



Full wwPDB X-ray Structure Validation Report ⓘ

May 21, 2020 – 05:33 am BST

PDB ID : 3T0E
Title : Crystal structure of a complete ternary complex of T cell receptor, peptide-MHC and CD4
Authors : Yin, Y.; Mariuzza, R.A.
Deposited on : 2011-07-20
Resolution : 4.00 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.11
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

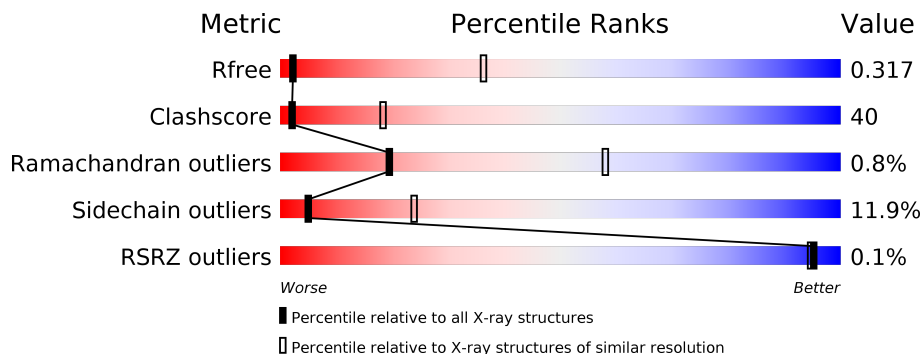
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.00 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1087 (4.30-3.70)
Clashscore	141614	1148 (4.30-3.70)
Ramachandran outliers	138981	1108 (4.30-3.70)
Sidechain outliers	138945	1099 (4.30-3.70)
RSRZ outliers	127900	1028 (4.34-3.66)

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 respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	182	
2	B	221	
3	C	206	
4	D	245	
5	E	373	

2 Entry composition i

There are 5 unique types of molecules in this entry. The entry contains 9259 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 HLA class II histocompatibility antigen, DR alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	178	1446	940	232	269	5	0	0	0

- Molecule 2 is a protein called HLA class II histocompatibility antigen, DRB1-4 beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	195	1578	1001	271	301	5	0	0	0

There are 29 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	1	PHE	-	EXPRESSION TAG	UNP P13760
B	2	SER	-	EXPRESSION TAG	UNP P13760
B	3	TRP	-	EXPRESSION TAG	UNP P13760
B	4	GLY	-	EXPRESSION TAG	UNP P13760
B	5	ALA	-	EXPRESSION TAG	UNP P13760
B	6	GLU	-	EXPRESSION TAG	UNP P13760
B	7	GLY	-	EXPRESSION TAG	UNP P13760
B	8	GLN	-	EXPRESSION TAG	UNP P13760
B	9	ARG	-	EXPRESSION TAG	UNP P13760
B	10	PRO	-	EXPRESSION TAG	UNP P13760
B	11	GLY	-	EXPRESSION TAG	UNP P13760
B	12	PHE	-	EXPRESSION TAG	UNP P13760
B	13	GLY	-	EXPRESSION TAG	UNP P13760
B	14	SER	-	EXPRESSION TAG	UNP P13760
B	15	GLY	-	EXPRESSION TAG	UNP P13760
B	16	GLY	-	EXPRESSION TAG	UNP P13760
B	17	GLY	-	EXPRESSION TAG	UNP P13760
B	18	SER	-	EXPRESSION TAG	UNP P13760
B	19	LEU	-	EXPRESSION TAG	UNP P13760
B	20	VAL	-	EXPRESSION TAG	UNP P13760

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Chain	Residue	Modelled	Actual	Comment	Reference
B	21	PRO	-	EXPRESSION TAG	UNP P13760
B	22	ARG	-	EXPRESSION TAG	UNP P13760
B	23	GLY	-	EXPRESSION TAG	UNP P13760
B	24	SER	-	EXPRESSION TAG	UNP P13760
B	25	GLY	-	EXPRESSION TAG	UNP P13760
B	26	GLY	-	EXPRESSION TAG	UNP P13760
B	27	GLY	-	EXPRESSION TAG	UNP P13760
B	28	GLY	-	EXPRESSION TAG	UNP P13760
B	29	SER	-	EXPRESSION TAG	UNP P13760

- Molecule 3 is a protein called T-cell receptor alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	C	193	1455	905	244	299	7	4	0	0

- Molecule 4 is a protein called T-cell receptor beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	D	245	1920	1210	327	375	8	0	0	0

- Molecule 5 is a protein called T-cell surface glycoprotein CD4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
5	E	365	2860	1818	491	541	10	0	0	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	40	TYR	GLN	ENGINEERED MUTATION	UNP P01730
E	45	TRP	THR	ENGINEERED MUTATION	UNP P01730
E	364	ALA	-	EXPRESSION TAG	UNP P01730
E	365	ALA	-	EXPRESSION TAG	UNP P01730
E	366	ASP	-	EXPRESSION TAG	UNP P01730
E	367	TYR	-	EXPRESSION TAG	UNP P01730
E	368	LYS	-	EXPRESSION TAG	UNP P01730
E	369	ASP	-	EXPRESSION TAG	UNP P01730
E	370	ASP	-	EXPRESSION TAG	UNP P01730
E	371	ASP	-	EXPRESSION TAG	UNP P01730
E	372	ASP	-	EXPRESSION TAG	UNP P01730

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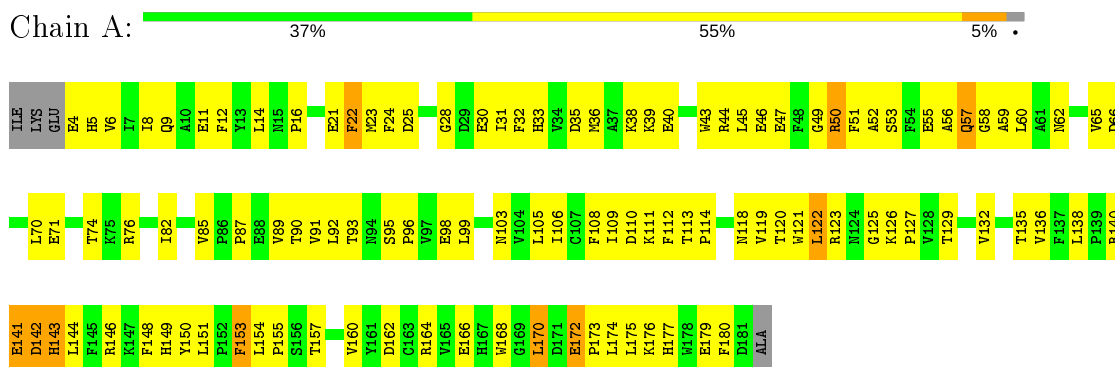
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Chain	Residue	Modelled	Actual	Comment	Reference
E	373	LYS	-	EXPRESSION TAG	UNP P01730

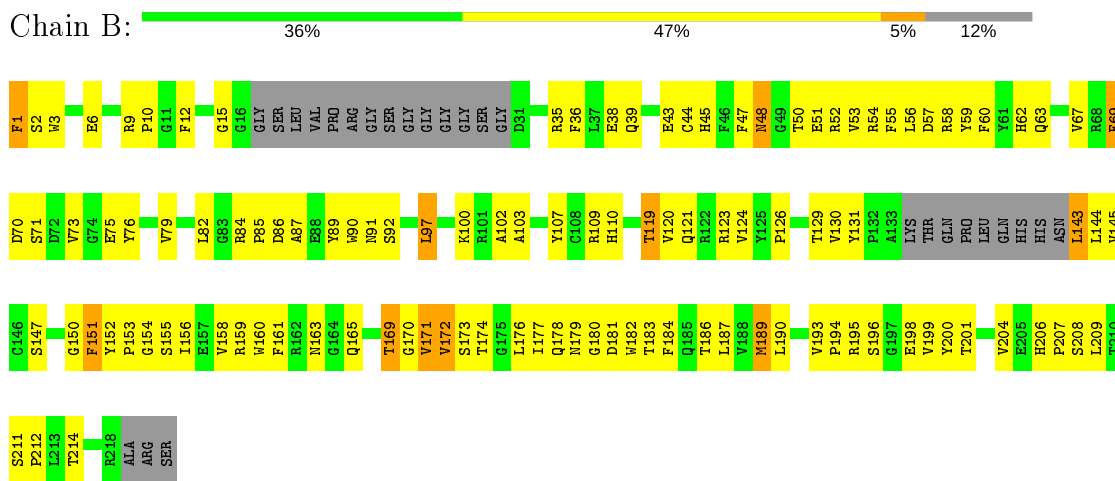
3 Residue-property plots

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

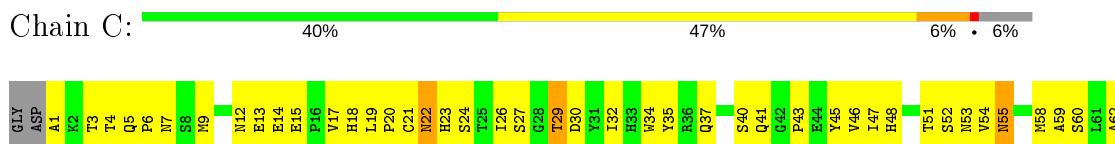
- Molecule 1: HLA class II histocompatibility antigen, DR alpha chain

