



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 06:43 PM GMT

PDB ID : 1C4Z
Title : STRUCTURE OF E6AP: INSIGHTS INTO 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

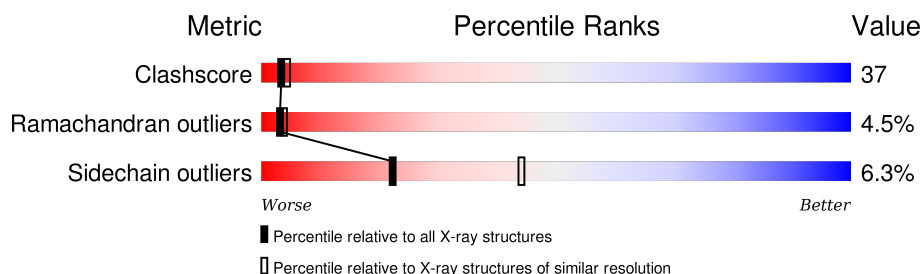
1 Overall quality at a glance

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	102246	2679 (2.60-2.60)
Ramachandran outliers	100387	2635 (2.60-2.60)
Sidechain outliers	100360	2635 (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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

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.

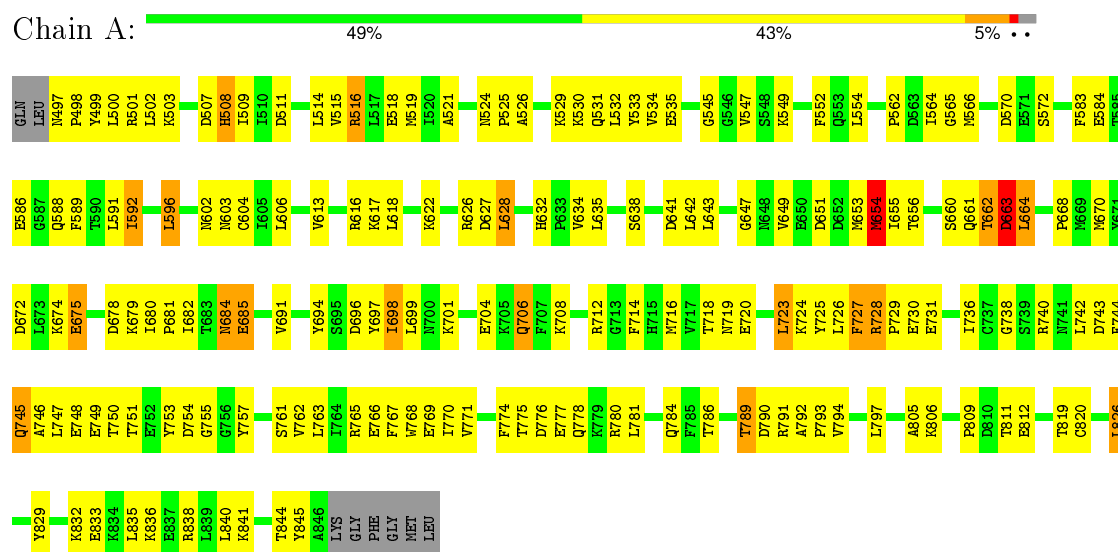
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	117	Total	O	0	0
			117	117		
3	B	99	Total	O	0	0
			99	99		
3	C	113	Total	O	0	0
			113	113		
3	D	30	Total	O	0	0
			30	30		

3 Residue-property plots

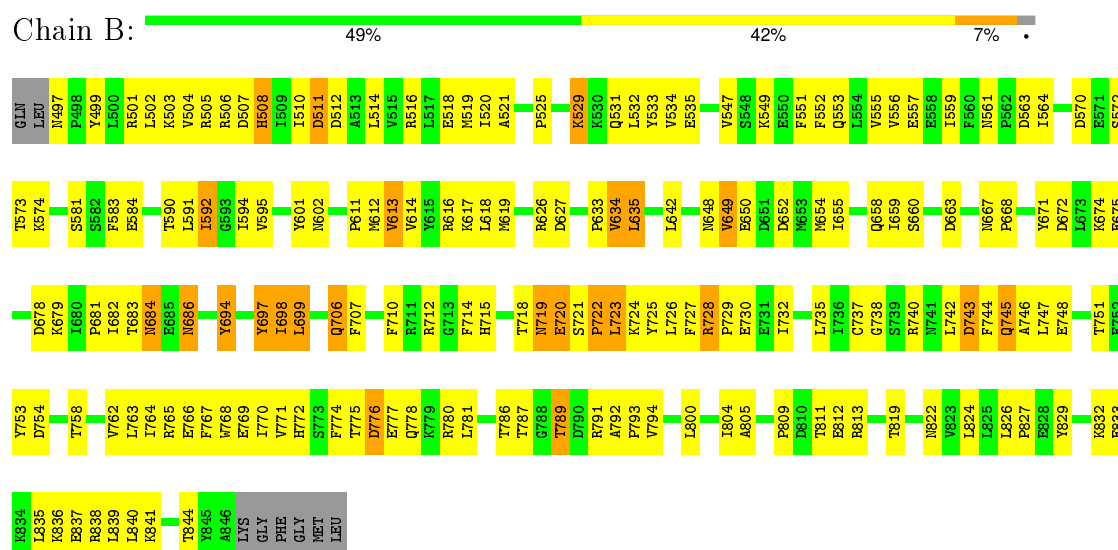
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

Note EDS was not executed.

