



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 12:36 AM GMT

PDB ID : 2AXZ
Title : Crystal structure of PrgX/cCF10 complex
Authors : Shi, K.; Brown, C.K.; Gu, Z.Y.; Kozlowicz, B.K.; Dunny, G.M.; Ohlendorf, D.H.; Earhart, C.A.
Deposited on : 2005-09-06
Resolution : 3.00 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
<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) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

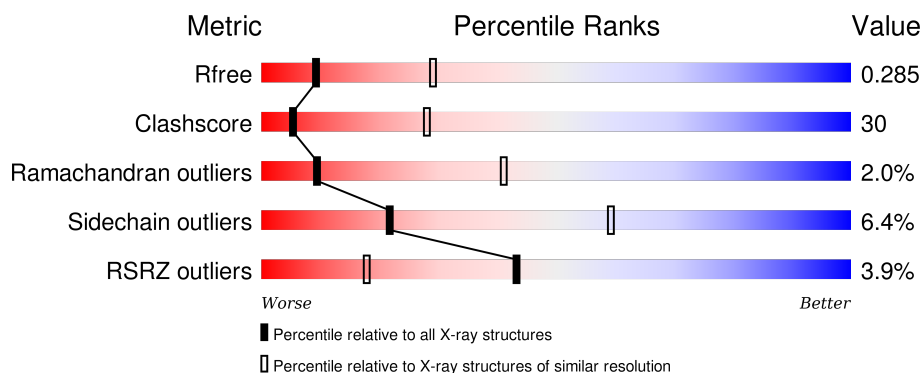
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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.



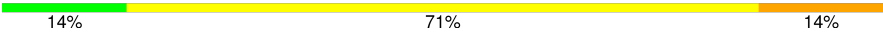
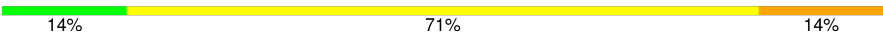

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	1578 (3.00-3.00)
Clashscore	102246	1912 (3.00-3.00)
Ramachandran outliers	100387	1853 (3.00-3.00)
Sidechain outliers	100360	1856 (3.00-3.00)
RSRZ outliers	91569	1592 (3.00-3.00)

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.

Mol	Chain	Length	Quality of chain
1	A	317	
1	B	317	
1	C	317	
1	D	317	
2	E	7	

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Mol	Chain	Length	Quality of chain
2	F	7	 14% 71% 14%
2	H	7	 14% 71% 14%
3	I	8	 13% 88% 13%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 10170 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 PrgX.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	306	Total	C	N	O	Se	0	0	0
			2532	1645	406	475	6			
1	B	305	Total	C	N	O	Se	0	0	0
			2523	1640	405	472	6			
1	C	279	Total	C	N	O	Se	0	0	0
			2309	1499	374	432	4			
1	D	305	Total	C	N	O	Se	0	0	0
			2523	1640	405	472	6			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	MET	MODIFIED RESIDUE	UNP Q04114
A	27	MSE	MET	MODIFIED RESIDUE	UNP Q04114
A	67	MSE	MET	MODIFIED RESIDUE	UNP Q04114
A	175	MSE	MET	MODIFIED RESIDUE	UNP Q04114
A	203	MSE	MET	MODIFIED RESIDUE	UNP Q04114
A	297	MSE	MET	MODIFIED RESIDUE	UNP Q04114
B	1	MSE	MET	MODIFIED RESIDUE	UNP Q04114
B	27	MSE	MET	MODIFIED RESIDUE	UNP Q04114
B	67	MSE	MET	MODIFIED RESIDUE	UNP Q04114
B	175	MSE	MET	MODIFIED RESIDUE	UNP Q04114
B	203	MSE	MET	MODIFIED RESIDUE	UNP Q04114
B	297	MSE	MET	MODIFIED RESIDUE	UNP Q04114
C	1	MSE	MET	MODIFIED RESIDUE	UNP Q04114
C	27	MSE	MET	MODIFIED RESIDUE	UNP Q04114
C	67	MSE	MET	MODIFIED RESIDUE	UNP Q04114
C	175	MSE	MET	MODIFIED RESIDUE	UNP Q04114
C	203	MSE	MET	MODIFIED RESIDUE	UNP Q04114
C	297	MSE	MET	MODIFIED RESIDUE	UNP Q04114
D	1	MSE	MET	MODIFIED RESIDUE	UNP Q04114
D	27	MSE	MET	MODIFIED RESIDUE	UNP Q04114
D	67	MSE	MET	MODIFIED RESIDUE	UNP Q04114

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Chain	Residue	Modelled	Actual	Comment	Reference
D	175	MSE	MET	MODIFIED RESIDUE	UNP Q04114
D	203	MSE	MET	MODIFIED RESIDUE	UNP Q04114
D	297	MSE	MET	MODIFIED RESIDUE	UNP Q04114

- Molecule 2 is a protein called LVTLVFV peptide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	E	7	Total	C	N	O	0	0	0
			56	40	7	9			
2	F	7	Total	C	N	O	0	0	0
			56	40	7	9			
2	H	7	Total	C	N	O	0	0	0
			56	40	7	9			

- Molecule 3 is a protein called TPPKEVT(MSE) peptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	I	8	Total	C	N	O	Se	0	0	0
			62	39	9	13	1			

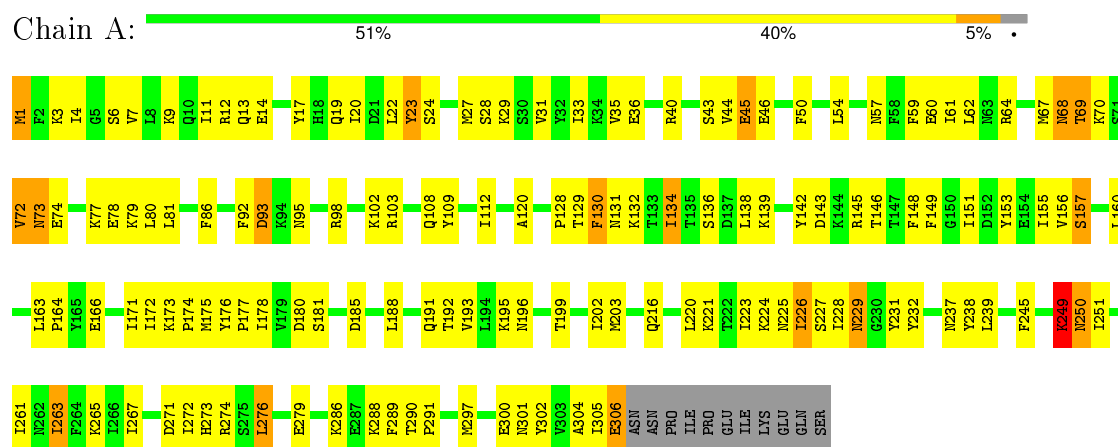
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	23	Total	O	0	0
			23	23		
4	B	18	Total	O	0	0
			18	18		
4	C	5	Total	O	0	0
			5	5		
4	D	7	Total	O	0	0
			7	7		