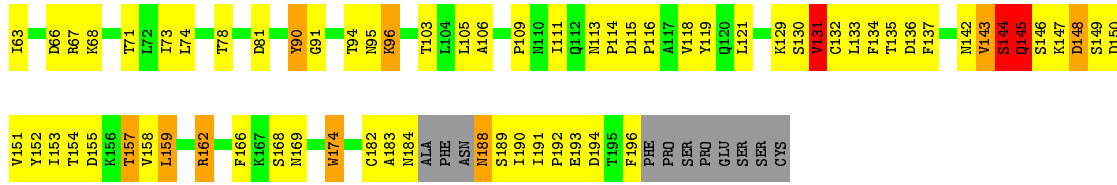


- Molecule 2: HLA class II histocompatibility antigen, DRB1-4 beta chain

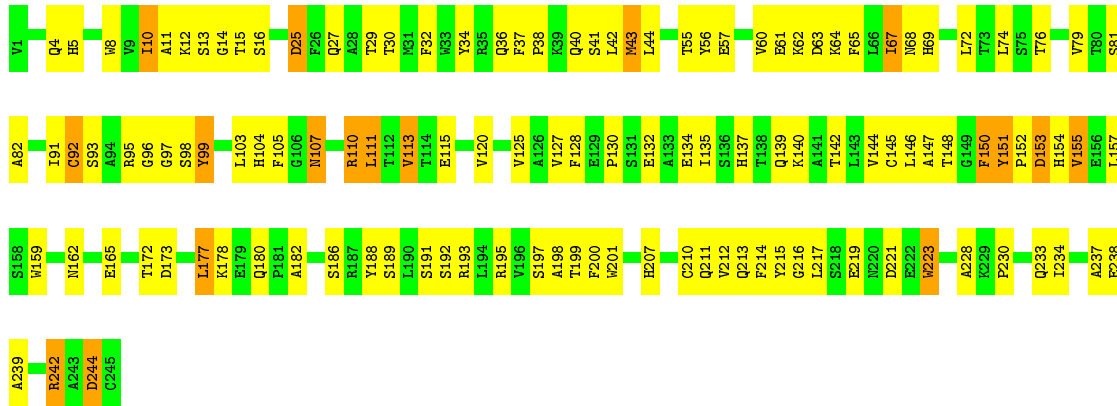


- Molecule 3: T-cell receptor alpha chain

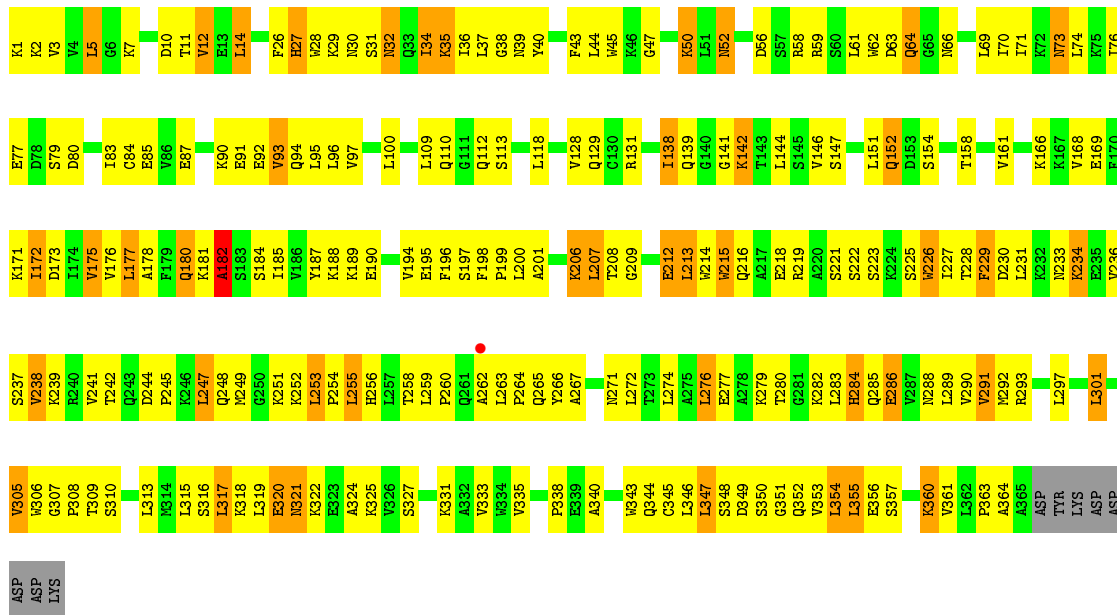




• Molecule 4: T-cell receptor beta chain



• Molecule 5: T-cell surface glycoprotein CD4



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	146.15Å 146.15Å 231.44Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.67 – 4.00 47.67 – 4.00	Depositor EDS
% Data completeness (in resolution range)	99.8 (47.67-4.00) 99.8 (47.67-4.00)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.65 (at 4.00Å)	Xtrriage
Refinement program	PHENIX (phenix.refine: 1.7.1_743)	Depositor
R, R_{free}	0.238 , 0.305 0.249 , 0.317	Depositor DCC
R_{free} test set	1066 reflections (4.88%)	wwPDB-VP
Wilson B-factor (Å ²)	179.8	Xtrriage
Anisotropy	0.150	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 204.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	9259	wwPDB-VP
Average B, all atoms (Å ²)	218.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.42% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.31	0/1491	0.52	0/2036
2	B	0.33	0/1622	0.53	0/2204
3	C	0.37	1/1485 (0.1%)	0.61	2/2030 (0.1%)
4	D	0.27	0/1973	0.50	0/2690
5	E	0.30	0/2912	0.55	0/3935
All	All	0.31	1/9483 (0.0%)	0.54	2/12895 (0.0%)

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
3	C	0	3
5	E	0	1
All	All	0	4

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	1	ALA	C-O	7.25	1.37	1.23

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
3	C	131	VAL	N-CA-C	6.10	127.47	111.00
3	C	145	GLN	N-CA-C	5.19	125.02	111.00

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	C	130	SER	Peptide
3	C	144	SER	Peptide
3	C	145	GLN	Peptide
5	E	182	ALA	Peptide

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	1446	0	1370	125	0
2	B	1578	0	1451	129	0
3	C	1455	0	1345	116	0
4	D	1920	0	1809	142	0
5	E	2860	0	2944	265	0
All	All	9259	0	8919	725	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 40.