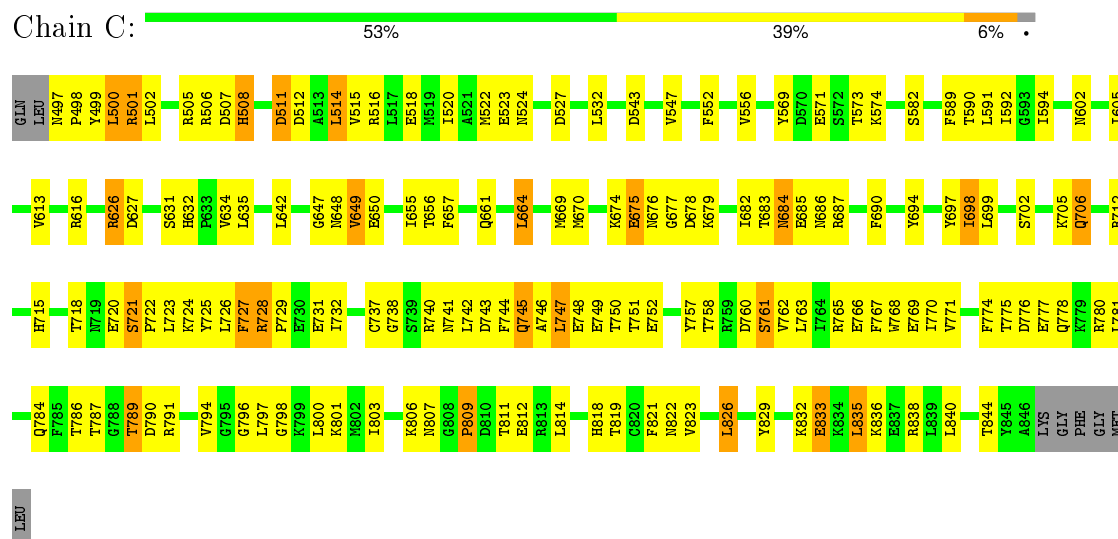
• Molecule 1: UBIQUITIN-PROTEIN LIGASE E3A



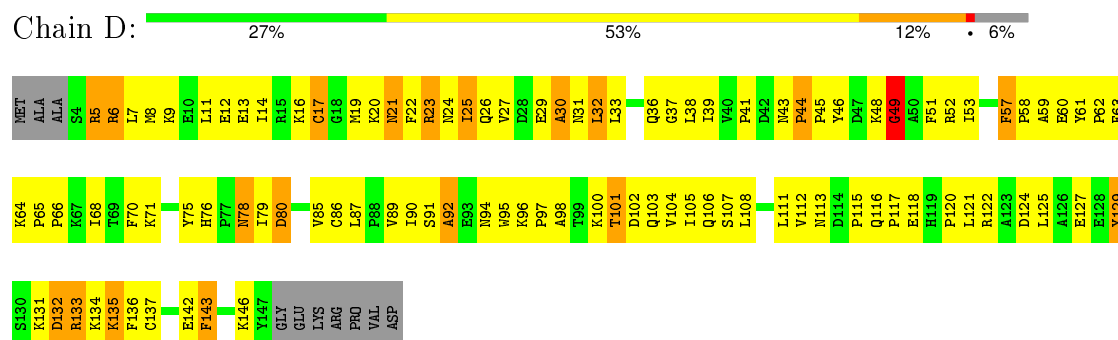
• Molecule 1: UBIQUITIN-PROTEIN LIGASE E3A



• Molecule 1: UBIQUITIN-PROTEIN LIGASE E3A



• Molecule 2: UBIQUITIN CONJUGATING ENZYME E2



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	103.40 Å 112.70 Å 123.80 Å 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	0.53	0/2923	0.81	5/3943 (0.1%)
1	B	0.52	0/2923	0.80	2/3943 (0.1%)
1	C	0.56	1/2923 (0.0%)	0.83	2/3943 (0.1%)
2	D	0.44	0/1127	0.81	2/1536 (0.1%)
All	All	0.53	1/9896 (0.0%)	0.81	11/13365 (0.1%)

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 (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	626	ARG	CD-NE	-5.69	1.36	1.46

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	745	GLN	N-CA-C	-8.83	87.16	111.00
1	B	745	GLN	N-CA-C	-8.48	88.10	111.00
1	A	745	GLN	N-CA-C	-8.19	88.88	111.00
1	C	626	ARG	NE-CZ-NH1	7.19	123.89	120.30
1	A	663	ASP	CA-C-N	-7.18	101.40	117.20
1	A	628	LEU	CA-CB-CG	5.77	128.57	115.30
1	A	663	ASP	O-C-N	5.62	131.68	122.70
2	D	49	GLY	N-CA-C	-5.52	99.29	113.10
1	A	663	ASP	C-N-CA	5.40	135.21	121.70
2	D	80	ASP	CB-CG-OD1	-5.32	113.52	118.30
1	B	697	TYR	N-CA-C	-5.12	97.18	111.00

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	224	9
1	B	2861	0	2827	206	22
1	C	2861	0	2827	179	30
2	D	1098	0	1063	155	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	712	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 37.