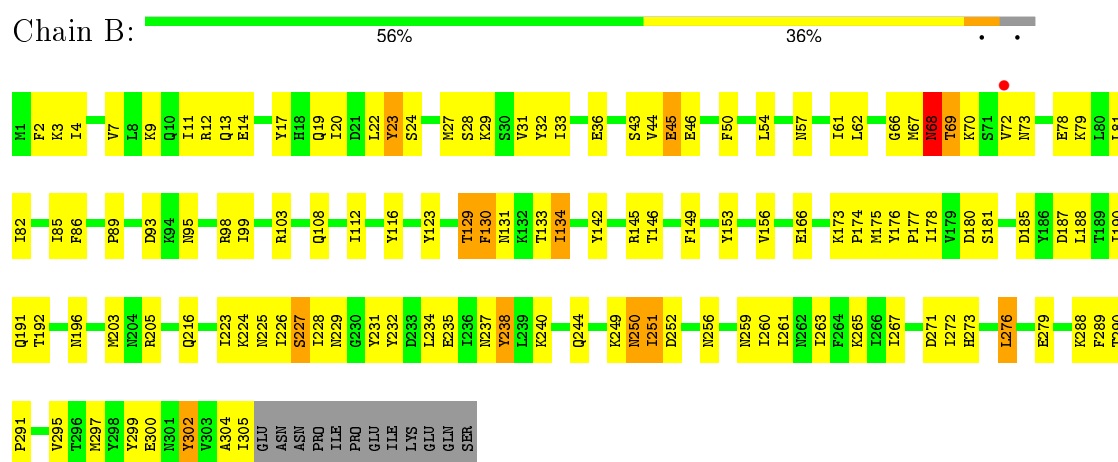
3 Residue-property plots

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.

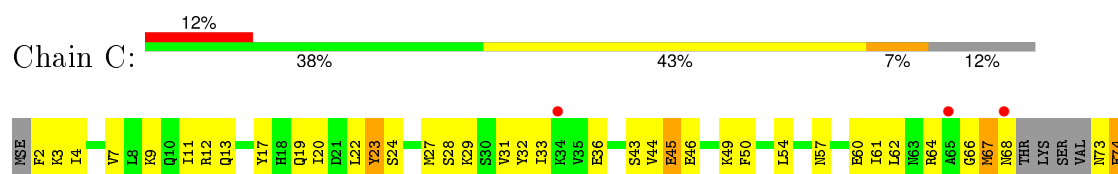
• Molecule 1: PrgX

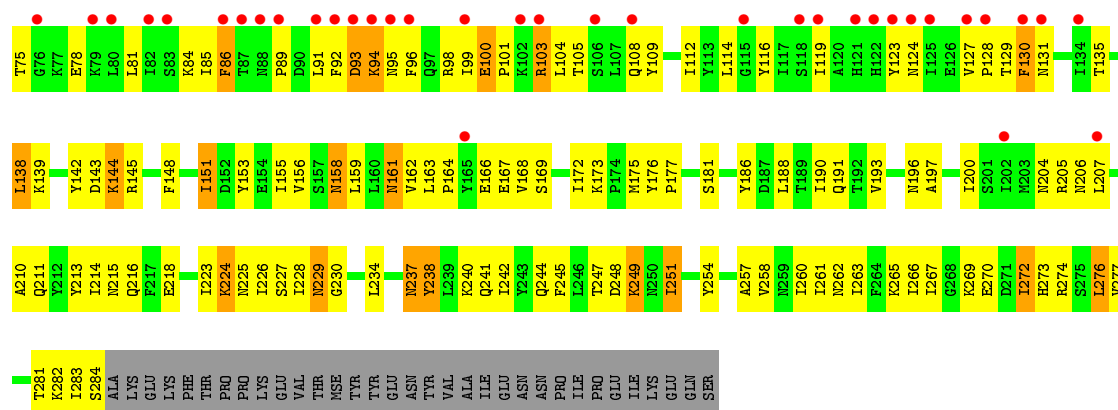


• Molecule 1: PrgX

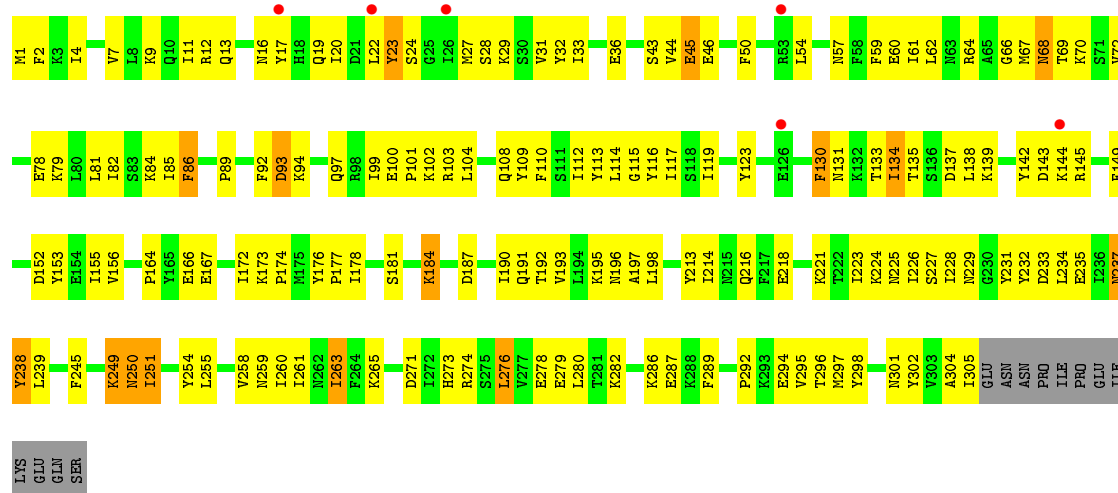


• Molecule 1: PrgX

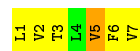




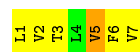
• Molecule 1: PrgX



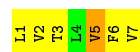
• Molecule 2: LVTLVFV peptide




• Molecule 2: LVTLVFV peptide




• Molecule 2: LVTLVFV peptide



- Molecule 3: TPPKEVT(MSE) peptide

Chain I: 



T290	P291	P292	K293	E294	V295	T296	M297
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4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	71.08 Å 83.90 Å 286.80 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 3.00 36.21 – 2.76	Depositor EDS
% Data completeness (in resolution range)	(Not available) (40.00-3.00) 87.3 (36.21-2.76)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.52 (at 2.77 Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.228 , 0.288 0.232 , 0.285	Depositor DCC
R_{free} test set	1626 reflections (4.97%)	DCC
Wilson B-factor (Å ²)	61.4	Xtriage
Anisotropy	0.209	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 69.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 39347 reflections	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	10170	wwPDB-VP
Average B, all atoms (Å ²)	71.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.41% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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	0.28	0/2579	0.50	0/3475
1	B	0.27	0/2570	0.50	0/3463
1	C	0.28	0/2350	0.50	0/3165
1	D	0.27	0/2570	0.49	0/3463
2	E	0.42	0/56	0.68	0/75
2	F	0.43	0/56	0.67	0/75
2	H	0.43	0/56	0.61	0/75
3	I	0.40	0/62	0.70	0/81
All	All	0.28	0/10299	0.50	0/13872

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	2532	0	2570	153	0
1	B	2523	0	2564	144	0
1	C	2309	0	2342	180	0
1	D	2523	0	2564	171	0
2	E	56	0	67	11	0
2	F	56	0	67	11	0
2	H	56	0	67	15	0
3	I	62	0	64	24	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	23	0	0	2	0
4	B	18	0	0	1	0
4	C	5	0	0	1	0
4	D	7	0	0	0	0
All	All	10170	0	10305	614	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 30.