All (725) 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:175:LEU:CD1	1:A:177:HIS:CE1	1.75	1.56
1:A:175:LEU:HD11	1:A:177:HIS:CE1	0.95	1.46
1:A:175:LEU:CD1	1:A:177:HIS:NE2	1.81	1.42
1:A:175:LEU:HD12	1:A:177:HIS:NE2	1.31	1.42
1:A:162:ASP:CG	1:A:177:HIS:ND1	2.02	1.13
5:E:110:GLN:HE21	5:E:178:ALA:HB1	1.15	1.10
5:E:236:VAL:HB	5:E:251:LYS:HA	1.35	1.06
2:B:172:VAL:HG21	5:E:45:TRP:CE3	1.90	1.05
5:E:3:VAL:HG12	5:E:94:GLN:HB3	1.37	1.04
1:A:175:LEU:HD11	1:A:177:HIS:ND1	1.72	1.02
1:A:71:GLU:HB3	2:B:15:GLY:HA3	1.42	0.99
2:B:6:GLU:HG2	2:B:107:TYR:CD1	1.98	0.98
2:B:123:ARG:HG3	2:B:123:ARG:HH11	1.28	0.98
1:A:175:LEU:HD12	1:A:177:HIS:HE2	1.30	0.97
5:E:109:LEU:HD21	5:E:276:LEU:HD11	1.46	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:178:ALA:HA	5:E:283:LEU:HD11	1.47	0.95
5:E:215:TRP:HB2	5:E:225:SER:HB3	1.48	0.95
5:E:285:GLN:HG2	5:E:286:GLU:N	1.80	0.93
1:A:175:LEU:HD11	1:A:177:HIS:HE1	1.20	0.93
1:A:162:ASP:OD2	1:A:177:HIS:ND1	2.03	0.91
5:E:180:GLN:HG3	5:E:199:PRO:HB2	1.54	0.90
2:B:51:GLU:HG2	2:B:52:ARG:H	1.37	0.89
2:B:57:ASP:OD1	2:B:100:LYS:NZ	2.06	0.89
3:C:146:SER:CB	3:C:147:LYS:HA	2.02	0.88
3:C:145:GLN:HG3	3:C:189:SER:HB2	1.55	0.87
4:D:95:ARG:HH21	4:D:98:SER:HA	1.38	0.87
4:D:14:GLY:HA2	4:D:82:ALA:HB3	1.57	0.86
1:A:175:LEU:CD1	1:A:177:HIS:CD2	2.57	0.86
4:D:4:GLN:OE1	4:D:92:CYS:N	2.08	0.86
5:E:37:LEU:HD11	5:E:44:LEU:HD11	1.57	0.85
5:E:177:LEU:HD23	5:E:201:ALA:HB3	1.58	0.84
5:E:317:LEU:HD12	5:E:333:VAL:HG11	1.62	0.82
5:E:188:LYS:HG3	5:E:194:VAL:HG22	1.61	0.82
3:C:109:PRO:HG3	3:C:158:VAL:HG21	1.61	0.82
5:E:318:LYS:O	5:E:325:LYS:NZ	2.12	0.82
5:E:347:LEU:HD12	5:E:354:LEU:HD21	1.60	0.82
2:B:50:THR:HG23	2:B:109:ARG:HG2	1.62	0.81
4:D:61:GLU:O	4:D:62:LYS:HG2	1.80	0.81
5:E:182:ALA:H	5:E:285:GLN:HG3	1.45	0.80
5:E:12:VAL:HG12	5:E:74:LEU:HD11	1.64	0.80
5:E:187:TYR:HD1	5:E:290:VAL:CG2	1.95	0.80
5:E:285:GLN:HG2	5:E:286:GLU:H	1.42	0.79
4:D:62:LYS:HG3	4:D:63:ASP:H	1.47	0.79
5:E:255:LEU:H	5:E:255:LEU:HD23	1.48	0.79
5:E:318:LYS:O	5:E:319:LEU:HB3	1.83	0.79
2:B:12:PHE:HE1	2:B:89:TYR:HB2	1.49	0.78
3:C:17:VAL:HG13	3:C:74:LEU:HB2	1.66	0.78
5:E:301:LEU:HD21	5:E:335:VAL:HB	1.64	0.78
3:C:145:GLN:HE21	3:C:189:SER:H	1.30	0.78
5:E:209:GLY:HA3	5:E:276:LEU:HA	1.66	0.77
1:A:162:ASP:OD2	1:A:177:HIS:CE1	2.37	0.77
4:D:99:TYR:H	4:D:99:TYR:HD1	1.32	0.77
2:B:174:THR:CG2	2:B:187:LEU:H	1.97	0.77
2:B:163:ASN:HD21	2:B:199:VAL:H	1.28	0.77
2:B:70:ASP:HB3	2:B:73:VAL:HG23	1.66	0.77
2:B:6:GLU:HG2	2:B:107:TYR:HD1	1.49	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:279:LYS:O	5:E:280:THR:OG1	2.02	0.77
1:A:121:TRP:CG	1:A:151:LEU:HD22	2.21	0.76
3:C:46:VAL:HG12	3:C:47:ILE:HG22	1.66	0.76
2:B:69:PHE:HB2	2:B:76:TYR:CD1	2.20	0.76
1:A:175:LEU:HD12	1:A:177:HIS:CD2	2.18	0.76
5:E:263:LEU:HB3	5:E:264:PRO:HD2	1.68	0.76
4:D:12:LYS:HG2	4:D:13:SER:H	1.50	0.75
5:E:128:VAL:HG12	5:E:129:GLN:H	1.50	0.75
2:B:69:PHE:HB2	2:B:76:TYR:CE1	2.22	0.75
5:E:315:LEU:HD12	5:E:346:LEU:O	1.87	0.74
5:E:38:GLY:HA3	5:E:45:TRP:CZ2	2.22	0.74
5:E:50:LYS:H	5:E:50:LYS:HD2	1.50	0.74
4:D:151:TYR:CD1	4:D:152:PRO:HA	2.22	0.74
5:E:64:GLN:H	5:E:64:GLN:HE21	1.35	0.73
5:E:187:TYR:HD1	5:E:290:VAL:HG22	1.52	0.73
4:D:162:ASN:HA	4:D:207:HIS:HB3	1.70	0.73
4:D:213:GLN:NE2	4:D:233:GLN:O	2.20	0.73
5:E:187:TYR:CZ	5:E:354:LEU:HD12	2.24	0.73
5:E:318:LYS:HG3	5:E:319:LEU:N	2.03	0.72
2:B:172:VAL:HG21	5:E:45:TRP:HE3	1.53	0.72
1:A:52:ALA:HB1	2:B:3:TRP:HB2	1.70	0.71
2:B:76:TYR:HB2	2:B:91:ASN:HD21	1.55	0.71
3:C:145:GLN:HG3	3:C:189:SER:CB	2.19	0.71
5:E:347:LEU:HB3	5:E:354:LEU:HD23	1.71	0.71
5:E:348:SER:HA	5:E:354:LEU:HD22	1.72	0.71
5:E:5:LEU:HD12	5:E:96:LEU:HB2	1.70	0.71
5:E:253:LEU:HD12	5:E:254:PRO:HA	1.72	0.71
3:C:145:GLN:NE2	3:C:189:SER:H	1.88	0.71
4:D:178:LYS:HG2	4:D:188:TYR:HE1	1.56	0.71
5:E:195:GLU:HG2	5:E:258:THR:HA	1.73	0.71
5:E:226:TRP:HD1	5:E:226:TRP:H	1.34	0.71
5:E:109:LEU:CD2	5:E:276:LEU:HD11	2.21	0.71
3:C:111:ILE:HD12	3:C:137:PHE:O	1.91	0.70
3:C:154:THR:HB	4:D:173:ASP:OD2	1.91	0.70
3:C:18:HIS:CD2	3:C:73:ILE:HG23	2.26	0.70
5:E:38:GLY:HA3	5:E:45:TRP:CE2	2.27	0.70
5:E:253:LEU:HA	5:E:254:PRO:C	2.11	0.70
1:A:62:ASN:O	1:A:65:VAL:HB	1.92	0.69
5:E:301:LEU:CD2	5:E:335:VAL:HB	2.22	0.69
5:E:100:LEU:HD23	5:E:118:LEU:HA	1.73	0.69
5:E:30:ASN:OD1	5:E:34:ILE:HB	1.93	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:43:GLU:OE2	2:B:58:ARG:NH1	2.25	0.69
5:E:182:ALA:N	5:E:285:GLN:HG3	2.07	0.69
1:A:89:VAL:O	1:A:176:LYS:NZ	2.26	0.69
2:B:150:GLY:HA2	2:B:183:THR:HB	1.75	0.69
4:D:36:GLN:HG3	4:D:41:SER:O	1.93	0.69
2:B:161:PHE:HB2	2:B:201:THR:HB	1.74	0.69
5:E:317:LEU:HD22	5:E:343:TRP:HE3	1.59	0.68
4:D:127:VAL:HG12	4:D:128:PHE:N	2.08	0.68
1:A:43:TRP:HH2	1:A:52:ALA:HB3	1.57	0.68
5:E:247:LEU:HB2	5:E:258:THR:O	1.92	0.68
2:B:181:ASP:O	2:B:182:TRP:HB2	1.93	0.67
3:C:145:GLN:NE2	3:C:188:ASN:HB2	2.09	0.67
4:D:238:GLU:HG2	4:D:239:ALA:H	1.59	0.67
5:E:194:VAL:HG11	5:E:289:LEU:HD12	1.74	0.67
1:A:123:ARG:O	1:A:126:LYS:HG2	1.94	0.67
1:A:43:TRP:CH2	1:A:52:ALA:HB3	2.29	0.67
2:B:123:ARG:HH11	2:B:123:ARG:CG	2.06	0.67
5:E:247:LEU:HD13	5:E:247:LEU:H	1.58	0.67
1:A:121:TRP:CD2	1:A:151:LEU:HD22	2.30	0.67
4:D:238:GLU:HG2	4:D:239:ALA:N	2.10	0.67
4:D:42:LEU:HD21	4:D:91:ILE:HD12	1.75	0.67
5:E:237:SER:H	5:E:251:LYS:CB	2.07	0.67
2:B:171:VAL:HG12	2:B:172:VAL:H	1.60	0.67
2:B:151:PHE:HE2	2:B:156:ILE:HG21	1.61	0.66
5:E:187:TYR:CE2	5:E:354:LEU:HD12	2.30	0.66
3:C:109:PRO:HG3	3:C:158:VAL:CG2	2.25	0.66
4:D:207:HIS:NE2	4:D:238:GLU:OE2	2.28	0.66
5:E:5:LEU:HD22	5:E:5:LEU:N	2.10	0.66
4:D:25:ASP:N	4:D:25:ASP:OD1	2.28	0.66
4:D:139:GLN:C	4:D:198:ALA:HB2	2.17	0.66
5:E:110:GLN:HG3	5:E:178:ALA:HB2	1.76	0.66
4:D:14:GLY:O	4:D:15:THR:OG1	2.14	0.65
3:C:40:SER:O	3:C:41:GLN:HG3	1.96	0.65
5:E:110:GLN:NE2	5:E:178:ALA:HB1	2.00	0.65
5:E:32:ASN:OD1	5:E:32:ASN:N	2.28	0.65
3:C:55:ASN:HB3	3:C:60:SER:OG	1.96	0.65
2:B:151:PHE:HD1	2:B:151:PHE:H	1.42	0.65
5:E:238:VAL:HG22	5:E:249:MET:HB2	1.76	0.65
2:B:69:PHE:CD2	2:B:69:PHE:C	2.70	0.65
3:C:6:PRO:O	3:C:103:THR:HG23	1.97	0.65
1:A:175:LEU:CD1	1:A:177:HIS:ND1	2.46	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:271:ASN:HA	5:E:286:GLU:HA	1.79	0.65
5:E:142:LYS:H	5:E:142:LYS:HZ3	1.42	0.64
5:E:244:ASP:HB3	5:E:245:PRO:HD3	1.79	0.64
2:B:187:LEU:HB3	2:B:189:MET:HE1	1.78	0.64
1:A:14:LEU:HD12	2:B:36:PHE:O	1.97	0.64
