.49
2:D:101:THR:C	2:D:104:VAL:HG22	2.37	0.49
1:A:841:LYS:O	1:A:845:TYR:HB2	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:622:LYS:HB2	1:C:498:PRO:HG3	1.93	0.49
1:A:656:THR:O	1:A:682:ILE:HD11	2.13	0.49
1:A:726:LEU:HD22	1:A:731:GLU:OE1	2.13	0.49
1:C:635:LEU:HD23	1:C:635:LEU:O	2.13	0.49
1:C:722:PRO:HB2	1:C:724:LYS:H	1.77	0.49
1:C:807:ASN:HA	3:C:343:HOH:O	2.13	0.49
1:B:694:TYR:O	1:B:697:TYR:O	2.30	0.48
1:C:569:TYR:CE1	1:C:574:LYS:HA	2.48	0.48
1:C:634:VAL:HG11	3:C:177:HOH:O	2.12	0.48
1:C:748:GLU:HA	1:C:768:TRP:CZ2	2.47	0.48
1:C:833:GLU:CD	1:C:833:GLU:H	2.21	0.48
1:A:507:ASP:O	1:A:508:HIS:HB2	2.13	0.48
1:C:744:PHE:HA	1:C:747:LEU:HB3	1.94	0.48
1:C:809:PRO:O	1:C:811:THR:HG23	2.13	0.48
1:B:503:LYS:HG3	1:B:535:GLU:O	2.14	0.48
1:B:659:ILE:C	1:B:659:ILE:HD12	2.38	0.48
1:B:742:LEU:HD11	1:B:780:ARG:CZ	2.44	0.48
1:B:775:THR:O	1:B:776:ASP:C	2.56	0.48
1:C:674:LYS:O	1:C:675:GLU:C	2.56	0.48
1:C:745:GLN:O	1:C:746:ALA:CB	2.54	0.48
2:D:44:PRO:HG3	2:D:113:ASN:HA	1.94	0.48
1:A:515:VAL:O	1:A:519:MET:HG3	2.13	0.48
1:A:566:MET:SD	1:A:588:GLN:HB3	2.54	0.48
1:A:753:TYR:N	1:A:753:TYR:CD1	2.82	0.48
1:A:835:LEU:C	1:A:835:LEU:CD2	2.87	0.48
1:C:737:CYS:O	1:C:791:ARG:HD2	2.13	0.48
1:B:555:VAL:HG11	1:B:595:VAL:HG21	1.94	0.48
1:C:649:VAL:H	1:C:684:ASN:ND2	1.96	0.48
1:A:497:ASN:N	1:A:497:ASN:HD22	2.12	0.48
1:A:655:ILE:HG13	1:A:682:ILE:HD12	1.96	0.48
1:B:838:ARG:HE	1:B:838:ARG:HA	1.77	0.48
1:A:727:PHE:CB	1:A:728:ARG:HD3	2.43	0.48
1:C:774:PHE:CE1	1:C:840:LEU:HD21	2.48	0.48
2:D:57:PHE:HB3	2:D:66:PRO:CG	2.42	0.48
1:C:543:ASP:OD1	1:C:547:VAL:HB	2.14	0.48
1:C:821:PHE:HB2	1:C:823:VAL:HG23	1.95	0.48
1:A:507:ASP:O	1:A:508:HIS:CB	2.62	0.47
1:A:653:MET:O	1:A:654:MET:C	2.56	0.47
1:A:763:LEU:HD13	1:A:763:LEU:C	2.39	0.47
1:B:649:VAL:N	1:B:684:ASN:HD21	2.11	0.47
1:B:679:LYS:O	1:B:681:PRO:HD3	2.13	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:835:LEU:C	1:C:835:LEU:CD2	2.87	0.47
2:D:11:LEU:C	2:D:13:GLU:H	2.22	0.47
2:D:25:ILE:CD1	2:D:26:GLN:H	2.27	0.47
1:A:723:LEU:H	1:A:723:LEU:CD2	2.20	0.47
1:A:784:GLN:HG3	3:A:93:HOH:O	2.13	0.47
1:B:743:ASP:OD1	1:C:740:ARG:NH1	2.47	0.47
1:B:778:GLN:HB3	3:B:155:HOH:O	2.14	0.47
2:D:142:GLU:O	2:D:146:LYS:HG2	2.14	0.47
1:A:552:PHE:HD2	1:A:604:CYS:HG	1.62	0.47
1:A:660:SER:HB3	1:A:670:MET:SD	2.55	0.47
2:D:11:LEU:C	2:D:13:GLU:N	2.72	0.47
2:D:25:ILE:HD12	2:D:26:GLN:H	1.79	0.47
2:D:60:GLU:CD	2:D:60:GLU:H	2.22	0.47