All (614) 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:227:SER:HB2	1:B:300:GLU:HG3	1.36	1.04
1:D:81:LEU:HA	1:D:84:LYS:HD3	1.42	1.01
1:C:20:ILE:H	1:C:20:ILE:HD12	1.29	0.97
1:C:163:LEU:HD12	1:C:164:PRO:HD2	1.46	0.97
1:B:20:ILE:HD12	1:B:20:ILE:H	1.29	0.95
1:C:251:ILE:H	1:C:251:ILE:HD13	1.30	0.95
1:A:229:ASN:HD22	1:A:232:TYR:H	1.10	0.95
1:D:20:ILE:H	1:D:20:ILE:HD12	1.30	0.94
1:A:20:ILE:HD12	1:A:20:ILE:H	1.31	0.94
1:D:103:ARG:HG3	1:D:104:LEU:HD12	1.46	0.94
1:C:158:ASN:HD22	1:C:159:LEU:N	1.70	0.90
1:D:1:MSE:HG3	1:D:2:PHE:H	1.41	0.86
1:D:192:THR:HG21	2:H:5:VAL:HG22	1.58	0.85
1:A:70:LYS:HB3	1:A:80:LEU:HD11	1.56	0.84
1:A:1:MSE:H3	1:A:1:MSE:HE3	1.42	0.84
1:A:196:ASN:HD21	2:E:3:THR:H	1.21	0.84
1:C:94:LYS:NZ	1:C:94:LYS:HA	1.92	0.83
1:C:263:ILE:HG13	1:D:263:ILE:HG13	1.59	0.83
1:B:131:ASN:HA	1:B:134:ILE:HD11	1.59	0.83
1:B:69:THR:HA	1:B:72:VAL:HG12	1.61	0.83
1:B:192:THR:HG21	2:F:5:VAL:HG22	1.60	0.81
1:D:62:LEU:HB3	1:D:67:MSE:HG3	1.61	0.81
1:C:62:LEU:HB3	1:C:67:MSE:HG3	1.61	0.81
1:A:192:THR:HG21	2:E:5:VAL:HG22	1.62	0.81
1:A:62:LEU:HB3	1:A:67:MSE:HG3	1.63	0.81
1:D:103:ARG:HH21	1:D:133:THR:HG21	1.44	0.81
1:B:62:LEU:HB3	1:B:67:MSE:HG3	1.62	0.80
1:C:98:ARG:HB3	1:C:98:ARG:NH1	1.95	0.80
1:A:229:ASN:ND2	1:A:232:TYR:H	1.80	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:265:LYS:HB2	1:D:273:HIS:CD2	2.17	0.79
1:C:85:ILE:HD12	1:C:91:LEU:HB2	1.66	0.78
1:A:131:ASN:HA	1:A:134:ILE:HD11	1.64	0.78
1:C:75:THR:HG21	1:C:108:GLN:HE21	1.46	0.78
1:B:250:ASN:ND2	1:B:251:ILE:HD13	1.99	0.77
3:I:292:PRO:O	3:I:295:VAL:HG22	1.86	0.76
1:B:79:LYS:NZ	1:B:108:GLN:HE22	1.83	0.76
1:B:196:ASN:HD21	2:F:3:THR:H	1.33	0.76
1:D:196:ASN:HD21	2:H:3:THR:H	1.34	0.75
1:B:252:ASP:OD1	3:I:292:PRO:HD3	1.87	0.75
1:A:265:LYS:HB2	1:A:273:HIS:CD2	2.21	0.74
1:C:257:ALA:O	1:C:261:ILE:HG13	1.88	0.74
1:C:262:ASN:HB2	3:I:293:LYS:NZ	2.03	0.73
1:A:77:LYS:NZ	1:A:77:LYS:HB2	2.02	0.73
1:C:49:LYS:HE3	1:D:1:MSE:HE1	1.71	0.73
1:C:86:PHE:CE1	1:C:119:ILE:HG12	2.24	0.72
1:C:263:ILE:HD12	1:D:260:ILE:HD13	1.71	0.72
1:B:250:ASN:HD22	1:B:251:ILE:HD13	1.55	0.72
1:B:252:ASP:CG	3:I:292:PRO:HD3	2.10	0.72
1:C:98:ARG:HB3	1:C:98:ARG:HH11	1.52	0.72
1:C:135:THR:O	1:C:139:LYS:HG2	1.89	0.72
1:A:11:ILE:HG13	1:B:149:PHE:CE2	2.26	0.71
1:B:192:THR:HG21	2:F:5:VAL:CG2	2.20	0.71
1:B:252:ASP:OD2	3:I:292:PRO:HD3	1.90	0.71
1:C:158:ASN:C	1:C:158:ASN:HD22	1.91	0.71
1:C:142:TYR:HA	1:C:145:ARG:HG2	1.72	0.71
1:B:196:ASN:ND2	2:F:3:THR:H	1.89	0.71
1:C:114:LEU:HD12	1:C:158:ASN:HD21	1.56	0.70
1:D:142:TYR:HA	1:D:145:ARG:HG2	1.73	0.70
1:C:164:PRO:HB2	1:C:167:GLU:OE2	1.91	0.70
1:A:229:ASN:HD21	1:A:231:TYR:HB2	1.56	0.70
1:C:262:ASN:HB2	3:I:293:LYS:HZ1	1.54	0.69
1:D:221:LYS:HG2	1:D:228:ILE:CD1	2.23	0.69
1:A:43:SER:HA	1:B:43:SER:HA	1.73	0.69
1:A:196:ASN:ND2	2:E:3:THR:H	1.90	0.69
1:A:79:LYS:NZ	1:A:108:GLN:HE22	1.89	0.69
1:B:224:LYS:O	1:B:225:ASN:HB2	1.93	0.69
1:C:181:SER:HB2	1:C:226:ILE:HD13	1.74	0.68
1:C:75:THR:HG21	1:C:108:GLN:NE2	2.08	0.68
1:C:155:ILE:O	1:C:158:ASN:ND2	2.25	0.68
1:A:224:LYS:O	1:A:225:ASN:HB2	1.92	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:192:THR:HG21	2:H:5:VAL:CG2	2.23	0.67
1:B:265:LYS:HB2	1:B:273:HIS:CD2	2.29	0.67
1:D:135:THR:O	1:D:139:LYS:HG2	1.95	0.67
1:D:110:PHE:HD2	1:D:155:ILE:HD13	1.60	0.67
1:A:19:GLN:HE22	1:A:33:ILE:HD11	1.60	0.66
1:C:103:ARG:HG3	1:C:104:LEU:HG	1.76	0.66
1:D:131:ASN:HA	1:D:134:ILE:HD11	1.78	0.66
1:A:191:GLN:HE22	1:A:228:ILE:HA	1.59	0.66
1:C:94:LYS:HA	1:C:94:LYS:HZ1	1.60	0.65
1:C:94:LYS:HA	1:C:94:LYS:HZ2	1.61	0.65
1:A:263:ILE:HG13	1:B:263:ILE:HG12	1.76	0.65