4:D:107:ASN:ND2	4:D:107:ASN:H	1.94	0.64
4:D:62:LYS:HG3	4:D:63:ASP:N	2.12	0.64
5:E:237:SER:HA	5:E:251:LYS:HE2	1.78	0.64
4:D:151:TYR:HD1	4:D:152:PRO:CA	2.11	0.64
4:D:64:LYS:HE3	4:D:81:SER:O	1.98	0.63
5:E:215:TRP:HE3	5:E:216:GLN:H	1.45	0.63
1:A:126:LYS:HG3	1:A:126:LYS:O	1.97	0.63
2:B:51:GLU:O	2:B:53:VAL:HG23	1.98	0.63
2:B:123:ARG:HG3	2:B:123:ARG:NH1	2.07	0.63
1:A:143:HIS:CD2	2:B:60:PHE:CE1	2.87	0.63
3:C:159:LEU:HD23	3:C:168:SER:O	1.99	0.63
5:E:234:LYS:O	5:E:252:LYS:HA	1.98	0.63
2:B:187:LEU:HD22	5:E:43:PHE:CE2	2.33	0.63
1:A:39:LYS:HG3	1:A:60:LEU:HD11	1.81	0.63
5:E:142:LYS:HD2	5:E:142:LYS:N	2.13	0.63
5:E:180:GLN:CG	5:E:199:PRO:HB2	2.28	0.62
5:E:151:LEU:HD13	5:E:151:LEU:O	2.00	0.62
3:C:34:TRP:O	3:C:46:VAL:HB	2.00	0.62
4:D:32:PHE:HB2	4:D:93:SER:OG	1.98	0.62
5:E:317:LEU:HD23	5:E:344:GLN:O	1.98	0.62
5:E:285:GLN:O	5:E:286:GLU:HB3	1.98	0.62
1:A:21:GLU:OE2	1:A:136:VAL:HB	1.99	0.62
3:C:144:SER:OG	3:C:189:SER:HB3	1.99	0.62
5:E:226:TRP:CD1	5:E:226:TRP:N	2.62	0.62
5:E:259:LEU:HD23	5:E:260:PRO:HD2	1.82	0.62
5:E:180:GLN:HG3	5:E:199:PRO:CB	2.27	0.62
5:E:79:SER:OG	5:E:97:VAL:HG22	2.00	0.62
1:A:108:PHE:CD1	1:A:148:PHE:HE2	2.18	0.62
1:A:28:GLY:O	1:A:146:ARG:NH2	2.32	0.62
1:A:162:ASP:OD1	1:A:177:HIS:ND1	2.32	0.62
5:E:241:VAL:HG12	5:E:242:THR:N	2.14	0.61
5:E:58:ARG:HD3	5:E:61:LEU:HD12	1.82	0.61
5:E:187:TYR:CD1	5:E:290:VAL:HG22	2.35	0.61
5:E:190:GLU:OE1	5:E:293:ARG:HG3	2.00	0.61
5:E:241:VAL:CG1	5:E:242:THR:N	2.62	0.61
5:E:212:GLU:HG2	5:E:213:LEU:N	2.15	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:36:ILE:O	5:E:47:GLY:N	2.27	0.61
5:E:73:ASN:HD22	5:E:73:ASN:C	2.03	0.61
2:B:9:ARG:HB3	2:B:10:PRO:CD	2.30	0.61
3:C:145:GLN:HE21	3:C:189:SER:N	1.96	0.61
3:C:166:PHE:CD2	4:D:140:LYS:HE2	2.36	0.61
4:D:68:ASN:HB3	4:D:76:THR:HB	1.82	0.61
5:E:131:ARG:HB3	5:E:158:THR:OG1	2.00	0.61
5:E:185:ILE:HG12	5:E:288:ASN:HB2	1.80	0.61
3:C:157:THR:HG23	4:D:193:ARG:NH2	2.16	0.61
1:A:170:LEU:HD23	1:A:170:LEU:H	1.65	0.61
3:C:17:VAL:CG1	3:C:74:LEU:HB2	2.30	0.61
2:B:206:HIS:O	2:B:208:SER:N	2.34	0.60
5:E:255:LEU:CD2	5:E:255:LEU:H	2.12	0.60
4:D:151:TYR:CD1	4:D:152:PRO:CA	2.84	0.60
4:D:157:LEU:HD13	4:D:192:SER:HB2	1.83	0.60
2:B:69:PHE:HD2	2:B:69:PHE:C	2.04	0.60
3:C:62:ALA:HB3	3:C:71:THR:HB	1.82	0.60
2:B:144:LEU:HD11	2:B:200:TYR:CD2	2.36	0.60
3:C:121:LEU:HD22	4:D:130:PRO:HA	1.82	0.60
4:D:223:TRP:CE3	4:D:223:TRP:HA	2.36	0.60
4:D:68:ASN:O	4:D:68:ASN:ND2	2.35	0.60
5:E:236:VAL:HB	5:E:251:LYS:CA	2.22	0.60
3:C:145:GLN:HB3	3:C:146:SER:O	2.02	0.60
5:E:348:SER:OG	5:E:349:ASP:N	2.32	0.60
1:A:148:PHE:HB3	1:A:150:TYR:HE2	1.66	0.60
4:D:178:LYS:HG2	4:D:188:TYR:CE1	2.36	0.60
5:E:37:LEU:HD11	5:E:44:LEU:CD1	2.30	0.59
1:A:108:PHE:HD1	1:A:148:PHE:HE2	1.51	0.59
2:B:89:TYR:O	2:B:92:SER:OG	2.16	0.59
5:E:237:SER:H	5:E:251:LYS:HB3	1.66	0.59
2:B:174:THR:HG21	2:B:187:LEU:H	1.65	0.59
5:E:112:GLN:NE2	5:E:280:THR:HB	2.17	0.59
5:E:76:ILE:HA	5:E:97:VAL:CG2	2.32	0.59
3:C:21:CYS:HB2	3:C:34:TRP:CZ2	2.38	0.59
3:C:119:TYR:CD2	4:D:134:GLU:HB2	2.38	0.59
3:C:111:ILE:CD1	3:C:169:ASN:H	2.16	0.59
5:E:229:PHE:HA	5:E:239:LYS:HB2	1.85	0.59
4:D:60:VAL:HG12	4:D:62:LYS:H	1.66	0.59
5:E:354:LEU:O	5:E:354:LEU:HD23	2.03	0.59
5:E:3:VAL:O	5:E:166:LYS:NZ	2.29	0.59
4:D:151:TYR:HD1	4:D:152:PRO:N	2.01	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:180:GLN:C	4:D:182:ALA:H	2.06	0.58
5:E:227:ILE:HA	5:E:241:VAL:HG13	1.85	0.58
5:E:187:TYR:HD1	5:E:290:VAL:HG21	1.68	0.58
2:B:194:PRO:HA	2:B:198:GLU:OE1	2.03	0.58
4:D:173:ASP:OD1	4:D:191:SER:OG	2.20	0.58
5:E:231:LEU:HD11	5:E:253:LEU:HD22	1.84	0.58
1:A:6:VAL:CG1	1:A:8:ILE:HG13	2.33	0.58
1:A:157:THR:HG22	1:A:180:PHE:HE2	1.69	0.58
2:B:172:VAL:HG22	2:B:173:SER:N	2.18	0.58
5:E:27:HIS:CE1	5:E:29:LYS:HE3	2.39	0.58
5:E:50:LYS:N	5:E:50:LYS:HD2	2.19	0.58
2:B:174:THR:HG22	2:B:187:LEU:H	1.67	0.58
4:D:95:ARG:NH2	4:D:98:SER:HA	2.14	0.58
4:D:29:THR:HG21	4:D:97:GLY:HA2	1.85	0.58
4:D:197:SER:OG	4:D:200:PHE:HB2	2.04	0.57
5:E:292:MET:HE2	5:E:357:SER:HB3	1.85	0.57
4:D:34:TYR:CE1	4:D:44:LEU:HD13	2.40	0.57
5:E:325:LYS:HD2	5:E:325:LYS:H	1.70	0.57
2:B:129:THR:HG22	2:B:130:VAL:H	1.69	0.57
3:C:188:ASN:N	3:C:188:ASN:HD22	2.02	0.57
4:D:127:VAL:HG12	4:D:128:PHE:H	1.68	0.57
5:E:128:VAL:HG12	5:E:129:GLN:N	2.18	0.57
5:E:110:GLN:HG3	5:E:178:ALA:CB	2.35	0.57
5:E:109:LEU:HD21	5:E:276:LEU:CD1	2.28	0.57
2:B:76:TYR:HB2	2:B:91:ASN:ND2	2.18	0.57
4:D:217:LEU:HD12	4:D:230:PRO:O	2.05	0.57
2:B:172:VAL:HG23	5:E:47:GLY:HA2	1.86	0.57
1:A:125:GLY:O	1:A:127:PRO:HD3	2.05	0.57
3:C:12:ASN:O	3:C:15:GLU:HB2	2.05	0.57
5:E:348:SER:HB2	5:E:354:LEU:N	2.20	0.57
2:B:154:GLY:HA3	2:B:184:PHE:CD2	2.40	0.56
1:A:120:THR:HB	1:A:164:ARG:HB3	1.88	0.56
1:A:90:THR:HG21	5:E:59:ARG:HE	1.71	0.56
5:E:178:ALA:HA	5:E:283:LEU:CD1	2.27	0.56
5:E:189:LYS:HE2	5:E:357:SER:HB2	1.87	0.56
4:D:10:ILE:HD12	4:D:11:ALA:H	1.71	0.56
5:E:290:VAL:HG12	5:E:308:PRO:HD2	1.85	0.56
2:B:151:PHE:HD1	2:B:151:PHE:N	2.04	0.56
4:D:223:TRP:HE3	4:D:223:TRP:HA	1.71	0.56
2:B:187:LEU:HD22	5:E:43:PHE:CD2	2.40	0.56
3:C:143:VAL:HG12	3:C:144:SER:N	2.21	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:61:GLU:O	4:D:62:LYS:CG	2.53	0.56
3:C:193:GLU:H	3:C:193:GLU:CD	2.09	0.56
5:E:154:SER:HB2	5:E:176:VAL:H	1.70	0.56
3:C:148:ASP:HB2	3:C:151:VAL:HB	1.88	0.55
1:A:92:LEU:HD22	5:E:43:PHE:HE1	1.71	0.55
5:E:284:HIS:C	5:E:284:HIS:HD1	2.09	0.55
5:E:50:LYS:H	5:E:50:LYS:CD	2.18	0.55
4:D:107:ASN:H	4:D:107:ASN:HD22	1.55	0.55
1:A:11:GLU:OE1	1:A:62:ASN:HB3	2.06	0.55
2:B:51:GLU:HG2	2:B:52:ARG:N	2.15	0.55
2:B:79:VAL:O	2:B:79:VAL:HG12	2.06	0.55
4:D:150:PHE:CE1	4:D:188:TYR:HB2	2.42	0.55
2:B:151:PHE:CD1	2:B:151:PHE:N	2.74	0.55
2:B:126:PRO:HD2	2:B:209:LEU:HD21	1.87	0.55
4:D:228:ALA:O	4:D:230:PRO:HD3	2.05	0.55
5:E:244:ASP:HB3	5:E:245:PRO:CD	2.35	0.55
1:A:119:VAL:HG21	1:A:149:HIS:CE1	2.42	0.55
3:C:53:ASN:ND2	3:C:62:ALA:HA	2.22	0.55
4:D:60:VAL:HG12	4:D:61:GLU:N	2.21	0.55
5:E:292:MET:HB3	5:E:355:LEU:CD1	2.37	0.55
2:B:10:PRO:HD3	4:D:96:GLY:O	2.06	0.55
5:E:285:GLN:CG	5:E:286:GLU:H	2.15	0.55
3:C:6:PRO:HG2	3:C:20:PRO:HG2	1.88	0.55
5:E:234:LYS:HE3	5:E:234:LYS:HA	1.88	0.55
5:E:70:ILE:HG22	5:E:71:ILE:N	2.22	0.55
1:A:51:PHE:O	2:B:1:PHE:HA	2.07	0.54
1:A:148:PHE:CE1	2:B:180:GLY:HA3	2.43	0.54
3:C:190:ILE:O	3:C:191:ILE:HG23	2.07	0.54
2:B:160:TRP:CG	2:B:190:LEU:HD22	2.43	0.54
3:C:162:ARG:HH11	3:C:162:ARG:HA	1.72	0.54