1:A:564:ILE:HG12	1:A:564:ILE:O	2.14	0.47
1:A:697:TYR:HA	1:A:701:LYS:HB2	1.97	0.47
1:A:714:PHE:HE2	1:A:723:LEU:HD11	1.79	0.47
1:B:551:PHE:O	1:B:555:VAL:HG23	2.15	0.47
1:C:497:ASN:HA	1:C:498:PRO:HD3	1.66	0.47
1:C:749:GLU:O	1:C:751:THR:N	2.47	0.47
1:C:752:GLU:HB2	1:C:803:ILE:HG12	1.96	0.47
2:D:111:LEU:CD1	2:D:116:GLN:HG2	2.43	0.47
1:A:503:LYS:H	1:A:516:ARG:CZ	2.22	0.47
1:B:754:ASP:HB3	1:B:805:ALA:HB2	1.96	0.47
1:C:649:VAL:HB	1:C:684:ASN:ND2	2.30	0.47
1:A:533:TYR:HA	1:B:626:ARG:HH21	1.77	0.47
1:B:698:ILE:HG22	1:B:699:LEU:HD13	1.95	0.47
1:B:794:VAL:HG21	1:C:728:ARG:NH1	2.28	0.47
1:C:521:ALA:HB2	1:C:716:MET:HE3	1.96	0.47
1:C:728:ARG:HD3	1:C:728:ARG:N	2.30	0.47
2:D:71:LYS:HE2	3:D:177:HOH:O	2.15	0.47
1:B:747:LEU:O	1:B:751:THR:OG1	2.33	0.47
1:A:685:GLU:OE1	1:A:685:GLU:N	2.48	0.47
1:B:723:LEU:HB3	1:B:732:ILE:HD11	1.97	0.47
2:D:103:GLN:O	2:D:105:ILE:O	2.33	0.47
1:C:763:LEU:CD1	1:C:826:LEU:HD13	2.43	0.47
1:C:589:PHE:CE2	1:C:706:GLN:HB2	2.50	0.46
2:D:25:ILE:CG1	2:D:26:GLN:H	2.27	0.46
1:B:516:ARG:HG2	1:B:516:ARG:NH1	2.30	0.46
1:B:748:GLU:HG3	1:B:768:TRP:CE2	2.50	0.46
1:B:775:THR:O	1:B:777:GLU:N	2.48	0.46
1:C:657:PHE:HE1	1:C:686:ASN:ND2	2.13	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:7:LEU:HD11	2:D:33:LEU:HD23	1.97	0.46
2:D:44:PRO:HG2	3:D:162:HOH:O	2.15	0.46
1:B:719:ASN:O	1:B:720:GLU:CB	2.62	0.46
2:D:9:LYS:HA	2:D:12:GLU:HG2	1.96	0.46
1:A:757:TYR:CE2	1:A:806:LYS:HA	2.50	0.46
1:C:500:LEU:O	1:C:501:ARG:HB2	2.16	0.46
2:D:68:ILE:HD12	2:D:87:LEU:HD21	1.97	0.46
2:D:133:ARG:HH11	2:D:133:ARG:CB	2.27	0.46
1:C:723:LEU:CA	1:C:726:LEU:HD12	2.44	0.46
1:C:829:TYR:CE2	1:C:838:ARG:HG3	2.51	0.46
1:B:612:MET:CE	1:B:730:GLU:HG3	2.45	0.46
1:A:596:LEU:HD12	1:A:606:LEU:CD1	2.44	0.46
1:C:507:ASP:O	1:C:508:HIS:ND1	2.47	0.46
1:C:698:ILE:H	1:C:702:SER:HB3	1.81	0.46
1:C:740:ARG:HB3	1:C:780:ARG:HH21	1.80	0.46
1:C:771:VAL:O	1:C:774:PHE:HB2	2.15	0.46
2:D:115:PRO:C	2:D:117:PRO:HD3	2.40	0.46
1:B:763:LEU:CD1	1:B:826:LEU:HD13	2.45	0.46
1:C:748:GLU:C	1:C:749:GLU:O	2.56	0.46
2:D:65:PRO:HB3	2:D:95:TRP:CD2	2.51	0.46
1:B:765:ARG:O	1:B:769:GLU:HG3	2.16	0.46
2:D:38:LEU:HD23	2:D:52:ARG:HA	1.97	0.46
1:A:838:ARG:HA	1:A:838:ARG:NE	2.31	0.46
1:B:770:ILE:HD13	1:B:836:LYS:HB2	1.98	0.46
2:D:143:PHE:CA	2:D:146:LYS:HE2	2.38	0.46
1:A:749:GLU:C	1:A:751:THR:N	2.71	0.45
1:B:552:PHE:O	1:B:556:VAL:HG23	2.16	0.45
1:B:765:ARG:HD3	3:B:329:HOH:O	2.16	0.45