1:D:19:GLN:HE22	1:D:33:ILE:HD11	1.60	0.65
1:B:67:MSE:C	1:B:69:THR:H	1.99	0.65
1:A:271:ASP:HB3	1:A:304:ALA:HB3	1.78	0.65
1:C:269:LYS:HB3	1:C:272:ILE:HG23	1.77	0.65
1:A:1:MSE:HE3	1:A:1:MSE:N	2.10	0.65
1:A:77:LYS:HB2	1:A:77:LYS:HZ3	1.59	0.65
1:C:20:ILE:CD1	1:C:20:ILE:H	2.06	0.65
1:C:163:LEU:HD12	1:C:164:PRO:CD	2.25	0.65
1:C:267:ILE:HA	1:D:237:ASN:ND2	2.12	0.65
1:D:78:GLU:OE1	1:D:99:ILE:HD11	1.97	0.65
1:C:109:TYR:HA	1:C:112:ILE:HD12	1.78	0.65
1:B:70:LYS:HE2	1:B:299:TYR:HD2	1.62	0.65
1:B:19:GLN:HE22	1:B:33:ILE:HD11	1.61	0.64
1:A:192:THR:HG21	2:E:5:VAL:CG2	2.26	0.64
1:D:79:LYS:NZ	1:D:108:GLN:HE22	1.95	0.64
1:C:265:LYS:HB2	1:C:273:HIS:CD2	2.33	0.64
1:C:19:GLN:HE22	1:C:33:ILE:HD11	1.62	0.64
1:A:279:GLU:OE1	2:E:1:LEU:HD23	1.98	0.64
1:B:271:ASP:HB3	1:B:304:ALA:HB3	1.79	0.64
1:C:191:GLN:OE1	1:C:228:ILE:HA	1.98	0.64
1:B:279:GLU:OE1	2:F:1:LEU:HD23	1.98	0.64
1:A:149:PHE:CE2	1:B:11:ILE:HG13	2.32	0.64
1:C:224:LYS:HB2	1:C:224:LYS:NZ	2.12	0.63
1:A:177:PRO:HB3	1:A:216:GLN:HE22	1.64	0.63
1:D:93:ASP:O	1:D:97:GLN:HG3	1.97	0.63
1:A:146:THR:HB	1:B:14:GLU:OE1	1.98	0.63
1:C:100:GLU:CD	1:C:101:PRO:HD3	2.19	0.63
1:C:166:GLU:HG2	1:C:167:GLU:OE2	1.99	0.63
1:D:235:GLU:O	1:D:238:TYR:HD1	1.82	0.63
1:A:199:THR:HG22	1:A:203:MSE:HE2	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:224:LYS:O	1:D:225:ASN:HB2	2.00	0.62
1:D:278:GLU:HG2	1:D:282:LYS:NZ	2.15	0.62
1:C:197:ALA:HB1	1:C:213:TYR:CZ	2.35	0.61
1:C:20:ILE:N	1:C:20:ILE:HD12	2.09	0.61
1:B:79:LYS:HZ2	1:B:108:GLN:HE22	1.48	0.61
1:C:229:ASN:HD22	1:C:230:GLY:N	1.98	0.61
1:A:72:VAL:C	1:A:74:GLU:H	2.02	0.61
1:B:156:VAL:HG21	1:B:175:MSE:SE	2.51	0.61
1:D:144:LYS:HD2	1:D:144:LYS:N	2.15	0.61
1:C:29:LYS:O	1:C:33:ILE:HG12	2.01	0.61
1:A:300:GLU:HG2	1:B:225:ASN:HA	1.83	0.61
1:B:271:ASP:HB2	4:B:318:HOH:O	2.00	0.61
1:B:67:MSE:O	1:B:69:THR:HG23	2.00	0.61
1:B:234:LEU:HD22	1:B:260:ILE:HG23	1.82	0.61
1:C:224:LYS:O	1:C:225:ASN:HB2	2.01	0.61
1:C:258:VAL:HA	1:C:261:ILE:HD12	1.83	0.61
1:B:69:THR:CG2	1:B:73:ASN:HD21	2.14	0.60
1:C:261:ILE:HG12	1:C:276:LEU:CD1	2.30	0.60
1:B:20:ILE:N	1:B:20:ILE:HD12	2.09	0.60
1:A:29:LYS:O	1:A:33:ILE:HG12	2.02	0.60
1:B:142:TYR:HA	1:B:145:ARG:HG2	1.84	0.60
1:D:216:GLN:HE21	1:D:216:GLN:HA	1.66	0.60
1:D:214:ILE:O	1:D:218:GLU:HG2	2.02	0.60
1:C:161:ASN:OD1	1:C:162:VAL:HG13	2.00	0.60
1:C:89:PRO:HB3	1:C:123:TYR:CE2	2.37	0.60
1:B:29:LYS:O	1:B:33:ILE:HG12	2.01	0.60
1:D:89:PRO:HB3	1:D:123:TYR:CE2	2.37	0.60
1:D:29:LYS:O	1:D:33:ILE:HG12	2.01	0.59
1:C:262:ASN:HB2	3:I:293:LYS:CE	2.31	0.59
1:D:20:ILE:HD12	1:D:20:ILE:N	2.10	0.59
1:B:57:ASN:O	1:B:61:ILE:HG13	2.01	0.59
1:C:277:VAL:HG13	3:I:294:GLU:CD	2.22	0.59
1:D:43:SER:OG	1:D:46:GLU:HG3	2.02	0.59
1:A:163:LEU:HD12	1:A:164:PRO:HD2	1.83	0.59
1:B:251:ILE:HD13	1:B:251:ILE:N	2.17	0.59
1:B:229:ASN:HD22	1:B:232:TYR:H	1.51	0.59
1:C:227:SER:HA	1:D:301:ASN:OD1	2.02	0.59
1:B:20:ILE:CD1	1:B:20:ILE:H	2.06	0.59
1:D:229:ASN:HD22	1:D:232:TYR:H	1.51	0.58
1:C:66:GLY:C	1:C:68:ASN:H	2.07	0.58
1:D:19:GLN:NE2	1:D:33:ILE:HD11	2.19	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:78:GLU:HB2	1:A:112:ILE:HD13	1.86	0.58
1:D:117:ILE:HD13	1:D:130:PHE:CE1	2.39	0.58
1:A:57:ASN:O	1:A:61:ILE:HG13	2.04	0.58
1:A:142:TYR:HA	1:A:145:ARG:HG2	1.86	0.58
1:D:176:TYR:OH	1:D:193:VAL:HB	2.04	0.58
1:D:191:GLN:HE22	1:D:228:ILE:HA	1.67	0.57
1:C:43:SER:OG	1:C:46:GLU:HG3	2.04	0.57
1:D:164:PRO:HD2	1:D:167:GLU:OE1	2.04	0.57
1:A:67:MSE:O	1:A:69:THR:N	2.37	0.57
1:A:43:SER:OG	1:A:46:GLU:HG3	2.05	0.57
1:C:269:LYS:HB3	1:C:272:ILE:CG2	2.35	0.57