1:A:175:LEU:CD1	1:A:177:HIS:CG	2.90	0.54
2:B:43:GLU:O	2:B:44:CYS:SG	2.66	0.54
4:D:15:THR:HG22	4:D:16:SER:N	2.22	0.54
3:C:37:GLN:HE22	4:D:36:GLN:HE22	1.54	0.54
3:C:51:THR:OG1	3:C:52:SER:N	2.41	0.54
3:C:131:VAL:HG21	4:D:128:PHE:CD1	2.43	0.54
5:E:241:VAL:CG1	5:E:242:THR:H	2.21	0.54
5:E:83:ILE:HG22	5:E:84:CYS:N	2.23	0.54
1:A:4:GLU:O	1:A:5:HIS:CG	2.61	0.54
2:B:158:VAL:HG22	2:B:204:VAL:HG22	1.89	0.54
2:B:84:ARG:N	2:B:85:PRO:HD2	2.23	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:151:VAL:HG12	3:C:153:ILE:HD11	1.90	0.54
3:C:190:ILE:HG12	3:C:191:ILE:N	2.22	0.54
1:A:46:GLU:O	1:A:49:GLY:N	2.39	0.53
3:C:90:TYR:HD1	3:C:91:GLY:N	2.06	0.53
3:C:115:ASP:OD1	4:D:137:HIS:CE1	2.61	0.53
5:E:142:LYS:HD2	5:E:142:LYS:H	1.72	0.53
3:C:78:THR:N	3:C:81:ASP:OD2	2.40	0.53
4:D:12:LYS:HG2	4:D:13:SER:N	2.22	0.53
1:A:168:TRP:N	1:A:168:TRP:CD1	2.73	0.53
1:A:58:GLY:HA3	4:D:99:TYR:OH	2.08	0.53
4:D:95:ARG:HH21	4:D:98:SER:CA	2.16	0.53
4:D:68:ASN:O	4:D:69:HIS:C	2.46	0.53
5:E:360:LYS:H	5:E:360:LYS:HD3	1.73	0.53
5:E:154:SER:HB2	5:E:175:VAL:HA	1.91	0.53
3:C:152:TYR:C	3:C:153:ILE:HD12	2.28	0.53
4:D:132:GLU:HA	4:D:135:ILE:HB	1.91	0.53
3:C:155:ASP:O	3:C:157:THR:HG22	2.09	0.53
5:E:316:SER:HB2	5:E:346:LEU:HD23	1.90	0.53
3:C:7:ASN:O	3:C:103:THR:HA	2.09	0.53
4:D:217:LEU:HD22	4:D:221:ASP:CG	2.29	0.53
5:E:297:LEU:H	5:E:297:LEU:HD23	1.74	0.53
4:D:13:SER:HB2	4:D:115:GLU:HA	1.91	0.53
5:E:161:VAL:HB	5:E:168:VAL:CG2	2.39	0.53
5:E:318:LYS:HG3	5:E:319:LEU:H	1.72	0.53
5:E:70:ILE:HG22	5:E:71:ILE:H	1.73	0.53
5:E:237:SER:H	5:E:251:LYS:HB2	1.72	0.52
1:A:129:THR:HB	1:A:132:VAL:CG1	2.39	0.52
3:C:3:THR:HG22	3:C:23:HIS:HB3	1.91	0.52
4:D:159:TRP:O	4:D:165:GLU:HA	2.10	0.52
5:E:177:LEU:CD2	5:E:201:ALA:HB3	2.34	0.52
5:E:172:ILE:H	5:E:172:ILE:HD12	1.74	0.52
5:E:319:LEU:O	5:E:320:GLU:HB3	2.09	0.52
4:D:34:TYR:HD1	4:D:44:LEU:HA	1.74	0.52
5:E:215:TRP:CB	5:E:225:SER:HB3	2.29	0.52
5:E:83:ILE:CG2	5:E:84:CYS:N	2.72	0.52
5:E:92:GLU:HG2	5:E:93:VAL:H	1.74	0.52
5:E:76:ILE:HD13	5:E:97:VAL:HG23	1.90	0.52
2:B:54:ARG:HH21	2:B:56:LEU:HD11	1.74	0.52
5:E:10:ASP:O	5:E:74:LEU:HD12	2.09	0.52
5:E:305:VAL:HG12	5:E:331:LYS:HG3	1.92	0.52
5:E:349:ASP:CG	5:E:350:SER:H	2.12	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:105:LEU:HB2	1:A:151:LEU:HB3	1.90	0.52
4:D:98:SER:OG	4:D:99:TYR:HD1	1.93	0.52
5:E:128:VAL:HG23	5:E:141:GLY:O	2.09	0.52
2:B:43:GLU:HB2	2:B:56:LEU:HB2	1.91	0.52
3:C:23:HIS:O	3:C:24:SER:C	2.48	0.52
3:C:182:CYS:O	3:C:183:ALA:HB3	2.10	0.52
2:B:212:PRO:O	2:B:214:THR:HG23	2.10	0.52
3:C:53:ASN:HD21	3:C:62:ALA:HA	1.74	0.52
4:D:60:VAL:CG1	4:D:61:GLU:N	2.72	0.52
2:B:9:ARG:HB3	2:B:10:PRO:HD2	1.92	0.51
2:B:206:HIS:CD2	2:B:207:PRO:HD2	2.46	0.51
4:D:10:ILE:HD12	4:D:11:ALA:N	2.25	0.51
4:D:159:TRP:CZ3	4:D:210:CYS:HB2	2.46	0.51
5:E:347:LEU:HB3	5:E:354:LEU:O	2.10	0.51
3:C:13:GLU:O	3:C:14:GLU:HB2	2.11	0.51
1:A:141:GLU:N	1:A:141:GLU:OE1	2.43	0.51
2:B:206:HIS:C	2:B:208:SER:H	2.14	0.51
4:D:93:SER:HB3	4:D:105:PHE:CD1	2.45	0.51
5:E:218:GLU:OE2	5:E:307:GLY:N	2.44	0.51
2:B:119:THR:OG1	2:B:120:VAL:N	2.44	0.51
4:D:157:LEU:HG	4:D:212:VAL:HG22	1.92	0.51
5:E:212:GLU:HG2	5:E:213:LEU:H	1.76	0.51
5:E:267:ALA:HB2	5:E:291:VAL:HG23	1.93	0.51
2:B:55:PHE:HB3	2:B:71:SER:HB2	1.92	0.51
3:C:135:THR:OG1	3:C:136:ASP:N	2.44	0.51
3:C:47:ILE:HG12	3:C:48:HIS:N	2.26	0.51
3:C:58:MET:O	3:C:59:ALA:HB2	2.11	0.51
4:D:177:LEU:HD12	4:D:177:LEU:O	2.11	0.51
5:E:253:LEU:HA	5:E:254:PRO:O	2.11	0.51
1:A:157:THR:HG22	1:A:180:PHE:CE2	2.45	0.51
5:E:215:TRP:HB2	5:E:225:SER:CB	2.32	0.51
5:E:317:LEU:HD22	5:E:343:TRP:CE3	2.44	0.51
5:E:87:GLU:O	5:E:87:GLU:HG3	2.10	0.51
3:C:105:LEU:HD12	3:C:106:ALA:N	2.25	0.50
3:C:129:LYS:HD2	3:C:129:LYS:N	2.26	0.50
4:D:214:PHE:CE2	4:D:216:GLY:HA3	2.46	0.50
1:A:57:GLN:OE1	4:D:55:THR:HG21	2.11	0.50
5:E:213:LEU:HD22	5:E:214:TRP:N	2.25	0.50
5:E:26:PHE:C	5:E:26:PHE:CD2	2.85	0.50
5:E:194:VAL:HG11	5:E:289:LEU:CD1	2.41	0.50
1:A:110:ASP:OD1	1:A:140:ARG:HD2	2.10	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:27:GLN:HA	4:D:27:GLN:HE21	1.77	0.50
5:E:181:LYS:O	5:E:182:ALA:CB	2.58	0.50
5:E:180:GLN:HB2	5:E:199:PRO:HG2	1.94	0.50
5:E:348:SER:CA	5:E:354:LEU:HD22	2.40	0.50
1:A:76:ARG:HH12	2:B:86:ASP:CG	2.15	0.50
3:C:153:ILE:N	3:C:153:ILE:HD12	2.27	0.50
5:E:221:SER:O	5:E:222:SER:HB3	2.12	0.50
5:E:225:SER:HA	5:E:242:THR:HG21	1.92	0.50
5:E:11:THR:HG23	5:E:71:ILE:O	2.12	0.50
1:A:142:ASP:C	1:A:143:HIS:ND1	2.65	0.50
3:C:116:PRO:HB3	3:C:137:PHE:HB3	1.94	0.50
3:C:113:ASN:HD22	3:C:166:PHE:HE1	1.60	0.50
5:E:245:PRO:HB3	5:E:266:TYR:CE1	2.46	0.50
1:A:103:ASN:HB3	1:A:153:PHE:CE2	2.46	0.50
1:A:122:LEU:HB3	1:A:127:PRO:HA	1.94	0.50
1:A:148:PHE:CD1	2:B:180:GLY:HA3	2.47	0.50
3:C:157:THR:HG23	4:D:193:ARG:HH22	1.76	0.50
5:E:238:VAL:HG22	5:E:249:MET:CB	2.41	0.50
1:A:38:LYS:HB3	1:A:40:GLU:HG2	1.93	0.50
1:A:22:PHE:CE2	1:A:59:ALA:HA	2.46	0.50
1:A:168:TRP:CH2	2:B:35:ARG:CZ	2.95	0.50
4:D:211:GLN:HG3	4:D:234:ILE:HG23	1.93	0.50
4:D:43:MET:HA	4:D:43:MET:CE	2.42	0.50
5:E:76:ILE:HA	5:E:97:VAL:HG21	1.93	0.50
4:D:95:ARG:HG3	4:D:103:LEU:HD12	1.92	0.50
5:E:346:LEU:HA	5:E:356:GLU:OE1	2.12	0.50
5:E:229:PHE:CA	5:E:239:LYS:HB2	2.42	0.49
5:E:39:ASN:HB3	5:E:62:TRP:CH2	2.47	0.49
5:E:213:LEU:HB2	5:E:272:LEU:HD13	1.92	0.49
1:A:46:GLU:C	1:A:46:GLU:OE1	2.51	0.49
3:C:111:ILE:HD13	3:C:168:SER:HA	1.94	0.49
4:D:145:CYS:HB2	4:D:159:TRP:CH2	2.48	0.49
4:D:201:TRP:CZ2	4:D:242:ARG:HB2	2.47	0.49
1:A:148:PHE:HB3	1:A:150:TYR:CE2	2.46	0.49
3:C:143:VAL:O	3:C:144:SER:CB	2.59	0.49
4:D:180:GLN:O	4:D:182:ALA:N	2.43	0.49
5:E:227:ILE:H	5:E:242:THR:HG23	1.78	0.49
5:E:309:THR:O	5:E:310:SER:C	2.50	0.49
2:B:171:VAL:O	2:B:172:VAL:HB	2.11	0.49
3:C:35:TYR:CD1	3:C:45:TYR:HA	2.48	0.49
1:A:9:GLN:HB2	1:A:24:PHE:CE2	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:52:ALA:O	1:A:53:SER:OG	2.25	0.49
2:B:110:HIS:CG	3:C:29:THR:HG22	2.48	0.49
4:D:244:ASP:N	4:D:244:ASP:OD1	2.44	0.49
3:C:144:SER:HB3	3:C:145:GLN:CG	2.43	0.49
1:A:121:TRP:CE2	1:A:151:LEU:HB2	2.48	0.49
3:C:118:VAL:HA	3:C:133:LEU:O	2.13	0.49
4:D:142:THR:OG1	4:D:195:ARG:NE	2.46	0.48
5:E:253:LEU:CD1	5:E:255:LEU:HD22	2.43	0.48
3:C:26:ILE:HD11	3:C:30:ASP:HB2	1.95	0.48
5:E:230:ASP:OD2	5:E:230:ASP:C	2.51	0.48
2:B:169:THR:OG1	2:B:170:GLY:N	2.44	0.48
2:B:126:PRO:CD	2:B:209:LEU:HD21	2.43	0.48
1:A:70:LEU:HB2	2:B:38:GLU:HB2	1.95	0.48