2:D:25:ILE:HG13	2:D:26:GLN:H	1.81	0.45
1:A:765:ARG:O	1:A:769:GLU:HG3	2.15	0.45
1:B:771:VAL:HA	1:B:774:PHE:HD2	1.74	0.45
1:C:497:ASN:N	3:C:4:HOH:O	2.49	0.45
1:C:589:PHE:CE2	1:C:706:GLN:CB	2.99	0.45
1:C:766:GLU:O	1:C:770:ILE:HG13	2.16	0.45
1:A:718:THR:O	1:A:718:THR:CG2	2.64	0.45
3:A:243:HOH:O	2:D:100:LYS:CG	2.64	0.45
1:C:715:HIS:HA	1:C:718:THR:HB	1.98	0.45
2:D:21:ASN:O	2:D:39:ILE:HA	2.16	0.45
2:D:101:THR:O	2:D:105:ILE:HD13	2.17	0.45
1:C:775:THR:O	1:C:776:ASP:C	2.59	0.45
1:C:800:LEU:O	1:C:801:LYS:C	2.59	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:742:LEU:HD11	1:A:780:ARG:NH1	2.31	0.45
1:B:505:ARG:C	1:B:506:ARG:O	2.55	0.45
1:B:745:GLN:OE1	1:B:772:HIS:CE1	2.69	0.45
1:B:824:LEU:CD1	1:B:826:LEU:HG	2.34	0.45
1:C:745:GLN:C	1:C:747:LEU:H	2.24	0.45
1:C:833:GLU:CD	1:C:833:GLU:N	2.74	0.45
1:C:757:TYR:CE2	1:C:806:LYS:HA	2.51	0.45
2:D:24:ASN:CG	3:D:168:HOH:O	2.60	0.45
2:D:57:PHE:HB3	2:D:66:PRO:HB3	1.98	0.45
2:D:41:PRO:HB2	2:D:46:TYR:O	2.17	0.45
1:A:499:TYR:CZ	1:B:626:ARG:HG3	2.52	0.45
1:A:628:LEU:HD22	1:A:632:HIS:HB2	1.98	0.45
1:A:714:PHE:CE2	1:A:723:LEU:HD11	2.52	0.45
1:A:769:GLU:OE2	1:A:832:LYS:NZ	2.46	0.45
1:C:766:GLU:CD	1:C:832:LYS:HB2	2.41	0.45
1:A:545:GLY:HA3	3:A:51:HOH:O	2.17	0.45
1:B:549:LYS:O	1:B:553:GLN:HG3	2.17	0.45
1:C:552:PHE:O	1:C:556:VAL:HG23	2.17	0.45
2:D:20:LYS:O	2:D:21:ASN:ND2	2.50	0.45
2:D:104:VAL:HG23	2:D:105:ILE:H	1.81	0.45
1:A:583:PHE:CZ	1:A:584:GLU:HG2	2.52	0.45
1:B:613:VAL:CG2	1:B:627:ASP:HB3	2.48	0.45
2:D:16:LYS:O	2:D:17:CYS:O	2.35	0.45
2:D:20:LYS:C	2:D:21:ASN:CG	2.83	0.45
2:D:29:GLU:O	2:D:30:ALA:HB2	2.17	0.45
1:A:641:ASP:OD1	2:D:96:LYS:HD2	2.17	0.44
1:A:757:TYR:O	1:A:761:SER:OG	2.33	0.44
1:B:614:VAL:HG23	3:B:269:HOH:O	2.16	0.44
1:B:728:ARG:HG2	1:B:728:ARG:HH11	1.83	0.44
1:C:775:THR:O	1:C:778:GLN:N	2.50	0.44
2:D:6:ARG:NH1	2:D:62:PRO:HB3	2.33	0.44
2:D:98:ALA:O	2:D:100:LYS:HD2	2.17	0.44
1:A:730:GLU:CG	3:A:179:HOH:O	2.65	0.44
1:B:573:THR:O	1:B:574:LYS:HB2	2.17	0.44
2:D:60:GLU:HG3	2:D:64:LYS:CD	2.45	0.44
1:A:516:ARG:NH1	1:A:516:ARG:CG	2.69	0.44
1:C:573:THR:O	1:C:574:LYS:HB2	2.17	0.44
1:C:744:PHE:HA	1:C:747:LEU:CB	2.47	0.44
1:C:784:GLN:HE22	1:C:789:THR:HA	1.80	0.44
2:D:78:ASN:ND2	2:D:116:GLN:H	2.14	0.44
1:A:684:ASN:H	1:A:684:ASN:ND2	2.13	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:747:LEU:HD13	1:A:747:LEU:O	2.16	0.44
1:B:833:GLU:OE2	1:B:833:GLU:N	2.51	0.44
1:C:675:GLU:HG3	1:C:676:ASN:OD1	2.18	0.44