All (712) 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:HG2	1:A:516:ARG:HH11	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:HD22	1:A:684:ASN:N	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:B:718:THR:HG21	1:B:723:LEU:HD21	1.61	0.81
1:A:697:TYR:O	1:A:698:ILE:HB	1.81	0.81
1:A:532:LEU:H	1:A:602:ASN:HD21	1.26	0.81
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:H	1:A:723:LEU:HD22	1.47	0.80
1:A:740:ARG:HH12	1:C:746:ALA:HB2	1.43	0.80
2:D:117:PRO:O	2:D:120:PRO:HD3	1.82	0.79
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:44:PRO:HB2	2:D:45:PRO:HD2	1.64	0.79
1:C:742:LEU:HD11	1:C:780:ARG:NH1	1.97	0.79
1:C:697:TYR:O	1:C:698:ILE:HB	1.83	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
1:B:532:LEU:H	1:B:602:ASN:ND2	1.82	0.76
1:A:763:LEU:HD11	1:A:826:LEU:HD13	1.66	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
2:D:36:GLN:NE2	2:D:52:ARG:HD3	2.04	0.73
1:A:745:GLN:O	1:A:746:ALA:HB3	1.88	0.73
1:A:516:ARG:HG2	1:A:516:ARG:NH1	1.98	0.73
1:C:745:GLN:O	1:C:746:ALA:HB3	1.89	0.73
1:C:718:THR:HG21	1:C:723:LEU:HD21	1.71	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
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
2:D:76:HIS:CE1	2:D:115:PRO:HG3	2.25	0.72
1:B:533:TYR:HA	1:C:626:ARG:NH2	2.05	0.72
2:D:36:GLN:CD	2:D:52:ARG:HD3	2.11	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
2:D:105:ILE:HG22	2:D:106:GLN:N	2.06	0.70
1:B:618:LEU:HD21	3:B:293:HOH:O	1.91	0.70
1:C:655:ILE:HG13	1:C:682:ILE:HD12	1.74	0.70
1:C:613:VAL:HG22	1:C:627:ASP:HB3	1.72	0.70
1:B:839:LEU:O	1:B:839:LEU:HD23	1.92	0.70
1:C:723:LEU:HD22	1:C:723:LEU:H	1.56	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:745:GLN:O	1:B:746:ALA:HB3	1.91	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:618:LEU:HD13	3:A:320:HOH:O	1.92	0.70
1:A:589:PHE:O	1:A:592:ILE:HD12	1.91	0.70
1:C:748:GLU:HA	1:C:768:TRP:CH2	2.26	0.70
1:C:723:LEU:HA	1:C:726:LEU:HD12	1.74	0.69
1:B:724:LYS:O	1:B:725:TYR:HB2	1.92	0.69
1:A:531:GLN:CD	1:B:626:ARG:HD2	2.11	0.69
1:A:586:GLU:HG2	3:A:275:HOH:O	1.91	0.69
1:B:723:LEU:H	1:B:723:LEU:HD22	1.54	0.69
1:A:661:GLN:OE1	3:A:225:HOH:O	2.09	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:91:SER:O	2:D:92:ALA:O	2.11	0.68
2:D:39:ILE:O	2:D:41:PRO:HD3	1.94	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:653:MET:HE2	2:D:97:PRO:HB2	1.77	0.67
1:C:721:SER:H	1:C:722:PRO:HD3	1.59	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:B:794:VAL:HG21	1:C:728:ARG:CZ	2.24	0.67
1:C:613:VAL:CG2	1:C:627:ASP:HB3	2.23	0.67
2:D:133:ARG:NH1	2:D:133:ARG:HB2	2.08	0.67
1:C:684:ASN:N	1:C:684:ASN:HD22	1.92	0.67
1:C:724:LYS:O	1:C:725:TYR:HB2	1.95	0.67
1:C:763:LEU:HD11	1:C:826:LEU:HD13	1.77	0.67
2:D:80:ASP:CG	2:D:121:LEU:HG	2.12	0.66
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
2:D:133:ARG:HG3	2:D:133:ARG:O	1.95	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:744:PHE:HA	1:A:747:LEU:HB3	1.78	0.66
1:A:514:LEU:HD21	1:A:591:LEU:HB2	1.78	0.66
2:D:133:ARG:HH11	2:D:133:ARG:HB2	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:C:766:GLU:OE2	1:C:832:LYS:HB2	1.96	0.65
1:B:533:TYR:HA	1:C:626:ARG:HH22	1.60	0.65
2:D:134:LYS:C	2:D:136:PHE:H	1.99	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: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:B:516:ARG:HD2	1:B:519:MET:HE3	1.77	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:C:497:ASN:HD22	1:C:498:PRO:CD	2.10	0.63
1:A:728:ARG:NH1	1:C:794:VAL:HG21	2.14	0.63
1:A:524:ASN:OD1	1:A:526:ALA:HB3	1.97	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
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:H	1:B:684:ASN:HD22	1.46	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:A:507:ASP:O	1:A:508:HIS:ND1	2.32	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
2:D:23:ARG:NH1	2:D:25:ILE:HG22	2.14	0.62
1:C:655:ILE:CG1	1:C:682:ILE:HD12	2.28	0.62
1:A:503:LYS:H	1:A:516:ARG:HH12	1.43	0.62
1:B:684:ASN:N	1:B:684:ASN:HD22	1.97	0.62
1:C:679:LYS:HD3	1:C:679:LYS:C	2.20	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:511:ASP:O	1:A:515:VAL:HG23	2.00	0.62
1:B:590:THR:O	1:B:594:ILE:HG13	1.98	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:C:590:THR:O	1:C:594:ILE:HG13	2.00	0.61
1:B:529:LYS:HG3	1:B:601:TYR:CE2	2.35	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:C:697:TYR:O	1:C:698:ILE:CB	2.49	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:B:697:TYR:O	1:B:698:ILE:HB	2.01	0.60
1:A:502:LEU:CA	1:A:516:ARG:HH12	2.14	0.60
1:C:591:LEU:HD21	3:C:214:HOH:O	2.02	0.60
1:C:497:ASN:HD21	1:C:499:TYR:H	1.50	0.60
1:C:505:ARG:NH1	1:C:508:HIS:CG	2.69	0.60