3:C:66:ASP:OD2	3:C:68:LYS:HB2	2.14	0.48
5:E:146:VAL:O	5:E:146:VAL:HG13	2.13	0.48
2:B:110:HIS:CD2	3:C:29:THR:HG22	2.48	0.48
2:B:153:PRO:O	2:B:206:HIS:NE2	2.46	0.48
5:E:194:VAL:CG2	5:E:262:ALA:HB2	2.43	0.48
5:E:251:LYS:O	5:E:252:LYS:HB2	2.13	0.48
2:B:124:VAL:HG23	2:B:152:TYR:H	1.77	0.48
4:D:150:PHE:CE2	4:D:155:VAL:HG21	2.48	0.48
5:E:247:LEU:HD13	5:E:247:LEU:N	2.28	0.48
5:E:290:VAL:HB	5:E:306:TRP:O	2.14	0.48
2:B:87:ALA:O	2:B:91:ASN:ND2	2.45	0.48
2:B:47:PHE:O	2:B:48:ASN:ND2	2.46	0.48
3:C:26:ILE:HG12	3:C:27:SER:N	2.29	0.48
4:D:113:VAL:CG1	4:D:113:VAL:O	2.63	0.47
5:E:349:ASP:C	5:E:351:GLY:N	2.66	0.47
4:D:111:LEU:HD23	4:D:111:LEU:O	2.15	0.47
4:D:148:THR:HG22	4:D:189:SER:OG	2.14	0.47
2:B:152:TYR:CG	2:B:153:PRO:HA	2.49	0.47
2:B:67:VAL:HG11	2:B:90:TRP:CZ3	2.50	0.47
4:D:44:LEU:HG	4:D:57:GLU:HG3	1.96	0.47
5:E:363:PRO:O	5:E:364:ALA:HB2	2.15	0.47
2:B:163:ASN:ND2	2:B:199:VAL:H	2.04	0.47
4:D:8:TRP:CZ3	4:D:110:ARG:HB3	2.49	0.47
4:D:127:VAL:CG1	4:D:128:PHE:N	2.78	0.47
4:D:15:THR:HG22	4:D:16:SER:H	1.78	0.47
5:E:109:LEU:HB2	5:E:112:GLN:OE1	2.15	0.47
5:E:284:HIS:ND1	5:E:284:HIS:C	2.67	0.47
3:C:111:ILE:HD11	3:C:169:ASN:ND2	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:292:MET:CE	5:E:357:SER:HB3	2.45	0.47
1:A:123:ARG:C	1:A:125:GLY:H	2.16	0.47
2:B:160:TRP:CB	2:B:190:LEU:HD22	2.44	0.47
5:E:338:PRO:HB2	5:E:361:VAL:HG11	1.97	0.47
1:A:119:VAL:HG11	1:A:149:HIS:CG	2.50	0.47
2:B:177:ILE:HG22	2:B:178:GLN:N	2.30	0.47
2:B:187:LEU:HD22	5:E:43:PHE:HE2	1.79	0.47
3:C:3:THR:CG2	3:C:23:HIS:HB3	2.44	0.47
5:E:40:TYR:O	5:E:43:PHE:HB2	2.15	0.47
1:A:135:THR:HG22	1:A:148:PHE:HB2	1.96	0.47
5:E:1:LYS:HG2	5:E:2:LYS:H	1.78	0.47
5:E:27:HIS:CD2	5:E:85:GLU:HB2	2.50	0.47
1:A:56:ALA:C	1:A:58:GLY:N	2.67	0.46
3:C:145:GLN:OE1	3:C:153:ILE:HG12	2.15	0.46
3:C:150:ASP:OD1	3:C:150:ASP:N	2.46	0.46
4:D:144:VAL:HG22	4:D:193:ARG:HG2	1.96	0.46
1:A:123:ARG:C	1:A:125:GLY:N	2.69	0.46
1:A:65:VAL:HG12	1:A:66:ASP:N	2.29	0.46
3:C:144:SER:HB3	3:C:145:GLN:CD	2.35	0.46
4:D:127:VAL:HG23	4:D:237:ALA:CB	2.46	0.46
5:E:348:SER:HB2	5:E:354:LEU:H	1.78	0.46
3:C:116:PRO:HG2	3:C:194:ASP:HB2	1.96	0.46
1:A:176:LYS:HE2	5:E:63:ASP:OD1	2.15	0.46
3:C:131:VAL:HG11	4:D:128:PHE:CD2	2.51	0.46
5:E:324:ALA:HB1	5:E:327:SER:HB2	1.97	0.46
2:B:120:VAL:HG12	2:B:121:GLN:HG3	1.96	0.46
2:B:123:ARG:CG	2:B:123:ARG:NH1	2.70	0.46
2:B:76:TYR:OH	2:B:100:LYS:HE3	2.16	0.46
3:C:145:GLN:HE21	3:C:188:ASN:HB2	1.81	0.46
4:D:115:GLU:CD	4:D:115:GLU:H	2.18	0.46
4:D:13:SER:O	4:D:82:ALA:O	2.32	0.46
3:C:145:GLN:CG	3:C:189:SER:HB2	2.35	0.46
5:E:177:LEU:O	5:E:178:ALA:HB2	2.16	0.46
5:E:226:TRP:CD1	5:E:242:THR:HG22	2.51	0.46
1:A:30:GLU:HG2	1:A:31:ILE:N	2.31	0.46
4:D:37:PHE:HB2	4:D:40:GLN:OE1	2.16	0.46
1:A:85:VAL:HG12	1:A:112:PHE:HA	1.98	0.46
1:A:129:THR:HB	1:A:132:VAL:HG11	1.98	0.46
1:A:143:HIS:CD2	2:B:60:PHE:CZ	3.04	0.46
1:A:141:GLU:O	1:A:143:HIS:CE1	2.68	0.46
1:A:170:LEU:HD12	1:A:172:GLU:O	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:55:PHE:H	2:B:71:SER:HB3	1.80	0.46
5:E:178:ALA:O	5:E:200:LEU:HA	2.15	0.46
5:E:12:VAL:CG1	5:E:74:LEU:HD21	2.46	0.46
1:A:170:LEU:HD13	1:A:174:LEU:HB2	1.98	0.45
4:D:150:PHE:HE1	4:D:188:TYR:HB2	1.81	0.45
5:E:142:LYS:HB3	5:E:142:LYS:NZ	2.31	0.45
5:E:181:LYS:O	5:E:182:ALA:HB3	2.16	0.45
5:E:282:LYS:HG3	5:E:282:LYS:O	2.16	0.45
5:E:74:LEU:CD2	5:E:95:LEU:HD21	2.46	0.45
3:C:111:ILE:HD11	3:C:169:ASN:H	1.82	0.45
5:E:346:LEU:HD12	5:E:347:LEU:H	1.81	0.45
1:A:160:VAL:HG22	1:A:179:GLU:HB3	1.97	0.45
5:E:212:GLU:HB2	5:E:228:THR:HA	1.98	0.45
1:A:135:THR:CG2	1:A:148:PHE:HB2	2.47	0.45
5:E:1:LYS:HG2	5:E:2:LYS:N	2.31	0.45
5:E:64:GLN:H	5:E:64:GLN:NE2	2.08	0.45
1:A:35:ASP:OD1	1:A:36:MET:N	2.50	0.45
5:E:292:MET:HB3	5:E:355:LEU:HD12	1.98	0.45
1:A:25:ASP:OD1	1:A:28:GLY:N	2.48	0.45
1:A:76:ARG:NH1	2:B:85:PRO:HG2	2.32	0.45
2:B:73:VAL:O	2:B:73:VAL:HG12	2.17	0.45
3:C:148:ASP:O	3:C:149:SER:HB3	2.17	0.45
5:E:230:ASP:O	5:E:236:VAL:O	2.35	0.45
2:B:130:VAL:HG23	2:B:145:VAL:O	2.17	0.45
3:C:6:PRO:HG2	3:C:20:PRO:CG	2.46	0.45
2:B:160:TRP:HB3	2:B:190:LEU:HD22	1.98	0.45
3:C:111:ILE:HD13	3:C:169:ASN:H	1.80	0.45
3:C:22:ASN:HA	3:C:22:ASN:HD22	1.69	0.45
5:E:2:LYS:HG2	5:E:3:VAL:N	2.32	0.45
3:C:131:VAL:O	3:C:132:CYS:C	2.56	0.45
1:A:143:HIS:ND1	1:A:143:HIS:N	2.65	0.44
4:D:67:ILE:HD13	4:D:67:ILE:N	2.32	0.44
5:E:194:VAL:HG23	5:E:262:ALA:HB2	1.99	0.44
5:E:318:LYS:HE2	5:E:320:GLU:H	1.82	0.44
1:A:103:ASN:HB3	1:A:153:PHE:HE2	1.80	0.44
4:D:14:GLY:HA2	4:D:82:ALA:CB	2.38	0.44
4:D:178:LYS:CG	4:D:188:TYR:HE1	2.26	0.44
5:E:138:ILE:C	5:E:138:ILE:HD13	2.38	0.44
4:D:214:PHE:CE2	4:D:216:GLY:CA	3.01	0.44
5:E:236:VAL:H	5:E:252:LYS:H	1.64	0.44
1:A:30:GLU:OE2	1:A:33:HIS:ND1	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:144:SER:OG	3:C:190:ILE:HG22	2.18	0.44
1:A:143:HIS:NE2	2:B:60:PHE:CE1	2.85	0.44
2:B:211:SER:HA	2:B:212:PRO:HD3	1.81	0.44
3:C:133:LEU:HD12	3:C:134:PHE:H	1.83	0.44
4:D:99:TYR:CD1	4:D:99:TYR:N	2.78	0.44
5:E:264:PRO:HB3	5:E:293:ARG:HH11	1.83	0.44
1:A:87:PRO:HD2	1:A:170:LEU:HD22	1.99	0.44
4:D:65:PHE:HD1	4:D:79:VAL:HG12	1.82	0.44
4:D:8:TRP:CE3	4:D:154:HIS:HB3	2.52	0.44
5:E:7:LYS:O	5:E:10:ASP:HB2	2.17	0.44
5:E:169:GLU:OE2	5:E:171:LYS:HE2	2.17	0.44
5:E:206:LYS:O	5:E:208:THR:HG23	2.17	0.44
5:E:340:ALA:HA	5:E:361:VAL:HB	1.98	0.44
4:D:65:PHE:HD1	4:D:79:VAL:CG1	2.31	0.44
1:A:30:GLU:HB2	1:A:138:LEU:HD21	2.00	0.44
1:A:118:ASN:HB2	1:A:166:GLU:HB2	1.99	0.44
1:A:45:LEU:HD22	1:A:45:LEU:HA	1.87	0.44
1:A:45:LEU:HD13	1:A:47:GLU:H	1.83	0.44
3:C:46:VAL:HG12	3:C:47:ILE:N	2.33	0.44
1:A:109:ILE:HD12	1:A:109:ILE:N	2.33	0.43
1:A:46:GLU:C	1:A:46:GLU:CD	2.76	0.43
2:B:181:ASP:O	2:B:182:TRP:CB	2.63	0.43
5:E:112:GLN:NE2	5:E:280:THR:O	2.32	0.43
2:B:130:VAL:O	2:B:131:TYR:HB3	2.18	0.43
1:A:113:THR:OG1	1:A:114:PRO:HA	2.18	0.43
1:A:144:LEU:HD23	2:B:63:GLN:NE2	2.33	0.43
5:E:236:VAL:HG23	5:E:253:LEU:H	1.83	0.43
5:E:349:ASP:CG	5:E:350:SER:N	2.71	0.43
1:A:74:THR:HG23	2:B:36:PHE:CE2	2.53	0.43
2:B:12:PHE:CE1	2:B:89:TYR:HB2	2.40	0.43
4:D:145:CYS:HB2	4:D:159:TRP:CZ2	2.53	0.43
4:D:62:LYS:CG	4:D:63:ASP:H	2.17	0.43
5:E:313:LEU:HB2	5:E:349:ASP:HB2	2.00	0.43
4:D:61:GLU:C	4:D:62:LYS:HG2	2.36	0.43
5:E:197:SER:HB2	5:E:256:HIS:CE1	2.53	0.43
2:B:58:ARG:O	2:B:59:TYR:CD2	2.71	0.43
4:D:40:GLN:O	4:D:41:SER:HB2	2.17	0.43
5:E:233:ASN:ND2	5:E:233:ASN:O	2.52	0.43