1:A:497:ASN:N	1:A:497:ASN:ND2	2.65	0.44
1:A:698:ILE:HG13	3:A:162:HOH:O	2.18	0.44
1:B:634:VAL:CG2	3:B:53:HOH:O	2.63	0.44
1:C:718:THR:CG2	1:C:723:LEU:HD21	2.45	0.44
2:D:60:GLU:HG3	2:D:64:LYS:NZ	2.33	0.44
1:B:505:ARG:HG2	1:B:512:ASP:OD1	2.17	0.44
1:C:502:LEU:HD23	1:C:502:LEU:HA	1.81	0.44
2:D:105:ILE:HD12	2:D:105:ILE:N	2.32	0.44
1:A:498:PRO:O	1:A:499:TYR:HB2	2.17	0.44
1:B:583:PHE:CZ	1:B:584:GLU:HG2	2.53	0.44
1:C:738:GLY:O	1:C:791:ARG:HD3	2.18	0.44
1:C:744:PHE:C	1:C:745:GLN:O	2.48	0.44
1:A:509:ILE:HD11	1:A:554:LEU:HD13	2.00	0.44
1:A:679:LYS:O	1:A:680:ILE:C	2.60	0.44
1:A:744:PHE:HA	1:A:747:LEU:CB	2.47	0.44
1:C:656:THR:HB	1:C:677:GLY:O	2.17	0.44
1:C:765:ARG:O	1:C:769:GLU:HG3	2.18	0.44
2:D:23:ARG:HD2	2:D:23:ARG:C	2.41	0.44
2:D:38:LEU:HD23	2:D:52:ARG:CA	2.48	0.44
2:D:105:ILE:CG2	2:D:106:GLN:N	2.77	0.44
1:A:530:LYS:NZ	3:A:285:HOH:O	2.43	0.44
1:A:811:THR:HG23	3:A:6:HOH:O	2.18	0.44
1:B:706:GLN:N	1:B:706:GLN:OE1	2.51	0.44
1:C:679:LYS:C	1:C:679:LYS:CD	2.88	0.44
1:B:635:LEU:HA	3:B:67:HOH:O	2.18	0.43
1:A:719:ASN:O	1:A:720:GLU:HB2	2.17	0.43
1:B:570:ASP:OD2	1:B:572:SER:HB3	2.17	0.43
1:B:715:HIS:CE1	1:B:719:ASN:HA	2.53	0.43
1:B:748:GLU:HA	1:B:768:TRP:CZ2	2.52	0.43
1:B:839:LEU:C	1:B:839:LEU:CD2	2.91	0.43
1:C:796:GLY:O	1:C:798:GLY:N	2.52	0.43
2:D:49:GLY:O	2:D:51:PHE:CE1	2.71	0.43
1:A:603:ASN:OD1	1:A:794:VAL:HB	2.18	0.43
1:A:714:PHE:CE1	3:A:320:HOH:O	2.56	0.43
1:B:511:ASP:OD1	1:B:511:ASP:N	2.36	0.43
1:C:767:PHE:CZ	1:C:771:VAL:HG21	2.53	0.43
2:D:38:LEU:HA	2:D:51:PHE:O	2.18	0.43
1:A:775:THR:O	1:A:776:ASP:C	2.61	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:514:LEU:O	1:B:518:GLU:HB2	2.18	0.43
1:C:742:LEU:HD11	1:C:780:ARG:HH12	1.80	0.43
2:D:75:TYR:CZ	2:D:125:LEU:HD22	2.54	0.43
2:D:105:ILE:HD12	2:D:105:ILE:H	1.82	0.43
1:A:626:ARG:NH1	3:A:124:HOH:O	2.51	0.43
1:A:730:GLU:OE1	1:A:730:GLU:N	2.45	0.43
1:A:767:PHE:HB2	1:A:835:LEU:HD11	2.01	0.43
1:C:677:GLY:O	1:C:678:ASP:C	2.60	0.43
2:D:6:ARG:HH21	2:D:100:LYS:HA	1.83	0.43
2:D:111:LEU:HD13	2:D:116:GLN:HG2	2.00	0.43
1:A:794:VAL:CG2	1:B:728:ARG:NH2	2.78	0.43
2:D:108:LEU:O	2:D:112:VAL:HG23	2.19	0.43
1:A:718:THR:HG21	1:A:723:LEU:HD21	2.00	0.43
1:A:744:PHE:H	1:A:797:LEU:HD12	1.84	0.43
1:B:677:GLY:O	1:B:678:ASP:C	2.61	0.43
1:B:841:LYS:HA	1:B:844:THR:CG2	2.49	0.43
2:D:23:ARG:C	2:D:23:ARG:CD	2.92	0.43
2:D:48:LYS:HA	2:D:48:LYS:HD3	1.81	0.43
1:A:706:GLN:OE1	1:A:706:GLN:N	2.32	0.43