1:A:684:ASN:HB2	1:A:685:GLU:OE1	2.01	0.60
2:D:7:LEU:HD13	2:D:32:LEU:O	2.02	0.60
1:A:728:ARG:H	1:A:728:ARG:HD3	1.67	0.60
1:B:764:ILE:O	1:B:767:PHE:HB3	2.02	0.59
2:D:78:ASN:HD21	2:D:116:GLN:H	1.50	0.59
1:B:771:VAL:O	1:B:774:PHE:HB2	2.01	0.59
1:A:746:ALA:HB2	1:B:740:ARG:HH12	1.67	0.59
1:A:719:ASN:OD1	1:A:720:GLU:HG3	2.01	0.59
1:C:675:GLU:HB3	3:C:341:HOH:O	2.01	0.59
1:C:670:MET:HE2	1:C:670:MET:HA	1.84	0.59
1:B:723:LEU:HD22	1:B:723:LEU:N	2.17	0.59
1:A:570:ASP:OD2	1:A:572:SER:HB3	2.03	0.59
1:A:770:ILE:HD13	1:A:836:LYS:HB2	1.84	0.59
1:A:723:LEU:HD22	1:A:723:LEU:N	2.16	0.59
1:A:778:GLN:HA	1:A:781:LEU:HD12	1.85	0.59
1:A:534:VAL:HB	1:A:547:VAL:HG12	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:741:ASN:HB2	3:C:23:HOH:O	2.02	0.59
1:A:675:GLU:HB3	3:A:163:HOH:O	2.02	0.59
1:C:505:ARG:HH12	1:C:508:HIS:CG	2.21	0.59
1:B:837:GLU:OE1	1:B:838:ARG:NH2	2.36	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:A:516:ARG:CG	1:A:516:ARG:HH11	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
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:841:LYS:HA	1:B:844:THR:HG22	1.85	0.58
1:B:649:VAL:H	1:B:684:ASN:HD21	1.52	0.58
1:A:532:LEU:H	1:A:602:ASN:ND2	2.00	0.58
1:A:730:GLU:HG2	3:A:179:HOH:O	2.04	0.58
1:A:712:ARG:O	1:A:716:MET:HG3	2.04	0.58
1:B:697:TYR:O	1:B:698:ILE:CB	2.52	0.57
1:B:506:ARG:O	1:B:507:ASP:HB2	2.04	0.57
1:C:786:THR:O	1:C:819:THR:HA	2.04	0.57
2:D:105:ILE:O	2:D:107:SER:N	2.36	0.57
2:D:25:ILE:HG13	2:D:26:GLN:N	2.19	0.57
1:B:748:GLU:HA	1:B:768:TRP:CH2	2.40	0.57
1:B:507:ASP:O	1:B:508:HIS:HB2	2.03	0.57
1:B:658:GLN:HG3	1:B:672:ASP:OD2	2.04	0.57
1:B:518:GLU:HA	1:B:518:GLU:OE1	2.04	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
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:C:520:ILE:O	1:C:523:GLU:O	2.22	0.56
1:A:835:LEU:HD23	1:A:835:LEU:C	2.26	0.56
1:C:648:ASN:HB2	3:C:94:HOH:O	2.04	0.56
1:A:674:LYS:HD3	1:A:680:ILE:HD13	1.88	0.56
1:A:584:GLU:N	3:A:258:HOH:O	2.38	0.56
1:B:655:ILE:CG1	1:B:682:ILE:HD12	2.36	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:583:PHE:CE1	1:A:584:GLU:HG2	2.40	0.56
1:A:706:GLN:H	1:A:706:GLN:CD	2.02	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:748:GLU:HG3	1:C:768:TRP:CE2	2.40	0.56
1:A:749:GLU:C	1:A:751:THR:H	2.09	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: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: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:684:ASN:N	1:A:684:ASN:ND2	2.45	0.55
1:A:806:LYS:HE2	3:A:111:HOH:O	2.06	0.55
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
1:C:723:LEU:O	1:C:726:LEU:CB	2.52	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:A:743:ASP:O	1:A:745:GLN:N	2.35	0.54
1:A:643:LEU:HD21	1:A:691:VAL:HG21	1.90	0.54
1:C:724:LYS:O	1:C:725:TYR:CB	2.55	0.54
1:C:706:GLN:H	1:C:706:GLN:CD	2.11	0.54
1:B:745:GLN:O	1:B:746:ALA:CB	2.56	0.54
1:A:724:LYS:O	1:A:725:TYR:CB	2.56	0.54
1:C:569:TYR:CZ	1:C:574:LYS:HA	2.43	0.54
1:C:506:ARG:O	1:C:507:ASP:CB	2.56	0.54
1:B:507:ASP:O	1:B:508:HIS:ND1	2.41	0.54
2:D:14:ILE:C	2:D:16:LYS:H	2.12	0.53
1:A:503:LYS:N	1:A:516:ARG:HH12	2.03	0.53
1:B:619:MET:HE3	1:B:726:LEU:O	2.07	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:723:LEU:HB3	1:C:732:ILE:HD11	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:616:ARG:HG2	1:C:729:PRO:HG2	1.91	0.53
2:D:24:ASN:O	2:D:25:ILE:HB	2.08	0.53
1:A:531:GLN:CD	1:B:626:ARG:NH1	2.62	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
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
2:D:39:ILE:HD13	2:D:53:ILE:HD11	1.90	0.53
1:B:789:THR:HG23	3:B:306:HOH:O	2.09	0.53
2:D:120:PRO:C	2:D:122:ARG:H	2.12	0.52
1:C:505:ARG:NH1	1:C:508:HIS:ND1	2.57	0.52
1:B:648:ASN:OD1	1:B:649:VAL:O	2.27	0.52
2:D:78:ASN:HD21	2:D:116:GLN:N	2.07	0.52
2:D:103:GLN:HB3	3:D:160:HOH:O	2.09	0.52
1:B:535:GLU:HA	3:B:317:HOH:O	2.09	0.52
2:D:80:ASP:OD1	2:D:121:LEU:CG	2.37	0.52
1:A:766:GLU:O	1:A:770:ILE:HG13	2.08	0.52
1:A:746:ALA:HB2	1:B:740:ARG:NH1	2.23	0.52
1:A:589:PHE:O	1:A:592:ILE:CD1	2.58	0.52
1:B:744:PHE:HA	1:B:747:LEU:HB3	1.92	0.52
1:B:516:ARG:HD2	1:B:519:MET:CE	2.39	0.52
1:A:529:LYS:HE2	1:A:720:GLU:OE2	2.09	0.52
1:A:740:ARG:NH1	1:C:746:ALA:CB	2.64	0.52
1:A:728:ARG:NH2	1:C:794:VAL:HG21	2.24	0.52
2:D:89:VAL:HG13	2:D:90:ILE:HG23	1.91	0.52
2:D:48:LYS:HA	3:D:159:HOH:O	2.09	0.52
1:A:694:TYR:O	1:A:697:TYR:O	2.28	0.52
1:A:663:ASP:HB3	1:A:664:LEU:HD12	1.92	0.52
1:B:837:GLU:OE2	1:B:838:ARG:NE	2.43	0.52
2:D:129:TYR:C	2:D:129:TYR:CD1	2.83	0.52
1:C:840:LEU:O	1:C:844:THR:HG22	2.10	0.52
1:C:721:SER:N	1:C:722:PRO:CD	2.61	0.52
1:A:763:LEU:HD13	1:A:763:LEU:O	2.10	0.52
1:C:760:ASP:O	1:C:761:SER:HB2	2.09	0.52
1:A:653:MET:HE1	2:D:98:ALA:N	2.25	0.51