5:E:292:MET:HB2	5:E:305:VAL:HG23	1.99	0.43
3:C:129:LYS:HD2	3:C:129:LYS:H	1.84	0.43
4:D:214:PHE:HE2	4:D:216:GLY:HA3	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:338:PRO:O	5:E:361:VAL:HG11	2.19	0.43
1:A:23:MET:HE2	1:A:30:GLU:HG3	2.00	0.43
1:A:55:GLU:HG3	1:A:56:ALA:N	2.33	0.43
3:C:23:HIS:NE2	3:C:32:ILE:HD13	2.33	0.43
5:E:355:LEU:HD13	5:E:355:LEU:O	2.19	0.43
5:E:52:ASN:HA	5:E:52:ASN:HD22	1.55	0.43
5:E:215:TRP:O	5:E:223:SER:HB2	2.19	0.43
5:E:227:ILE:O	5:E:227:ILE:HG22	2.19	0.43
5:E:248:GLN:CD	5:E:249:MET:H	2.23	0.43
2:B:208:SER:C	2:B:209:LEU:HD23	2.39	0.42
3:C:133:LEU:HD12	3:C:134:PHE:N	2.34	0.42
3:C:43:PRO:HG2	4:D:105:PHE:CE2	2.54	0.42
5:E:154:SER:HB2	5:E:176:VAL:N	2.33	0.42
1:A:154:LEU:HD23	1:A:155:PRO:N	2.33	0.42
2:B:102:ALA:O	2:B:103:ALA:C	2.57	0.42
3:C:191:ILE:HD12	3:C:192:PRO:O	2.19	0.42
5:E:113:SER:HA	5:E:147:SER:HA	2.00	0.42
5:E:14:LEU:HD22	5:E:14:LEU:H	1.84	0.42
5:E:245:PRO:HB2	5:E:259:LEU:HD21	2.01	0.42
2:B:172:VAL:HG22	2:B:173:SER:H	1.81	0.42
3:C:159:LEU:CD1	4:D:195:ARG:HB3	2.49	0.42
1:A:110:ASP:OD1	1:A:111:LYS:HG2	2.20	0.42
1:A:32:PHE:C	1:A:32:PHE:CD1	2.92	0.42
1:A:82:ILE:HD13	2:B:62:HIS:CG	2.54	0.42
2:B:51:GLU:O	2:B:52:ARG:C	2.58	0.42
3:C:146:SER:CB	3:C:147:LYS:CA	2.79	0.42
3:C:55:ASN:HB3	3:C:60:SER:CB	2.49	0.42
5:E:100:LEU:HD23	5:E:100:LEU:HA	1.84	0.42
5:E:182:ALA:CA	5:E:285:GLN:HG3	2.49	0.42
5:E:5:LEU:CD2	5:E:5:LEU:N	2.81	0.42
2:B:193:VAL:HG23	2:B:193:VAL:O	2.19	0.42
3:C:134:PHE:HZ	3:C:192:PRO:HD2	1.83	0.42
4:D:180:GLN:C	4:D:182:ALA:N	2.71	0.42
4:D:211:GLN:HG3	4:D:234:ILE:CG2	2.49	0.42
5:E:241:VAL:HG11	5:E:247:LEU:HD21	2.00	0.42
5:E:27:HIS:HE1	5:E:29:LYS:HE3	1.84	0.42
1:A:57:GLN:HE21	1:A:57:GLN:H	1.67	0.42
2:B:171:VAL:HG12	2:B:172:VAL:N	2.32	0.42
2:B:177:ILE:CG2	2:B:178:GLN:N	2.82	0.42
2:B:44:CYS:C	2:B:45:HIS:CD2	2.93	0.42
4:D:29:THR:HG23	4:D:30:THR:OG1	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:79:VAL:O	4:D:79:VAL:HG23	2.20	0.42
2:B:163:ASN:C	2:B:165:GLN:H	2.23	0.42
3:C:43:PRO:HG2	4:D:105:PHE:CD2	2.54	0.42
4:D:153:ASP:O	4:D:155:VAL:HG22	2.20	0.42
5:E:265:GLN:HG2	5:E:266:TYR:CD2	2.55	0.42
5:E:73:ASN:C	5:E:73:ASN:ND2	2.73	0.42
3:C:47:ILE:HD11	3:C:54:VAL:HG12	2.02	0.42
4:D:72:LEU:HD13	4:D:72:LEU:HA	1.88	0.42
5:E:152:GLN:HG2	5:E:152:GLN:H	1.60	0.42
5:E:172:ILE:HD12	5:E:172:ILE:N	2.34	0.42
1:A:12:PHE:HB2	2:B:38:GLU:O	2.19	0.42
1:A:45:LEU:CD1	1:A:47:GLU:H	2.33	0.42
2:B:195:ARG:N	2:B:198:GLU:OE1	2.50	0.42
5:E:207:LEU:HD22	5:E:277:GLU:OE2	2.20	0.42
5:E:35:LYS:HB3	5:E:35:LYS:HE2	1.76	0.42
5:E:28:TRP:CE3	5:E:83:ILE:O	2.72	0.42
1:A:110:ASP:OD1	1:A:111:LYS:N	2.52	0.42
2:B:75:GLU:HA	2:B:97:LEU:HD21	2.02	0.42
3:C:95:ASN:OD1	4:D:95:ARG:NH2	2.53	0.42
4:D:120:VAL:HG12	4:D:230:PRO:CB	2.50	0.42
4:D:125:VAL:HG22	4:D:147:ALA:HB2	2.00	0.42
4:D:151:TYR:CD2	4:D:186:SER:O	2.72	0.42
4:D:201:TRP:CG	4:D:201:TRP:O	2.73	0.42
4:D:30:THR:HG21	4:D:32:PHE:HE1	1.83	0.42
1:A:16:PRO:HD2	2:B:35:ARG:HD2	2.02	0.41
1:A:70:LEU:HB2	2:B:38:GLU:CB	2.50	0.41
3:C:174:TRP:CD2	4:D:146:LEU:HD11	2.55	0.41
3:C:26:ILE:HG23	3:C:67:ARG:HH22	1.85	0.41
5:E:319:LEU:C	5:E:321:ASN:H	2.22	0.41
5:E:345:CYS:HB3	5:E:357:SER:O	2.20	0.41
1:A:95:SER:HB2	1:A:96:PRO:CD	2.50	0.41
1:A:150:TYR:OH	2:B:179:ASN:O	2.29	0.41
3:C:158:VAL:HG22	3:C:169:ASN:OD1	2.19	0.41
3:C:96:LYS:HB3	3:C:96:LYS:HE2	1.72	0.41
5:E:31:SER:HB2	5:E:80:ASP:OD2	2.20	0.41
5:E:301:LEU:CG	5:E:335:VAL:HB	2.49	0.41
5:E:14:LEU:HD22	5:E:69:LEU:O	2.20	0.41
1:A:30:GLU:CD	1:A:44:ARG:HB2	2.40	0.41
3:C:113:ASN:HA	3:C:114:PRO:HD3	1.84	0.41
4:D:127:VAL:HG23	4:D:237:ALA:HB3	2.01	0.41
1:A:172:GLU:HA	1:A:173:PRO:HD3	1.91	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:195:ARG:O	2:B:196:SER:C	2.59	0.41
4:D:154:HIS:O	4:D:155:VAL:HG13	2.20	0.41
5:E:161:VAL:HB	5:E:168:VAL:HG21	2.02	0.41
5:E:285:GLN:O	5:E:286:GLU:CB	2.68	0.41
5:E:319:LEU:O	5:E:320:GLU:CB	2.68	0.41
5:E:301:LEU:HD11	5:E:335:VAL:N	2.35	0.41
5:E:253:LEU:HD13	5:E:255:LEU:HD22	2.02	0.41
5:E:34:ILE:HA	5:E:34:ILE:HD13	1.89	0.41
4:D:172:THR:HG22	4:D:173:ASP:N	2.36	0.41
1:A:119:VAL:HA	1:A:164:ARG:O	2.21	0.41
1:A:174:LEU:C	1:A:174:LEU:HD23	2.40	0.41
2:B:55:PHE:H	2:B:71:SER:CB	2.34	0.41
5:E:142:LYS:N	5:E:142:LYS:CD	2.84	0.41
5:E:74:LEU:HD21	5:E:95:LEU:HD21	2.02	0.41
5:E:301:LEU:HG	5:E:335:VAL:O	2.20	0.41
3:C:12:ASN:HB2	3:C:15:GLU:HG3	2.02	0.41
3:C:184:ASN:OD1	3:C:184:ASN:C	2.59	0.41
3:C:5:GLN:NE2	3:C:103:THR:OG1	2.54	0.41
3:C:9:MET:HE1	3:C:19:LEU:HG	2.03	0.41
4:D:98:SER:OG	4:D:99:TYR:CD1	2.73	0.41
5:E:182:ALA:HA	5:E:285:GLN:HG3	2.03	0.41
5:E:241:VAL:HG13	5:E:242:THR:H	1.84	0.41
5:E:90:LYS:O	5:E:91:GLU:C	2.59	0.41
2:B:176:LEU:HA	2:B:176:LEU:HD12	1.67	0.41
2:B:143:LEU:HD11	2:B:189:MET:HG2	2.02	0.41
5:E:128:VAL:CG1	5:E:129:GLN:H	2.29	0.41
5:E:184:SER:O	5:E:288:ASN:N	2.51	0.41
5:E:305:VAL:HG12	5:E:331:LYS:CG	2.50	0.41
2:B:130:VAL:HG22	2:B:131:TYR:N	2.35	0.40
2:B:152:TYR:CD1	2:B:153:PRO:HA	2.56	0.40
3:C:96:LYS:H	3:C:96:LYS:HG2	1.67	0.40
4:D:113:VAL:HG13	4:D:113:VAL:O	2.21	0.40
4:D:29:THR:HG21	4:D:97:GLY:CA	2.50	0.40
4:D:56:TYR:CD2	4:D:56:TYR:N	2.89	0.40
5:E:348:SER:CB	5:E:353:VAL:HA	2.51	0.40
2:B:172:VAL:HG22	5:E:45:TRP:HB2	2.02	0.40
1:A:22:PHE:CD1	1:A:22:PHE:C	2.95	0.40
3:C:144:SER:HB3	3:C:145:GLN:CB	2.51	0.40
1:A:89:VAL:HA	1:A:108:PHE:O	2.21	0.40
1:A:57:GLN:HG2	4:D:55:THR:HG21	2.04	0.40
1:A:98:GLU:HG2	1:A:99:LEU:H	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:143:VAL:O	3:C:144:SER:HB2	2.20	0.40
4:D:8:TRP:NE1	4:D:215:TYR:CE2	2.89	0.40
4:D:37:PHE:HB3	4:D:38:PRO:HD2	2.04	0.40
1:A:150:TYR:N	1:A:150:TYR:CD2	2.88	0.40
1:A:50:ARG:O	1:A:51:PHE:CD2	2.74	0.40
2:B:124:VAL:HG23	2:B:152:TYR:N	2.37	0.40
2:B:172:VAL:HG21	5:E:45:TRP:CD2	2.50	0.40
2:B:206:HIS:C	2:B:208:SER:N	2.74	0.40
2:B:44:CYS:O	2:B:45:HIS:CD2	2.74	0.40
3:C:153:ILE:HG22	3:C:154:THR:N	2.37	0.40
4:D:147:ALA:HB2	4:D:212:VAL:HG21	2.04	0.40
4:D:211:GLN:HG2	4:D:212:VAL:N	2.36	0.40
5:E:5:LEU:HD22	5:E:5:LEU:H	1.87	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	176/182 (97%)	154 (88%)	22 (12%)	0	100	100
2	B	189/221 (86%)	158 (84%)	29 (15%)	2 (1%)	14	51
3	C	189/206 (92%)	163 (86%)	24 (13%)	2 (1%)	14	51
4	D	243/245 (99%)	213 (88%)	30 (12%)	0	100	100
5	E	363/373 (97%)	295 (81%)	63 (17%)	5 (1%)	11	46
All	All	1160/1227 (94%)	983 (85%)	168 (14%)	9 (1%)	19	58