2:D:117:PRO:O	2:D:118:GLU:C	2.62	0.43
1:A:654:MET:HA	3:A:323:HOH:O	2.18	0.43
1:A:809:PRO:O	1:A:811:THR:HG23	2.18	0.43
1:B:714:PHE:HB2	3:B:293:HOH:O	2.19	0.43
2:D:60:GLU:N	2:D:60:GLU:OE2	2.52	0.43
1:A:550:GLU:O	1:A:551:PHE:C	2.62	0.42
1:A:654:MET:HE2	2:D:5:ARG:NH2	2.34	0.42
1:A:727:PHE:HB2	1:A:728:ARG:HD3	2.00	0.42
1:B:753:TYR:CE2	1:B:764:ILE:HD12	2.53	0.42
1:A:628:LEU:HD23	1:A:699:LEU:HD21	2.01	0.42
1:C:749:GLU:C	1:C:751:THR:N	2.76	0.42
1:C:787:THR:CG2	1:C:822:ASN:OD1	2.58	0.42
1:A:723:LEU:C	1:A:724:LYS:O	2.60	0.42
1:B:715:HIS:O	1:B:719:ASN:HB2	2.18	0.42
2:D:53:ILE:HD11	2:D:70:PHE:CE1	2.54	0.42
2:D:122:ARG:CD	2:D:125:LEU:HG	2.48	0.42
1:A:499:TYR:CE2	1:A:531:GLN:NE2	2.88	0.42
1:A:771:VAL:HA	1:A:774:PHE:CE2	2.53	0.42
1:B:786:THR:O	1:B:819:THR:HA	2.19	0.42
2:D:85:VAL:HG12	2:D:86:CYS:N	2.35	0.42
1:A:708:LYS:HD3	3:A:109:HOH:O	2.20	0.42
1:C:723:LEU:H	1:C:723:LEU:CD2	2.30	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:38:LEU:HD23	2:D:52:ARG:N	2.35	0.42
2:D:58:PRO:O	2:D:61:TYR:N	2.51	0.42
1:A:668:PRO:HB3	2:D:59:ALA:CB	2.46	0.42
1:A:747:LEU:O	1:A:751:THR:OG1	2.36	0.42
1:B:723:LEU:H	1:B:723:LEU:CD2	2.27	0.42
1:B:787:THR:HG22	1:B:822:ASN:CG	2.43	0.42
1:C:514:LEU:O	1:C:518:GLU:HB2	2.20	0.42
2:D:135:LYS:O	2:D:135:LYS:CD	2.66	0.42
1:A:728:ARG:HH11	1:A:728:ARG:HG2	1.84	0.42
1:B:735:LEU:HD11	1:C:727:PHE:CE2	2.55	0.42
1:C:562:PRO:O	1:C:563:ASP:C	2.63	0.42
2:D:70:PHE:CD2	2:D:79:ILE:HD13	2.55	0.42
1:A:686:ASN:OD1	1:A:686:ASN:C	2.63	0.42
1:B:590:THR:OG1	1:B:712:ARG:NH2	2.52	0.42
1:B:697:TYR:O	1:B:698:ILE:HG12	2.19	0.42
1:B:778:GLN:O	1:B:781:LEU:N	2.52	0.42
1:B:715:HIS:HA	1:B:718:THR:HB	2.02	0.41
1:C:649:VAL:CB	1:C:684:ASN:ND2	2.83	0.41
1:A:562:PRO:O	1:A:565:GLY:N	2.49	0.41
1:A:566:MET:CE	1:A:588:GLN:HB3	2.50	0.41
1:A:596:LEU:HG	1:A:736:ILE:HD13	2.02	0.41
1:A:747:LEU:HD13	1:A:747:LEU:C	2.46	0.41
1:A:748:GLU:C	1:A:749:GLU:O	2.58	0.41
1:B:534:VAL:HB	1:B:547:VAL:HG12	2.01	0.41
1:B:723:LEU:O	1:B:726:LEU:CB	2.62	0.41
1:B:735:LEU:CD2	1:C:728:ARG:NH2	2.83	0.41
1:A:841:LYS:HA	1:A:844:THR:CG2	2.50	0.41
1:A:844:THR:HB	3:A:129:HOH:O	2.19	0.41
1:B:505:ARG:HH12	1:B:508:HIS:CG	2.38	0.41
1:B:583:PHE:CE1	1:B:584:GLU:HG2	2.55	0.41
1:B:804:ILE:HG23	1:B:824:LEU:HD12	2.01	0.41
1:C:726:LEU:HD22	1:C:731:GLU:OE1	2.19	0.41
1:A:767:PHE:CD1	1:A:767:PHE:C	2.98	0.41
1:A:792:ALA:HA	1:A:793:PRO:HD3	1.79	0.41
1:B:499:TYR:HA	1:B:531:GLN:O	2.20	0.41