1:C:728:ARG:H	1:C:728:ARG:HD3	1.75	0.51
1:B:738:GLY:O	1:B:791:ARG:HD3	2.10	0.51
1:A:530:LYS:NZ	3:A:285:HOH:O	2.43	0.51
1:C:745:GLN:HB3	3:C:263:HOH:O	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:97:PRO:HG2	3:D:155:HOH:O	2.10	0.51
1:B:663:ASP:OD2	1:B:667:ASN:OD1	2.28	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:A:653:MET:CE	2:D:97:PRO:HB2	2.40	0.51
1:C:500:LEU:HG	1:C:527:ASP:O	2.11	0.51
1:C:720:GLU:O	1:C:721:SER:HB3	2.11	0.51
1:B:840:LEU:O	1:B:844:THR:HG22	2.11	0.51
1:B:827:PRO:HB2	1:B:829:TYR:CE1	2.46	0.51
1:B:681:PRO:HD2	3:B:290:HOH:O	2.11	0.51
1:A:838:ARG:HA	1:A:838:ARG:HE	1.75	0.51
1:A:841:LYS:HA	1:A:844:THR:HG22	1.93	0.51
1:B:694:TYR:O	1:B:694:TYR:HD2	1.94	0.51
1:B:614:VAL:N	3:B:269:HOH:O	2.44	0.50
1:B:748:GLU:OE1	1:B:772:HIS:CE1	2.64	0.50
1:A:549:LYS:HD3	1:A:820:CYS:HA	1.93	0.50
1:B:613:VAL:HG22	1:B:627:ASP:HB3	1.93	0.50
1:B:735:LEU:HD23	1:C:728:ARG:HH22	1.75	0.50
1:B:634:VAL:HG22	3:B:53:HOH:O	2.11	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:C:723:LEU:HD22	1:C:723:LEU:N	2.23	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:A:838:ARG:NH2	1:A:841:LYS:HD2	2.26	0.50
1:A:833:GLU:N	1:A:833:GLU:OE2	2.43	0.50
2:D:87:LEU:HD23	2:D:87:LEU:H	1.77	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
1:A:681:PRO:HD2	3:A:326:HOH:O	2.11	0.50
2:D:25:ILE:CG1	2:D:26:GLN:N	2.75	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:749:GLU:O	1:A:751:THR:N	2.45	0.50
2:D:108:LEU:C	2:D:108:LEU:HD23	2.33	0.50
2:D:75:TYR:CD2	2:D:143:PHE:HD1	2.30	0.49
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
1:B:617:LYS:HB3	1:B:707:PHE:CZ	2.46	0.49
2:D:31:ASN:O	2:D:33:LEU:N	2.43	0.49
1:A:662:THR:HG23	2:D:59:ALA:HB2	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
2:D:101:THR:HA	2:D:104:VAL:CG2	2.38	0.49
2:D:11:LEU:HD11	2:D:26:GLN:NE2	2.27	0.49
1:A:771:VAL:O	1:A:774:PHE:HB2	2.13	0.49
1:A:738:GLY:O	1:A:791:ARG:HD3	2.12	0.49
1:A:841:LYS:O	1:A:845:TYR:HB2	2.13	0.49
1:C:631:SER:C	1:C:632:HIS:ND1	2.66	0.49
1:A:622:LYS:HB2	1:C:498:PRO:HG3	1.93	0.49
1:C:670:MET:CE	1:C:670:MET:HA	2.42	0.49
1:A:656:THR:O	1:A:682:ILE:HD11	2.13	0.49
1:C:722:PRO:HB2	1:C:724:LYS:H	1.77	0.49
1:B:722:PRO:C	3:B:174:HOH:O	2.52	0.49
1:A:726:LEU:HD22	1:A:731:GLU:OE1	2.13	0.49
1:C:807:ASN:HA	3:C:343:HOH:O	2.13	0.49
1:C:635:LEU:HD23	1:C:635:LEU:O	2.13	0.49
2:D:38:LEU:HD23	2:D:51:PHE:C	2.33	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:748:GLU:HA	1:C:768:TRP:CZ2	2.47	0.48
1:C:634:VAL:HG11	3:C:177:HOH:O	2.12	0.48
1:C:744:PHE:HA	1:C:747:LEU:HB3	1.94	0.48
2:D:14:ILE:C	2:D:16:LYS:N	2.67	0.48
1:A:507:ASP:O	1:A:508:HIS:HB2	2.13	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:A:564:ILE:HG12	1:A:564:ILE:O	2.14	0.48
1:C:745:GLN:O	1:C:746:ALA:CB	2.54	0.48
2:D:104:VAL:C	2:D:105:ILE:O	2.45	0.48
2:D:44:PRO:HG3	2:D:113:ASN:HA	1.94	0.48
1:B:742:LEU:HD11	1:B:780:ARG:CZ	2.44	0.48
2:D:134:LYS:C	2:D:136:PHE:N	2.65	0.48
1:A:515:VAL:O	1:A:519:MET:HG3	2.13	0.48
1:A:570:ASP:C	1:A:570:ASP:OD2	2.52	0.48
1:C:737:CYS:O	1:C:791:ARG:HD2	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:C:649:VAL:H	1:C:684:ASN:ND2	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:555:VAL:HG11	1:B:595:VAL:HG21	1.94	0.48
1:B:838:ARG:HA	1:B:838:ARG:HE	1.77	0.48
1:A:655:ILE:HG13	1:A:682:ILE:HD12	1.96	0.48
1:A:497:ASN:HD22	1:A:497:ASN:N	2.12	0.48
2:D:57:PHE:HB3	2:D:66:PRO:CG	2.42	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
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:B:649:VAL:N	1:B:684:ASN:HD21	2.11	0.47
1:A:507:ASP:O	1:A:508:HIS:CB	2.62	0.47
2:D:25:ILE:CD1	2:D:26:GLN:H	2.27	0.47
1:B:679:LYS:O	1:B:681:PRO:HD3	2.13	0.47
2:D:142:GLU:O	2:D:146:LYS:HG2	2.14	0.47
1:A:766:GLU:CD	1:A:832:LYS:HB2	2.34	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
1:A:723:LEU:CD2	1:A:723:LEU:H	2.20	0.47
1:A:784:GLN:HG3	3:A:93:HOH:O	2.13	0.47
1:B:824:LEU:C	1:B:824:LEU:HD13	2.34	0.47
2:D:25:ILE:HD12	2:D:26:GLN:H	1.79	0.47
1:A:660:SER:HB3	1:A:670:MET:SD	2.55	0.47
1:A:552:PHE:HD2	1:A:604:CYS:HG	1.62	0.47
1:A:617:LYS:NZ	3:A:240:HOH:O	2.39	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: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
2:D:111:LEU:CD1	2:D:116:GLN:HG2	2.43	0.47
1:B:551:PHE:O	1:B:555:VAL:HG23	2.15	0.47
1:C:752:GLU:HB2	1:C:803:ILE:HG12	1.96	0.47
1:A:503:LYS:H	1:A:516:ARG:CZ	2.22	0.47
1:C:649:VAL:HB	1:C:684:ASN:ND2	2.30	0.47
1:B:754:ASP:HB3	1:B:805:ALA:HB2	1.96	0.47
1:A:533:TYR:HA	1:B:626:ARG:HH21	1.77	0.47
2:D:71:LYS:HE2	3:D:177:HOH:O	2.15	0.47
1:B:794:VAL:HG21	1:C:728:ARG:NH1	2.28	0.47
1:C:728:ARG:N	1:C:728:ARG:HD3	2.30	0.47