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	E	182	ALA

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Mol	Chain	Res	Type
5	E	286	GLU
5	E	352	GLN
3	C	144	SER
2	B	172	VAL
3	C	143	VAL
5	E	93	VAL
5	E	175	VAL
2	B	171	VAL

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	159/166 (96%)	146 (92%)	13 (8%)	11	38
2	B	167/189 (88%)	151 (90%)	16 (10%)	8	30
3	C	160/183 (87%)	142 (89%)	18 (11%)	6	25
4	D	212/216 (98%)	189 (89%)	23 (11%)	6	27
5	E	324/332 (98%)	272 (84%)	52 (16%)	2	15
All	All	1022/1086 (94%)	900 (88%)	122 (12%)	5	24

All (122) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	22	PHE
1	A	50	ARG
1	A	57	GLN
1	A	91	VAL
1	A	93	THR
1	A	106	ILE
1	A	122	LEU
1	A	141	GLU
1	A	142	ASP
1	A	143	HIS
1	A	153	PHE

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Mol	Chain	Res	Type
1	A	170	LEU
1	A	172	GLU
2	B	1	PHE
2	B	2	SER
2	B	39	GLN
2	B	48	ASN
2	B	69	PHE
2	B	82	LEU
2	B	97	LEU
2	B	119	THR
2	B	143	LEU
2	B	147	SER
2	B	151	PHE
2	B	155	SER
2	B	159	ARG
2	B	169	THR
2	B	186	THR
2	B	189	MET
3	C	4	THR
3	C	22	ASN
3	C	29	THR
3	C	55	ASN
3	C	63	ILE
3	C	90	TYR
3	C	94	THR
3	C	96	LYS
3	C	131	VAL
3	C	142	ASN
3	C	144	SER
3	C	148	ASP
3	C	157	THR
3	C	159	LEU
3	C	162	ARG
3	C	174	TRP
3	C	188	ASN
3	C	196	PHE
4	D	5	HIS
4	D	10	ILE
4	D	25	ASP
4	D	43	MET
4	D	67	ILE
4	D	74	LEU

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Mol	Chain	Res	Type
4	D	92	CYS
4	D	99	TYR
4	D	104	HIS
4	D	107	ASN
4	D	110	ARG
4	D	111	LEU
4	D	113	VAL
4	D	150	PHE
4	D	151	TYR
4	D	153	ASP
4	D	155	VAL
4	D	177	LEU
4	D	199	THR
4	D	219	GLU
4	D	223	TRP
4	D	242	ARG
4	D	244	ASP
5	E	5	LEU
5	E	12	VAL
5	E	14	LEU
5	E	27	HIS
5	E	32	ASN
5	E	34	ILE
5	E	35	LYS
5	E	50	LYS
5	E	52	ASN
5	E	56	ASP
5	E	64	GLN
5	E	66	ASN
5	E	73	ASN
5	E	77	GLU
5	E	138	ILE
5	E	139	GLN
5	E	142	LYS
5	E	144	LEU
5	E	152	GLN
5	E	172	ILE
5	E	173	ASP
5	E	177	LEU
5	E	180	GLN
5	E	196	PHE
5	E	198	PHE

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Mol	Chain	Res	Type
5	E	206	LYS
5	E	207	LEU
5	E	212	GLU
5	E	213	LEU
5	E	215	TRP
5	E	219	ARG
5	E	226	TRP
5	E	229	PHE
5	E	234	LYS
5	E	238	VAL
5	E	247	LEU
5	E	253	LEU
5	E	255	LEU
5	E	274	LEU
5	E	276	LEU
5	E	284	HIS
5	E	291	VAL
5	E	301	LEU
5	E	305	VAL
5	E	317	LEU
5	E	320	GLU
5	E	321	ASN
5	E	322	LYS
5	E	347	LEU
5	E	354	LEU
5	E	355	LEU
5	E	360	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (30) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	149	HIS
2	B	48	ASN
2	B	163	ASN
2	B	178	GLN
2	B	179	ASN
3	C	5	GLN
3	C	18	HIS
3	C	22	ASN
3	C	33	HIS
3	C	37	GLN
3	C	53	ASN

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Mol	Chain	Res	Type
3	C	113	ASN
3	C	145	GLN
4	D	27	GLN
4	D	68	ASN
4	D	100	ASN
4	D	107	ASN
4	D	137	HIS
4	D	213	GLN
5	E	25	GLN
5	E	30	ASN
5	E	52	ASN
5	E	64	GLN
5	E	66	ASN
5	E	73	ASN
5	E	110	GLN
5	E	139	GLN
5	E	152	GLN
5	E	180	GLN
5	E	288	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 carbohydrates 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

There are no chain breaks in this entry.

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

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

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å ²)	Q<0.9
1	A	178/182 (97%)	-0.28	0	100 100	99, 205, 259, 320	0
2	B	195/221 (88%)	-0.22	0	100 100	144, 185, 249, 292	0
3	C	193/206 (93%)	-0.30	0	100 100	146, 207, 283, 424	1 (0%)
4	D	245/245 (100%)	-0.36	0	100 100	157, 220, 293, 346	0
5	E	365/373 (97%)	-0.31	1 (0%)	94 90	160, 229, 319, 365	0
All	All	1176/1227 (95%)	-0.30	1 (0%)	95 94	99, 212, 295, 424	1 (0%)

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
5	E	262	ALA	2.4

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.