1:A:638:SER:HB3	2:D:63:PHE:HD1	1.85	0.41
1:B:518:GLU:OE1	1:B:716:MET:HE1	2.21	0.41
1:B:559:ILE:HG21	1:B:592:ILE:HD13	2.03	0.41
1:B:649:VAL:HG12	1:B:650:GLU:N	2.35	0.41
1:B:742:LEU:O	1:B:743:ASP:C	2.63	0.41
1:B:792:ALA:HA	1:B:793:PRO:HD3	1.75	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:505:ARG:HH12	1:B:508:HIS:CD2	2.38	0.41
1:B:684:ASN:N	1:B:684:ASN:ND2	2.65	0.41
1:B:686:ASN:C	1:B:686:ASN:HD22	2.26	0.41
1:C:543:ASP:CG	1:C:547:VAL:HB	2.45	0.41
1:C:761:SER:N	3:C:69:HOH:O	2.53	0.41
2:D:60:GLU:HG3	2:D:64:LYS:CE	2.51	0.41
1:C:757:TYR:O	1:C:761:SER:HB2	2.19	0.41
1:C:814:LEU:HD21	1:C:838:ARG:CZ	2.50	0.41
2:D:65:PRO:HA	2:D:66:PRO:HD3	1.82	0.41
2:D:70:PHE:CE2	2:D:79:ILE:CD1	3.03	0.41
1:A:501:ARG:NH1	1:A:535:GLU:OE2	2.53	0.41
1:A:672:ASP:HB3	1:A:674:LYS:O	2.21	0.41
1:B:505:ARG:NH1	1:B:508:HIS:CG	2.89	0.41
1:B:516:ARG:HH11	1:B:516:ARG:CG	2.30	0.41
1:B:527:ASP:C	1:B:529:LYS:H	2.28	0.41
1:C:640:LYS:NZ	1:C:644:GLU:OE1	2.52	0.41
1:A:499:TYR:CD2	1:A:499:TYR:N	2.86	0.41
1:A:617:LYS:NZ	3:A:240:HOH:O	2.39	0.41
1:A:728:ARG:NH2	1:C:794:VAL:CG2	2.84	0.41
1:A:767:PHE:CE1	1:A:771:VAL:HG21	2.55	0.41
1:A:789:THR:OG1	1:A:790:ASP:N	2.53	0.41
1:B:561:ASN:OD1	1:B:563:ASP:HB2	2.20	0.41
1:B:674:LYS:HE2	3:B:29:HOH:O	2.19	0.41
1:B:763:LEU:HD22	1:B:835:LEU:HD12	2.03	0.41
1:C:497:ASN:ND2	1:C:497:ASN:C	2.77	0.41
1:C:500:LEU:C	1:C:500:LEU:CD2	2.94	0.41
1:C:507:ASP:O	1:C:508:HIS:CG	2.74	0.41
2:D:7:LEU:HD22	2:D:57:PHE:CZ	2.55	0.41
2:D:58:PRO:O	2:D:59:ALA:C	2.63	0.41
1:A:774:PHE:HE1	1:A:840:LEU:HD21	1.86	0.41
1:A:836:LYS:O	1:A:840:LEU:HG	2.21	0.41
1:A:742:LEU:HA	1:A:797:LEU:HD11	2.02	0.40
1:C:626:ARG:NE	3:C:15:HOH:O	2.46	0.40
1:A:762:VAL:O	1:A:766:GLU:HG3	2.22	0.40
1:B:679:LYS:O	1:B:681:PRO:CD	2.69	0.40
1:B:737:CYS:O	1:B:791:ARG:HD2	2.21	0.40
1:C:523:GLU:O	1:C:524:ASN:C	2.63	0.40
1:A:525:PRO:O	1:A:526:ALA:C	2.64	0.40
1:A:531:GLN:OE1	1:B:626:ARG:HD2	2.20	0.40
1:B:611:PRO:HG2	3:B:269:HOH:O	2.22	0.40
1:B:707:PHE:O	1:B:710:PHE:HB3	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:502:LEU:HD23	1:C:516:ARG:HG2	2.04	0.40
1:C:728:ARG:HA	1:C:729:PRO:HD3	1.86	0.40
1:A:582:SER:OG	1:A:585:THR:OG1	2.38	0.40
1:B:516:ARG:NH1	1:B:516:ARG:CG	2.83	0.40
1:B:527:ASP:C	1:B:529:LYS:N	2.79	0.40
1:C:777:GLU:O	1:C:781:LEU:HG	2.21	0.40
2:D:45:PRO:HB3	2:D:137:CYS:HA	2.02	0.40
1:A:668:PRO:HG3	2:D:33:LEU:CD1	2.52	0.40
1:A:786:THR:O	1:A:819:THR:HG22	2.21	0.40