1:B:698:ILE:HG22	1:B:699:LEU:HD13	1.95	0.47
1:B:747:LEU:O	1:B:751:THR:OG1	2.33	0.47
2:D:103:GLN:O	2:D:105:ILE:O	2.33	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:685:GLU:N	1:A:685:GLU:OE1	2.48	0.47
1:B:723:LEU:HB3	1:B:732:ILE:HD11	1.97	0.47
1:C:763:LEU:CD1	1:C:826:LEU:HD13	2.43	0.47
2:D:25:ILE:CG1	2:D:26:GLN:H	2.27	0.46
1:C:589:PHE:CE2	1:C:706:GLN:HB2	2.50	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
2:D:44:PRO:HG2	3:D:162:HOH:O	2.15	0.46
2:D:7:LEU:HD11	2:D:33:LEU:HD23	1.97	0.46
1:B:516:ARG:HG2	1:B:516:ARG:NH1	2.30	0.46
1:C:657:PHE:HE1	1:C:686:ASN:ND2	2.13	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
2:D:133:ARG:HH11	2:D:133:ARG:CB	2.27	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
1:C:723:LEU:CA	1:C:726:LEU:HD12	2.44	0.46
1:C:749:GLU:C	1:C:751:THR:H	2.18	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:C:740:ARG:HB3	1:C:780:ARG:HH21	1.80	0.46
1:C:698:ILE:H	1:C:702:SER:HB3	1.81	0.46
1:B:839:LEU:HD23	1:B:839:LEU:C	2.35	0.46
1:C:507:ASP:O	1:C:508:HIS:ND1	2.47	0.46
1:C:771:VAL:O	1:C:774:PHE:HB2	2.15	0.46
1:A:596:LEU:HD12	1:A:606:LEU:CD1	2.44	0.46
1:B:763:LEU:CD1	1:B:826:LEU:HD13	2.45	0.46
2:D:65:PRO:HB3	2:D:95:TRP:CD2	2.51	0.46
2:D:38:LEU:HD23	2:D:52:ARG:HA	1.97	0.46
1:B:765:ARG:O	1:B:769:GLU:HG3	2.16	0.46
2:D:143:PHE:CA	2:D:146:LYS:HE2	2.38	0.46
1:B:770:ILE:HD13	1:B:836:LYS:HB2	1.98	0.46
1:A:838:ARG:HA	1:A:838:ARG:NE	2.31	0.46
2:D:25:ILE:HG13	2:D:26:GLN:H	1.81	0.45
1:B:765:ARG:HD3	3:B:329:HOH:O	2.16	0.45
1:B:552:PHE:O	1:B:556:VAL:HG23	2.16	0.45
1:C:766:GLU:O	1:C:770:ILE:HG13	2.16	0.45
2:D:71:LYS:HD3	2:D:71:LYS:C	2.36	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
2:D:101:THR:O	2:D:105:ILE:HD13	2.17	0.45
1:C:715:HIS:HA	1:C:718:THR:HB	1.98	0.45
1:A:718:THR:O	1:A:718:THR:CG2	2.64	0.45
2:D:21:ASN:O	2:D:39:ILE:HA	2.16	0.45
3:A:243:HOH:O	2:D:100:LYS:CG	2.64	0.45
1:B:505:ARG:O	1:B:506:ARG:C	2.55	0.45
1:B:824:LEU:CD1	1:B:826:LEU:HG	2.34	0.45
1:B:745:GLN:OE1	1:B:772:HIS:CE1	2.69	0.45
1:A:742:LEU:HD11	1:A:780:ARG:NH1	2.31	0.45
2:D:57:PHE:HB3	2:D:66:PRO:HB3	1.98	0.45
1:C:757:TYR:CE2	1:C:806:LYS:HA	2.51	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:714:PHE:CE2	1:A:723:LEU:HD11	2.52	0.45
1:A:628:LEU:HD22	1:A:632:HIS:HB2	1.98	0.45
2:D:104:VAL:HG23	2:D:105:ILE:H	1.81	0.45
2:D:20:LYS:O	2:D:21:ASN:ND2	2.50	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:16:LYS:O	2:D:17:CYS:O	2.35	0.45
1:B:613:VAL:CG2	1:B:627:ASP:HB3	2.48	0.45
1:A:583:PHE:CZ	1:A:584:GLU:HG2	2.52	0.45
2:D:29:GLU:O	2:D:30:ALA:HB2	2.17	0.45
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
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:757:TYR:O	1:A:761:SER:OG	2.33	0.44
1:A:641:ASP:OD1	2:D:96:LYS:HD2	2.17	0.44
1:C:775:THR:O	1:C:778:GLN:N	2.50	0.44
2:D:60:GLU:HG3	2:D:64:LYS:CD	2.45	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
1:A:516:ARG:NH1	1:A:516:ARG:CG	2.69	0.44
1:C:744:PHE:HA	1:C:747:LEU:CB	2.47	0.44
2:D:101:THR:C	2:D:104:VAL:HG22	2.37	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:573:THR:O	1:C:574:LYS:HB2	2.17	0.44
1:A:684:ASN:ND2	1:A:684:ASN:H	2.13	0.44
1:A:747:LEU:O	1:A:747:LEU:HD13	2.16	0.44
1:C:675:GLU:HG3	1:C:676:ASN:OD1	2.18	0.44
1:B:833:GLU:N	1:B:833:GLU:OE2	2.51	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: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:A:497:ASN:N	1:A:497:ASN:ND2	2.65	0.44
2:D:105:ILE:N	2:D:105:ILE:HD12	2.32	0.44
1:C:502:LEU:HA	1:C:502:LEU:HD23	1.81	0.44
1:B:505:ARG:HG2	1:B:512:ASP:OD1	2.17	0.44
1:A:498:PRO:O	1:A:499:TYR:HB2	2.17	0.44
1:C:738:GLY:O	1:C:791:ARG:HD3	2.18	0.44
1:B:583:PHE:CZ	1:B:584:GLU:HG2	2.53	0.44
2:D:105:ILE:CG2	2:D:106:GLN:N	2.77	0.44
2:D:38:LEU:HD23	2:D:52:ARG:CA	2.48	0.44
1:A:744:PHE:HA	1:A:747:LEU:CB	2.47	0.44
1:A:509:ILE:HD11	1:A:554:LEU:HD13	2.00	0.44
1:C:656:THR:HB	1:C:677:GLY:O	2.17	0.44
1:C:833:GLU:H	1:C:833:GLU:CD	2.21	0.44
1:C:765:ARG:O	1:C:769:GLU:HG3	2.18	0.44
1:A:811:THR:HG23	3:A:6:HOH:O	2.18	0.44
1:B:706:GLN:OE1	1:B:706:GLN:N	2.51	0.44
1:B:635:LEU:HA	3:B:67:HOH:O	2.18	0.43
1:B:659:ILE:C	1:B:659:ILE:HD12	2.38	0.43
2:D:49:GLY:O	2:D:51:PHE:CE1	2.71	0.43
1:B:748:GLU:HA	1:B:768:TRP:CZ2	2.52	0.43
1:B:775:THR:O	1:B:776:ASP:C	2.56	0.43
1:B:715:HIS:CE1	1:B:719:ASN:HA	2.53	0.43
1:A:719:ASN:O	1:A:720:GLU:HB2	2.17	0.43
1:C:674:LYS:O	1:C:675:GLU:C	2.56	0.43
1:C:796:GLY:O	1:C:798:GLY:N	2.52	0.43
1:B:570:ASP:OD2	1:B:572:SER:HB3	2.17	0.43
2:D:38:LEU:HA	2:D:51:PHE:O	2.18	0.43
1:A:714:PHE:CE1	3:A:320:HOH:O	2.56	0.43
1:A:603:ASN:OD1	1:A:794:VAL:HB	2.18	0.43
1:C:767:PHE:CZ	1:C:771:VAL:HG21	2.53	0.43
1:B:511:ASP:N	1:B:511:ASP:OD1	2.36	0.43