1:B:297:MSE:HE2	2:F:6:PHE:HE1	1.69	0.57
1:D:1:MSE:HG3	1:D:2:PHE:N	2.17	0.57
1:C:261:ILE:HG12	1:C:276:LEU:HD11	1.87	0.57
1:C:138:LEU:HD23	1:C:142:TYR:HD2	1.69	0.57
1:D:70:LYS:HE2	2:H:7:VAL:HG13	1.86	0.57
1:B:19:GLN:NE2	1:B:33:ILE:HD11	2.20	0.56
1:D:173:LYS:HB2	1:D:174:PRO:HD3	1.85	0.56
1:C:176:TYR:HB3	1:C:216:GLN:OE1	2.05	0.56
1:B:103:ARG:HG2	1:B:103:ARG:HH11	1.68	0.56
1:D:166:GLU:CD	1:D:166:GLU:H	2.08	0.56
1:B:78:GLU:HB2	1:B:112:ILE:HD13	1.87	0.56
1:B:43:SER:OG	1:B:46:GLU:HG3	2.05	0.56
1:D:99:ILE:HG13	1:D:116:TYR:CE2	2.40	0.56
1:A:267:ILE:HA	1:B:237:ASN:ND2	2.21	0.56
1:C:19:GLN:NE2	1:C:33:ILE:HD11	2.20	0.56
1:A:19:GLN:NE2	1:A:33:ILE:HD11	2.19	0.56
1:C:86:PHE:CD1	1:C:119:ILE:HG12	2.41	0.56
1:B:224:LYS:O	1:B:225:ASN:CB	2.54	0.56
1:B:173:LYS:HB2	1:B:174:PRO:HD3	1.88	0.56
1:C:44:VAL:HG11	1:D:4:ILE:HD11	1.87	0.56
1:C:151:ILE:HD13	1:C:151:ILE:O	2.06	0.56
1:A:267:ILE:HG21	1:B:234:LEU:HD23	1.86	0.56
1:A:271:ASP:HB3	1:A:304:ALA:CB	2.36	0.56
1:D:196:ASN:ND2	2:H:3:THR:H	2.04	0.55
1:A:7:VAL:O	1:A:11:ILE:HD13	2.07	0.55
1:C:272:ILE:HD12	1:C:272:ILE:O	2.07	0.55
1:D:57:ASN:O	1:D:61:ILE:HG13	2.06	0.55
1:D:271:ASP:HB3	1:D:304:ALA:HB3	1.87	0.55
1:C:260:ILE:HG12	1:D:263:ILE:HD11	1.87	0.55
1:D:261:ILE:HD12	1:D:280:LEU:HD22	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:114:LEU:CD1	1:C:158:ASN:HD21	2.18	0.55
1:C:196:ASN:N	1:C:196:ASN:HD22	2.04	0.55
1:A:11:ILE:HG22	1:A:54:LEU:HD22	1.89	0.55
1:A:191:GLN:NE2	1:A:228:ILE:HA	2.21	0.55
1:D:2:PHE:HD1	1:D:67:MSE:CE	2.20	0.55
1:C:267:ILE:HA	1:D:237:ASN:HD21	1.70	0.55
1:C:43:SER:HA	1:D:43:SER:HA	1.88	0.55
1:C:81:LEU:HD22	1:C:116:TYR:OH	2.07	0.55
1:A:20:ILE:HD12	1:A:20:ILE:N	2.12	0.54
1:A:263:ILE:CG2	1:B:234:LEU:HD21	2.36	0.54
1:A:160:LEU:HD21	1:A:172:ILE:HD11	1.89	0.54
1:A:173:LYS:HB2	1:A:174:PRO:HD3	1.90	0.54
1:C:238:TYR:O	1:C:242:ILE:HG12	2.07	0.54
1:C:28:SER:OG	1:C:31:VAL:HG22	2.07	0.54
1:A:20:ILE:H	1:A:20:ILE:CD1	2.08	0.54
1:B:66:GLY:C	1:B:68:ASN:H	2.09	0.54
1:D:224:LYS:O	1:D:225:ASN:CB	2.55	0.54
1:C:156:VAL:HG11	1:C:172:ILE:HG12	1.89	0.54
1:D:20:ILE:CD1	1:D:20:ILE:H	2.07	0.54
1:D:117:ILE:HD13	1:D:130:PHE:CD1	2.42	0.54
1:D:223:ILE:O	1:D:226:ILE:HG12	2.08	0.54
3:I:291:PRO:O	3:I:295:VAL:HG13	2.07	0.54
1:D:196:ASN:ND2	2:H:2:VAL:HA	2.23	0.54
1:A:69:THR:O	1:A:70:LYS:HB2	2.07	0.54
1:D:221:LYS:HG2	1:D:228:ILE:HD11	1.90	0.54
1:D:216:GLN:NE2	1:D:216:GLN:HA	2.22	0.54
1:D:279:GLU:OE1	2:H:1:LEU:HD23	2.08	0.53
1:B:68:ASN:O	1:B:69:THR:O	2.26	0.53
1:A:199:THR:CG2	1:A:203:MSE:HE2	2.38	0.53
1:C:205:ARG:HH22	1:C:283:ILE:HG23	1.74	0.53
1:C:281:THR:O	1:C:283:ILE:N	2.42	0.53
1:C:73:ASN:O	1:C:74:GLU:HB2	2.08	0.53
1:B:28:SER:OG	1:B:31:VAL:HG22	2.08	0.53
1:A:156:VAL:HG21	1:A:175:MSE:SE	2.57	0.53
1:C:57:ASN:O	1:C:61:ILE:HG13	2.07	0.53
1:A:176:TYR:OH	1:A:193:VAL:HB	2.08	0.53
1:A:28:SER:OG	1:A:31:VAL:HG22	2.08	0.53
1:D:251:ILE:HD13	1:D:251:ILE:O	2.09	0.53
1:C:108:GLN:O	1:C:112:ILE:HG13	2.09	0.53
1:B:229:ASN:HB3	1:B:232:TYR:HB2	1.90	0.53
1:D:181:SER:HB2	1:D:226:ILE:HD13	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:131:ASN:CA	1:B:134:ILE:HD11	2.35	0.52
1:B:256:ASN:O	1:B:260:ILE:HG13	2.09	0.52
1:D:251:ILE:HD12	1:D:255:LEU:HG	1.89	0.52
1:B:176:TYR:HB3	1:B:216:GLN:HE21	1.74	0.52
1:A:72:VAL:HA	1:A:77:LYS:HZ1	1.74	0.52
1:D:191:GLN:NE2	1:D:228:ILE:HA	2.24	0.52
1:D:11:ILE:HG22	1:D:54:LEU:HD22	1.90	0.52
1:C:81:LEU:HD23	1:C:85:ILE:HG12	1.92	0.52
1:C:229:ASN:C	1:C:229:ASN:HD22	2.13	0.52
1:C:4:ILE:HD11	1:D:44:VAL:HG11	1.91	0.52
1:A:224:LYS:O	1:A:225:ASN:CB	2.57	0.52
1:B:251:ILE:HD11	3:I:290:THR:C	2.30	0.52