1:B:510:ILE:HG23	1:B:591:LEU:HD23	2.04	0.40
1:B:786:THR:O	1:B:819:THR:HG22	2.22	0.40

All (31) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:813:ARG:NH1	1:C:762:VAL:CG1[3_656]	0.85	1.35
1:B:660:SER:OG	1:C:523:GLU:OE1[4_456]	0.89	1.31
1:B:813:ARG:NH2	1:C:762:VAL:CG2[3_656]	0.98	1.22
1:B:813:ARG:NH1	1:C:762:VAL:CB[3_656]	1.10	1.10
1:B:813:ARG:CZ	1:C:762:VAL:CB[3_656]	1.15	1.05
1:B:652:ASP:O	1:C:712:ARG:NH1[4_456]	1.22	0.98
1:B:813:ARG:CZ	1:C:762:VAL:CG2[3_656]	1.36	0.84
1:A:651:ASP:OD2	1:C:705:LYS:NZ[3_746]	1.47	0.73
1:A:508:HIS:NE2	1:C:818:HIS:NE2[2_654]	1.60	0.60
1:B:660:SER:OG	1:C:523:GLU:CD[4_456]	1.70	0.50
1:B:654:MET:CB	1:C:518:GLU:CG[4_456]	1.79	0.41
1:B:813:ARG:CZ	1:C:762:VAL:CG1[3_656]	1.79	0.41
1:B:654:MET:CA	1:C:518:GLU:CG[4_456]	1.83	0.37
1:B:660:SER:O	1:C:523:GLU:OE2[4_456]	1.84	0.36
1:B:654:MET:N	1:C:518:GLU:CD[4_456]	1.87	0.33
1:A:679:LYS:CE	1:C:669:MET:CE[3_746]	1.89	0.31
1:A:518:GLU:OE2	1:C:811:THR:CG2[2_654]	1.91	0.29
1:B:654:MET:N	1:C:518:GLU:OE2[4_456]	1.91	0.29
1:B:655:ILE:CD1	1:C:522:MET:CE[4_456]	1.92	0.28
1:B:813:ARG:NH2	1:C:762:VAL:CB[3_656]	1.93	0.27
1:B:654:MET:N	1:C:518:GLU:CG[4_456]	1.94	0.26
1:A:679:LYS:CG	1:C:669:MET:CE[3_746]	2.01	0.19
1:A:518:GLU:OE1	1:C:811:THR:CG2[2_654]	2.05	0.15
1:B:660:SER:C	1:C:523:GLU:OE2[4_456]	2.09	0.11

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:813:ARG:NE	1:C:762:VAL:CB[3_656]	2.09	0.11
1:A:508:HIS:NE2	1:C:818:HIS:CE1[2_654]	2.11	0.09
1:B:813:ARG:NE	1:C:762:VAL:CG2[3_656]	2.11	0.09
1:A:518:GLU:CD	1:C:811:THR:CG2[2_654]	2.14	0.06
1:B:654:MET:C	1:C:518:GLU:CG[4_456]	2.14	0.06
1:A:584:GLU:OE1	1:C:838:ARG:NH1[2_654]	2.16	0.04
1:B:694:TYR:OH	3:C:97:HOH:O[4_456]	2.19	0.01

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	348/358 (97%)	306 (88%)	32 (9%)	10 (3%)	3	6
1	B	348/358 (97%)	305 (88%)	32 (9%)	11 (3%)	3	5
1	C	348/358 (97%)	309 (89%)	26 (8%)	13 (4%)	2	3
2	D	142/154 (92%)	91 (64%)	32 (22%)	19 (13%)	0	0
All	All	1186/1228 (97%)	1011 (85%)	122 (10%)	53 (4%)	2	2

All (53) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	508	HIS
1	A	698	ILE
1	A	776	ASP
1	B	508	HIS
1	B	675	GLU
1	B	698	ILE
1	B	776	ASP
1	C	508	HIS
1	C	675	GLU
1	C	698	ILE

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Mol	Chain	Res	Type
1	C	721	SER
1	C	758	THR
2	D	17	CYS
2	D	25	ILE
2	D	30	ALA
2	D	32	LEU
2	D	92	ALA
2	D	132	ASP
1	A	654	MET