2:D:75:TYR:CZ	2:D:125:LEU:HD22	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:105:ILE:H	2:D:105:ILE:HD12	1.82	0.43
1:C:742:LEU:HD11	1:C:780:ARG:HH12	1.80	0.43
1:B:514:LEU:O	1:B:518:GLU:HB2	2.18	0.43
1:A:626:ARG:NH1	3:A:124:HOH:O	2.51	0.43
1:A:767:PHE:HB2	1:A:835:LEU:HD11	2.01	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:730:GLU:OE1	1:A:730:GLU:N	2.45	0.43
1:A:835:LEU:CD2	1:A:835:LEU:C	2.87	0.43
1:A:763:LEU:C	1:A:763:LEU:HD13	2.39	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:B:841:LYS:HA	1:B:844:THR:CG2	2.49	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
2:D:48:LYS:HA	2:D:48:LYS:HD3	1.81	0.43
1:A:653:MET:O	1:A:654:MET:C	2.56	0.43
2:D:11:LEU:C	2:D:13:GLU:H	2.22	0.43
1:C:835:LEU:CD2	1:C:835:LEU:C	2.87	0.43
1:A:706:GLN:N	1:A:706:GLN:OE1	2.32	0.43
2:D:11:LEU:C	2:D:13:GLU:N	2.72	0.43
2:D:60:GLU:N	2:D:60:GLU:OE2	2.52	0.43
1:B:714:PHE:HB2	3:B:293:HOH:O	2.19	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:C:684:ASN:N	1:C:684:ASN:ND2	2.64	0.42
2:D:60:GLU:H	2:D:60:GLU:CD	2.22	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:C:787:THR:CG2	1:C:822:ASN:OD1	2.58	0.42
1:A:628:LEU:HD23	1:A:699:LEU:HD21	2.01	0.42
2:D:122:ARG:CD	2:D:125:LEU:HG	2.48	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
1:A:749:GLU:C	1:A:751:THR:N	2.71	0.42
1:A:789:THR:OG1	1:A:790:ASP:N	2.53	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
2:D:85:VAL:HG12	2:D:86:CYS:N	2.35	0.42
1:B:786:THR:O	1:B:819:THR:HA	2.19	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)
1:B:684:ASN:N	1:B:684:ASN:ND2	2.65	0.42
1:A:708:LYS:HD3	3:A:109:HOH:O	2.20	0.42
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
2:D:135:LYS:CD	2:D:135:LYS:O	2.66	0.42
1:C:514:LEU:O	1:C:518:GLU:HB2	2.20	0.42
1:A:728:ARG:HH11	1:A:728:ARG:HG2	1.84	0.42
2:D:70:PHE:CD2	2:D:79:ILE:HD13	2.55	0.42
1:B:735:LEU:HD11	1:C:727:PHE:CE2	2.55	0.42
2:D:115:PRO:C	2:D:117:PRO:HD3	2.40	0.42
1:B:778:GLN:O	1:B:781:LEU:N	2.52	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:C:649:VAL:CB	1:C:684:ASN:ND2	2.83	0.41
1:B:715:HIS:HA	1:B:718:THR:HB	2.02	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: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:B:534:VAL:HB	1:B:547:VAL:HG12	2.01	0.41
1:A:562:PRO:O	1:A:565:GLY:N	2.49	0.41
1:B:804:ILE:HG23	1:B:824:LEU:HD12	2.01	0.41
1:A:769:GLU:OE2	1:A:832:LYS:NZ	2.46	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:C:726:LEU:HD22	1:C:731:GLU:OE1	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:499:TYR:HA	1:B:531:GLN:O	2.20	0.41
1:A:792:ALA:HA	1:A:793:PRO:HD3	1.79	0.41
1:C:748:GLU:C	1:C:749:GLU:O	2.56	0.41
1:B:649:VAL:HG12	1:B:650:GLU:N	2.35	0.41
1:B:559:ILE:HG21	1:B:592:ILE:HD13	2.03	0.41
1:A:638:SER:HB3	2:D:63:PHE:HD1	1.85	0.41
1:B:792:ALA:HA	1:B:793:PRO:HD3	1.75	0.41
2:D:60:GLU:HG3	2:D:64:LYS:CE	2.51	0.41
1:B:505:ARG:HH12	1:B:508:HIS:CD2	2.38	0.41
1:C:761:SER:N	3:C:69:HOH:O	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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
1:B:516:ARG:HH11	1:B:516:ARG:CG	2.30	0.41
1:B:505:ARG:NH1	1:B:508:HIS:CG	2.89	0.41
1:A:672:ASP:HB3	1:A:674:LYS:O	2.21	0.41
1:A:501:ARG:NH1	1:A:535:GLU:OE2	2.53	0.41
1:A:499:TYR:N	1:A:499:TYR:CD2	2.86	0.41
1:B:763:LEU:HD22	1:B:835:LEU:HD12	2.03	0.41
1:A:767:PHE:CE1	1:A:771:VAL:HG21	2.55	0.41
2:D:7:LEU:HD22	2:D:57:PHE:CZ	2.55	0.41
1:A:728:ARG:NH2	1:C:794:VAL:CG2	2.84	0.41
1:C:507:ASP:O	1:C:508:HIS:CG	2.74	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:A:836:LYS:O	1:A:840:LEU:HG	2.21	0.41
1:A:774:PHE:HE1	1:A:840:LEU:HD21	1.86	0.41
1:C:745:GLN:C	1:C:747:LEU:H	2.24	0.40
1:C:626:ARG:NE	3:C:15:HOH:O	2.46	0.40
1:A:742:LEU:HA	1:A:797:LEU:HD11	2.02	0.40
1:C:775:THR:O	1:C:776:ASP:C	2.59	0.40
1:C:800:LEU:O	1:C:801:LYS:C	2.59	0.40
1:A:762:VAL:O	1:A:766:GLU:HG3	2.22	0.40
1:B:505:ARG:C	1:B:506:ARG:O	2.55	0.40
1:B:737:CYS:O	1:B:791:ARG:HD2	2.21	0.40
1:B:679:LYS:O	1:B:681:PRO:CD	2.69	0.40
1:C:833:GLU:N	1:C:833:GLU:CD	2.74	0.40
1:A:531:GLN:OE1	1:B:626:ARG:HD2	2.20	0.40
2:D:24:ASN:CG	3:D:168:HOH:O	2.60	0.40
1:B:611:PRO:HG2	3:B:269:HOH:O	2.22	0.40
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:C:679:LYS:CD	1:C:679:LYS:C	2.88	0.40
1:B:707:PHE:O	1:B:710:PHE:HB3	2.22	0.40
2:D:45:PRO:HB3	2:D:137:CYS:HA	2.02	0.40
1:B:516:ARG:CG	1:B:516:ARG:NH1	2.83	0.40
1:C:777:GLU:O	1:C:781:LEU:HG	2.21	0.40
1:C:744:PHE:C	1:C:745:GLN:O	2.48	0.40
1:C:766:GLU:CD	1:C:832:LYS:HB2	2.41	0.40
1:A:668:PRO:HG3	2:D:33:LEU:CD1	2.52	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:786:THR:O	1:B:819:THR:HG22	2.22	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