1:D:28:SER:OG	1:D:31:VAL:HG22	2.09	0.52
1:D:108:GLN:O	1:D:112:ILE:HG13	2.09	0.52
1:C:7:VAL:O	1:C:11:ILE:HD13	2.09	0.52
1:D:142:TYR:HA	1:D:145:ARG:CG	2.37	0.52
1:B:7:VAL:O	1:B:11:ILE:HD13	2.09	0.52
1:A:274:ARG:HD3	4:A:340:HOH:O	2.09	0.52
1:D:297:MSE:HE3	2:H:6:PHE:HE1	1.75	0.52
1:D:153:TYR:HA	1:D:156:VAL:HG12	1.92	0.52
1:D:153:TYR:HA	1:D:156:VAL:CG1	2.40	0.52
1:C:166:GLU:CD	1:C:166:GLU:H	2.14	0.51
1:C:86:PHE:HE1	1:C:119:ILE:HG12	1.73	0.51
1:A:79:LYS:HZ2	1:A:108:GLN:HE22	1.57	0.51
1:D:274:ARG:NH1	1:D:274:ARG:HB2	2.24	0.51
1:D:139:LYS:HE3	1:D:143:ASP:OD1	2.10	0.51
1:A:166:GLU:CD	1:A:166:GLU:H	2.14	0.51
1:D:81:LEU:HD13	1:D:81:LEU:C	2.30	0.51
1:D:7:VAL:O	1:D:11:ILE:HD13	2.10	0.51
1:B:302:TYR:HE1	2:F:3:THR:HG1	1.59	0.51
1:A:14:GLU:OE1	1:B:146:THR:HB	2.11	0.51
1:C:142:TYR:HA	1:C:145:ARG:CG	2.41	0.51
1:C:84:LYS:HB3	1:C:84:LYS:NZ	2.24	0.51
1:C:224:LYS:O	1:C:225:ASN:CB	2.57	0.51
1:C:99:ILE:C	1:C:101:PRO:HD2	2.31	0.51
1:D:9:LYS:O	1:D:13:GLN:HG3	2.11	0.51
1:B:81:LEU:HD13	1:B:81:LEU:O	2.11	0.51
1:C:267:ILE:HG13	1:C:269:LYS:HG2	1.92	0.51
1:D:292:PRO:HG2	1:D:294:GLU:O	2.11	0.51
2:H:7:VAL:HG12	2:H:7:VAL:OXT	2.11	0.50
1:D:238:TYR:CE2	1:D:261:ILE:HD11	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:288:LYS:NZ	1:A:288:LYS:HB2	2.26	0.50
1:A:300:GLU:HG3	1:B:227:SER:CB	2.42	0.50
1:C:176:TYR:OH	1:C:193:VAL:HB	2.12	0.50
1:A:73:ASN:O	1:A:74:GLU:HB3	2.12	0.50
1:C:283:ILE:O	1:C:283:ILE:HG22	2.11	0.50
1:B:67:MSE:C	1:B:69:THR:N	2.64	0.50
1:C:9:LYS:HB2	1:C:36:GLU:CG	2.42	0.50
1:B:205:ARG:HH11	1:B:205:ARG:HG2	1.76	0.50
1:A:138:LEU:HD13	1:A:171:ILE:HD11	1.93	0.50
3:I:297:MSE:HG3	3:I:297:MSE:OXT	2.11	0.49
1:B:78:GLU:CB	1:B:112:ILE:HD13	2.42	0.49
1:A:4:ILE:HD11	1:B:44:VAL:HG11	1.92	0.49
1:C:9:LYS:O	1:C:13:GLN:HG3	2.13	0.49
1:D:86:PHE:CE2	1:D:119:ILE:HG12	2.48	0.49
1:B:185:ASP:HB3	2:F:7:VAL:HG11	1.94	0.49
1:D:245:PHE:CD1	1:D:254:TYR:HB2	2.47	0.49
1:B:288:LYS:NZ	1:B:288:LYS:HB2	2.26	0.49
1:D:79:LYS:HZ1	1:D:108:GLN:HE22	1.61	0.49
1:D:9:LYS:HB2	1:D:36:GLU:CG	2.42	0.49
1:C:93:ASP:CG	1:C:94:LYS:H	2.16	0.49
1:B:85:ILE:HD12	1:B:116:TYR:CE1	2.47	0.49
1:B:9:LYS:HB2	1:B:36:GLU:CG	2.42	0.49
1:A:9:LYS:HB2	1:A:36:GLU:CG	2.43	0.49
1:C:11:ILE:HG22	1:C:54:LEU:HD22	1.93	0.49
1:A:151:ILE:O	1:A:155:ILE:HG13	2.13	0.49
1:A:196:ASN:ND2	2:E:2:VAL:HA	2.28	0.49
1:C:238:TYR:CE2	1:C:276:LEU:HD11	2.48	0.49
1:C:139:LYS:HA	1:C:143:ASP:OD2	2.12	0.49
1:B:85:ILE:HD12	1:B:116:TYR:HE1	1.78	0.49
1:A:44:VAL:HG11	1:B:4:ILE:HD11	1.93	0.49
1:A:102:LYS:HE2	1:A:109:TYR:CZ	2.48	0.49
1:A:153:TYR:O	1:A:157:SER:HB2	2.13	0.49
1:A:263:ILE:HG23	1:B:234:LEU:HD21	1.95	0.49
1:C:265:LYS:HG2	1:C:270:GLU:OE2	2.12	0.49
3:I:292:PRO:HA	3:I:295:VAL:HG13	1.95	0.48
1:C:95:ASN:ND2	1:C:116:TYR:OH	2.46	0.48
1:C:2:PHE:O	1:C:4:ILE:N	2.44	0.48
1:A:163:LEU:HD12	1:A:164:PRO:CD	2.44	0.48
1:D:103:ARG:HG2	1:D:103:ARG:HH11	1.77	0.48
1:A:1:MSE:H3	1:A:1:MSE:CE	2.22	0.48
1:D:133:THR:HG22	1:D:137:ASP:OD2	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:69:THR:HB	1:B:73:ASN:ND2	2.28	0.48
1:B:251:ILE:HD12	3:I:290:THR:N	2.28	0.48
1:B:81:LEU:HD13	1:B:85:ILE:HG13	1.95	0.48
1:D:79:LYS:HZ3	2:H:7:VAL:H	1.62	0.48
1:B:9:LYS:O	1:B:13:GLN:HG3	2.14	0.48
1:C:188:LEU:C	1:C:188:LEU:HD13	2.33	0.48
1:C:98:ARG:CB	1:C:98:ARG:HH11	2.24	0.48
1:A:221:LYS:HE2	1:A:228:ILE:CD1	2.43	0.48
1:B:240:LYS:O	1:B:244:GLN:HG3	2.14	0.48
1:B:89:PRO:HB3	1:B:123:TYR:CD2	2.49	0.48
1:C:245:PHE:O	1:C:249:LYS:HD3	2.14	0.48
1:A:301:ASN:OD1	1:B:228:ILE:HG12	2.14	0.48
1:D:133:THR:HG22	1:D:137:ASP:CG	2.34	0.47