1	A	664	LEU
1	A	675	GLU
1	B	719	ASN
1	B	720	GLU
1	C	647	GLY
1	C	750	THR
2	D	6	ARG
2	D	19	MET
2	D	124	ASP
1	A	727	PHE
1	A	750	THR
1	B	727	PHE
1	C	761	SER
1	C	797	LEU
2	D	5	ARG
2	D	21	ASN
2	D	43	ASN
2	D	44	PRO
2	D	94	ASN
1	B	501	ARG
2	D	49	GLY
2	D	78	ASN
2	D	101	THR
2	D	118	GLU
1	A	704	GLU
1	C	727	PHE
2	D	135	LYS
1	B	758	THR
1	C	501	ARG
1	A	647	GLY
1	B	649	VAL
1	B	722	PRO
1	C	524	ASN

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Mol	Chain	Res	Type
1	C	649	VAL

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	317/323 (98%)	296 (93%)	21 (7%)	15	34
1	B	317/323 (98%)	294 (93%)	23 (7%)	13	29
1	C	317/323 (98%)	294 (93%)	23 (7%)	13	29
2	D	108/138 (78%)	103 (95%)	5 (5%)	24	49
All	All	1059/1107 (96%)	987 (93%)	72 (7%)	14	32

All (72) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	500	LEU
1	A	516	ARG
1	A	592	ILE
1	A	596	LEU
1	A	613	VAL
1	A	635	LEU
1	A	642	LEU
1	A	654	MET
1	A	655	ILE
1	A	662	THR
1	A	663	ASP
1	A	678	ASP
1	A	684	ASN
1	A	685	GLU
1	A	699	LEU
1	A	706	GLN
1	A	723	LEU
1	A	728	ARG
1	A	789	THR
1	A	812	GLU

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Mol	Chain	Res	Type
1	A	826	LEU
1	B	502	LEU
1	B	511	ASP
1	B	529	LYS
1	B	557	GLU
1	B	581	SER
1	B	592	ILE
1	B	613	VAL
1	B	633	PRO
1	B	634	VAL
1	B	635	LEU
1	B	637	GLN
1	B	642	LEU
1	B	668	PRO
1	B	680	ILE
1	B	684	ASN
1	B	686	ASN
1	B	699	LEU
1	B	706	GLN
1	B	723	LEU
1	B	728	ARG
1	B	789	THR
1	B	812	GLU
1	B	835	LEU
1	C	500	LEU
1	C	502	LEU
1	C	511	ASP
1	C	514	LEU
1	C	582	SER
1	C	592	ILE
1	C	596	LEU
1	C	642	LEU
1	C	662	THR
1	C	664	LEU
1	C	684	ASN
1	C	685	GLU
1	C	699	LEU
1	C	706	GLN
1	C	723	LEU
1	C	728	ARG
1	C	747	LEU
1	C	789	THR

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Mol	Chain	Res	Type
1	C	809	PRO
1	C	812	GLU
1	C	826	LEU
1	C	833	GLU
1	C	835	LEU
2	D	57	PHE
2	D	60	GLU
2	D	102	ASP
2	D	129	TYR
2	D	133	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (25) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	531	GLN
1	A	602	ASN
1	A	658	GLN
1	A	661	GLN
1	A	684	ASN
1	B	531	GLN
1	B	553	GLN
1	B	602	ASN
1	B	684	ASN
1	B	686	ASN
1	B	715	HIS
1	B	772	HIS
1	B	784	GLN
1	C	497	ASN
1	C	531	GLN
1	C	602	ASN
1	C	684	ASN
1	C	715	HIS
1	C	719	ASN
1	C	784	GLN
1	C	818	HIS
2	D	26	GLN
2	D	36	GLN
2	D	76	HIS
2	D	78	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](#)

There are no ligands in this entry.

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.