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:813:ARG:NE	1:C:762:VAL:CB[3_656]	2.09	0.11
1:B:660:SER:C	1:C:523:GLU:OE2[4_456]	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

5.3.1 Protein backbone

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

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
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

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Mol	Chain	Res	Type
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
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.

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	317/323 (98%)	299 (94%)	18 (6%)	25	49
1	B	317/323 (98%)	295 (93%)	22 (7%)	19	38
1	C	317/323 (98%)	296 (93%)	21 (7%)	21	40
2	D	108/138 (78%)	102 (94%)	6 (6%)	26	50
All	All	1059/1107 (96%)	992 (94%)	67 (6%)	22	44

All (67) 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	635	LEU
1	A	642	LEU
1	A	654	MET
1	A	662	THR
1	A	663	ASP
1	A	678	ASP
1	A	684	ASN
1	A	685	GLU
1	A	706	GLN
1	A	723	LEU
1	A	728	ARG
1	A	789	THR
1	A	812	GLU
1	A	826	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	642	LEU
1	B	668	PRO
1	B	678	ASP

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Mol	Chain	Res	Type
1	B	684	ASN
1	B	686	ASN
1	B	694	TYR
1	B	699	LEU
1	B	706	GLN
1	B	723	LEU
1	B	728	ARG
1	B	743	ASP
1	B	789	THR
1	B	812	GLU
1	C	500	LEU
1	C	511	ASP
1	C	514	LEU
1	C	582	SER
1	C	592	ILE
1	C	642	LEU
1	C	664	LEU
1	C	678	ASP
1	C	684	ASN
1	C	685	GLU
1	C	694	TYR
1	C	699	LEU
1	C	706	GLN
1	C	728	ARG
1	C	747	LEU
1	C	789	THR
1	C	809	PRO
1	C	812	GLU
1	C	826	LEU
1	C	833	GLU
1	C	835	LEU
2	D	23	ARG
2	D	57	PHE
2	D	102	ASP
2	D	129	TYR
2	D	133	ARG
2	D	143	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	531	GLN

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Mol	Chain	Res	Type
1	A	602	ASN
1	A	684	ASN
1	B	531	GLN
1	B	602	ASN
1	B	684	ASN
1	B	686	ASN
1	B	772	HIS
1	C	497	ASN
1	C	531	GLN
1	C	602	ASN
1	C	661	GLN
1	C	684	ASN
1	C	784	GLN
1	C	818	HIS
2	D	21	ASN
2	D	26	GLN
2	D	36	GLN
2	D	76	HIS
2	D	78	ASN

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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section will therefore be empty.

6.4 Ligands [i](#)

EDS was not executed - this section will therefore be empty.

6.5 Other polymers [i](#)

EDS was not executed - this section will therefore be empty.