1:D:276:LEU:HD13	2:H:1:LEU:HD11	1.96	0.47
1:B:295:VAL:HB	1:B:305:ILE:HD12	1.96	0.47
1:C:281:THR:C	1:C:283:ILE:H	2.17	0.47
1:B:11:ILE:HG22	1:B:54:LEU:HD22	1.95	0.47
1:B:181:SER:HB2	1:B:226:ILE:HD13	1.95	0.47
1:C:167:GLU:OE2	1:C:167:GLU:N	2.47	0.47
1:A:78:GLU:CB	1:A:112:ILE:HD13	2.44	0.47
1:B:235:GLU:O	1:B:238:TYR:HD1	1.97	0.47
1:D:229:ASN:HB3	1:D:232:TYR:HB2	1.97	0.47
1:D:184:LYS:N	1:D:184:LYS:HD2	2.28	0.47
1:A:276:LEU:HD13	2:E:1:LEU:HD11	1.96	0.47
1:A:69:THR:O	1:A:70:LYS:CB	2.62	0.47
1:C:223:ILE:O	1:C:226:ILE:HG12	2.15	0.47
1:A:95:ASN:O	1:A:98:ARG:HB3	2.15	0.47
1:D:249:LYS:NZ	1:D:249:LYS:HB2	2.30	0.47
1:A:202:ILE:HD12	1:A:239:LEU:HB3	1.97	0.47
1:B:129:THR:O	1:B:133:THR:HG23	2.15	0.47
1:B:66:GLY:C	1:B:68:ASN:N	2.68	0.47
1:A:72:VAL:O	1:A:74:GLU:N	2.48	0.47
1:D:130:PHE:O	1:D:134:ILE:HG13	2.15	0.47
1:D:134:ILE:O	1:D:138:LEU:HG	2.15	0.47
1:C:237:ASN:O	1:C:241:GLN:HG2	2.15	0.47
1:A:220:LEU:HB3	1:A:226:ILE:HD13	1.96	0.47
1:D:69:THR:O	1:D:72:VAL:HG12	2.14	0.47
1:C:251:ILE:N	1:C:251:ILE:HD13	2.14	0.47
1:C:277:VAL:HG13	3:I:294:GLU:OE1	2.15	0.47
1:C:251:ILE:H	1:C:251:ILE:CD1	2.07	0.47
1:B:12:ARG:HD2	1:B:22:LEU:HD13	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:45:GLU:H	1:D:45:GLU:CD	2.19	0.47
1:A:103:ARG:HG2	1:A:103:ARG:HH11	1.80	0.47
1:C:164:PRO:HB3	1:C:166:GLU:OE2	2.16	0.46
1:B:271:ASP:HB3	1:B:304:ALA:CB	2.45	0.46
1:D:296:THR:HG22	1:D:304:ALA:HB2	1.96	0.46
1:C:144:LYS:HE3	1:D:16:ASN:OD1	2.15	0.46
1:D:102:LYS:HE2	1:D:109:TYR:CE1	2.49	0.46
1:A:72:VAL:C	1:A:74:GLU:N	2.68	0.46
1:A:9:LYS:O	1:A:13:GLN:HG3	2.15	0.46
1:A:195:LYS:HE2	1:A:232:TYR:CE2	2.50	0.46
1:A:229:ASN:HB3	1:A:232:TYR:HB2	1.97	0.46
1:B:67:MSE:O	1:B:69:THR:N	2.37	0.46
3:I:296:THR:O	3:I:297:MSE:OXT	2.33	0.46
1:A:271:ASP:HB2	4:A:318:HOH:O	2.14	0.46
1:C:224:LYS:HZ2	1:C:224:LYS:HB2	1.80	0.46
1:B:297:MSE:HE2	2:F:6:PHE:CE1	2.50	0.46
1:A:251:ILE:HD11	1:D:258:VAL:HG13	1.97	0.46
1:A:178:ILE:O	1:A:223:ILE:HD11	2.16	0.46
1:A:131:ASN:CA	1:A:134:ILE:HD11	2.39	0.46
1:D:144:LYS:HD2	1:D:144:LYS:H	1.79	0.46
1:C:74:GLU:O	1:C:78:GLU:HG2	2.15	0.46
1:C:19:GLN:HG3	4:C:319:HOH:O	2.16	0.46
1:C:163:LEU:HD23	1:C:168:VAL:HG22	1.97	0.46
1:C:92:PHE:CE1	1:C:119:ILE:HB	2.51	0.46
1:D:70:LYS:HG2	2:H:7:VAL:CG2	2.46	0.46
1:D:274:ARG:HH11	1:D:274:ARG:HB2	1.79	0.46
1:D:102:LYS:HE2	1:D:109:TYR:CZ	2.51	0.46
1:C:105:THR:HB	1:C:109:TYR:CD2	2.50	0.46
1:D:197:ALA:HB1	1:D:213:TYR:CE2	2.51	0.46
3:I:292:PRO:HA	3:I:295:VAL:CG1	2.46	0.46
1:D:78:GLU:HB2	1:D:112:ILE:HD13	1.98	0.46
1:D:282:LYS:HG2	1:D:287:GLU:OE2	2.15	0.46
1:A:237:ASN:ND2	1:B:267:ILE:HA	2.31	0.46
1:C:151:ILE:O	1:C:155:ILE:HG13	2.16	0.46
1:A:70:LYS:HB3	1:A:80:LEU:CD1	2.38	0.46
1:D:12:ARG:HD2	1:D:22:LEU:HD13	1.98	0.46
1:B:153:TYR:CD2	1:B:190:ILE:HG22	2.51	0.46
1:C:96:PHE:HD1	1:C:116:TYR:HB3	1.81	0.45
1:B:272:ILE:O	1:B:276:LEU:HD22	2.17	0.45
1:C:127:VAL:N	1:C:128:PRO:HD3	2.32	0.45
1:C:148:PHE:HB3	1:C:175:MSE:HE3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:82:ILE:HD13	1:D:115:GLY:HA3	1.98	0.45
1:C:62:LEU:O	1:C:67:MSE:HG2	2.17	0.45
1:D:187:ASP:HA	1:D:190:ILE:HD11	1.98	0.45
1:C:254:TYR:O	1:C:258:VAL:HG23	2.17	0.45
1:D:229:ASN:ND2	1:D:232:TYR:H	2.12	0.45
1:D:221:LYS:HG2	1:D:228:ILE:HD13	1.97	0.45
1:B:297:MSE:SE	1:B:305:ILE:HD11	2.66	0.45
1:C:207:LEU:CD2	1:C:207:LEU:H	2.29	0.45
1:D:278:GLU:HG2	1:D:282:LYS:HZ3	1.82	0.45
1:C:176:TYR:HB3	1:C:177:PRO:HA	1.99	0.45
1:C:156:VAL:HG21	1:C:175:MSE:SE	2.66	0.45
1:C:12:ARG:HD2	1:C:22:LEU:HD13	1.99	0.45
1:C:197:ALA:HB1	1:C:213:TYR:CE2	2.52	0.45
1:D:152:ASP:O	1:D:156:VAL:HG12	2.17	0.45
1:D:250:ASN:HD22	1:D:251:ILE:N	2.14	0.45
1:C:204:ASN:HB2	1:C:206:ASN:ND2	2.32	0.45
1:B:130:PHE:O	1:B:134:ILE:HG13	2.16	0.45
1:A:300:GLU:O	1:B:227:SER:HB2	2.17	0.45
1:C:66:GLY:C	1:C:68:ASN:N	2.69	0.45
1:C:45:GLU:CD	1:C:45:GLU:H	2.19	0.45
1:C:153:TYR:CD2	1:C:190:ILE:HG22	2.51	0.45
3:I:295:VAL:C	3:I:297:MSE:H	2.21	0.44
1:B:79:LYS:HZ1	1:B:108:GLN:HE22	1.63	0.44
1:D:66:GLY:C	1:D:68:ASN:H	2.21	0.44
1:A:138:LEU:HD13	1:A:171:ILE:CD1	2.47	0.44
1:A:176:TYR:HB3	1:A:177:PRO:HA	2.00	0.44
1:D:195:LYS:HD2	1:D:235:GLU:CD	2.38	0.44
1:A:142:TYR:HA	1:A:145:ARG:CG	2.47	0.44
1:C:20:ILE:HG13	1:C:23:TYR:OH	2.18	0.44
1:A:300:GLU:O	1:B:227:SER:HA	2.18	0.44
1:B:238:TYR:CE2	1:B:261:ILE:HD11	2.53	0.44
1:D:195:LYS:HE3	2:H:1:LEU:O	2.17	0.44
1:D:251:ILE:CD1	1:D:255:LEU:HG	2.47	0.44
1:C:274:ARG:HH11	1:C:274:ARG:HB2	1.83	0.44
1:D:295:VAL:HB	1:D:305:ILE:CD1	2.48	0.44
1:A:72:VAL:HA	1:A:77:LYS:NZ	2.32	0.44
1:A:148:PHE:CD2	1:A:175:MSE:HE3	2.52	0.44
1:D:72:VAL:HG22	1:D:72:VAL:O	2.17	0.44
1:A:92:PHE:CZ	1:A:120:ALA:HB2	2.53	0.44
1:B:45:GLU:H	1:B:45:GLU:CD	2.21	0.44
1:A:23:TYR:OH	1:A:29:LYS:HD2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:62:LEU:O	1:A:67:MSE:HG2	2.17	0.44
1:D:156:VAL:HG13	1:D:193:VAL:HG22	1.98	0.44
1:B:176:TYR:HB3	1:B:177:PRO:HA	1.99	0.44
1:A:305:ILE:HG22	1:A:306:GLU:N	2.32	0.44
1:A:23:TYR:CD2	1:A:23:TYR:C	2.91	0.44
1:B:78:GLU:O	1:B:82:ILE:HG13	2.18	0.44
1:A:3:LYS:HD2	1:A:6:SER:OG	2.18	0.44
3:I:292:PRO:HA	3:I:295:VAL:HG22	2.00	0.44
1:A:279:GLU:OE1	2:E:1:LEU:HA	2.18	0.44
1:A:199:THR:HG22	1:A:203:MSE:CE	2.48	0.44
1:C:227:SER:H	1:D:301:ASN:HD21	1.64	0.44
1:A:78:GLU:OE1	1:A:98:ARG:NH1	2.51	0.44
1:B:20:ILE:HG13	1:B:23:TYR:OH	2.18	0.43
1:D:20:ILE:HG13	1:D:23:TYR:OH	2.18	0.43
1:C:269:LYS:HE3	1:C:272:ILE:HG21	1.98	0.43
1:D:238:TYR:CE1	1:D:239:LEU:HG	2.53	0.43
1:D:156:VAL:HG21	1:D:172:ILE:HG12	1.99	0.43
1:D:57:ASN:HB3	1:D:60:GLU:HB2	1.99	0.43
1:A:12:ARG:HD2	1:A:22:LEU:HD13	2.00	0.43
1:C:169:SER:O	1:C:173:LYS:HD3	2.18	0.43
1:C:45:GLU:CB	1:D:1:MSE:HE3	2.48	0.43
1:A:228:ILE:HD11	1:B:231:TYR:OH	2.18	0.43
1:B:187:ASP:O	1:B:191:GLN:HG3	2.18	0.43
1:D:23:TYR:OH	1:D:29:LYS:HD2	2.18	0.43
1:D:229:ASN:HD21	1:D:231:TYR:HB2	1.83	0.43
1:A:45:GLU:H	1:A:45:GLU:CD	2.20	0.43
1:D:23:TYR:C	1:D:23:TYR:CD2	2.92	0.43
1:D:289:PHE:CZ	2:H:2:VAL:HG21	2.52	0.43
1:C:262:ASN:HD21	1:C:266:ILE:HD11	1.84	0.43
1:C:100:GLU:N	1:C:101:PRO:HD2	2.34	0.43
1:C:229:ASN:C	1:C:229:ASN:ND2	2.72	0.43
1:D:176:TYR:HB3	1:D:177:PRO:HA	2.00	0.43
1:A:64:ARG:HG2	1:A:64:ARG:HH11	1.82	0.43
1:C:207:LEU:N	1:C:207:LEU:HD22	2.34	0.43
1:A:180:ASP:OD2	1:A:181:SER:N	2.52	0.43
1:A:20:ILE:HG13	1:A:23:TYR:OH	2.17	0.43
1:D:131:ASN:CA	1:D:134:ILE:HD11	2.47	0.43
1:D:70:LYS:HD3	2:H:7:VAL:HG11	2.01	0.43
1:B:177:PRO:HB3	1:B:216:GLN:HE22	1.83	0.43
1:B:289:PHE:CZ	2:F:2:VAL:HG21	2.53	0.43
1:C:23:TYR:C	1:C:23:TYR:CD2	2.92	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:251:ILE:CD1	1:B:251:ILE:N	2.81	0.43
3:I:292:PRO:C	3:I:295:VAL:HG22	2.39	0.43
1:C:262:ASN:HB2	3:I:293:LYS:HE3	2.01	0.43
1:D:113:TYR:CE2	1:D:117:ILE:HD11	2.54	0.43
1:D:223:ILE:HB	1:D:226:ILE:CG1	2.49	0.43
1:A:69:THR:HG22	1:A:70:LYS:N	2.33	0.43
1:A:60:GLU:OE2	1:B:149:PHE:HB3	2.18	0.43
1:C:283:ILE:O	1:C:284:SER:C	2.57	0.43
1:B:22:LEU:HD22	1:B:32:TYR:OH	2.18	0.43
1:D:197:ALA:HB1	1:D:213:TYR:CZ	2.53	0.43
1:C:234:LEU:HD11	1:D:234:LEU:HD11	2.01	0.43
1:C:49:LYS:HE3	1:D:1:MSE:CE	2.46	0.43
1:A:300:GLU:HG2	1:B:225:ASN:C	2.39	0.43
1:B:288:LYS:HB2	1:B:288:LYS:HZ2	1.83	0.43
1:B:272:ILE:HG22	1:B:276:LEU:HD22	2.01	0.43
1:A:225:ASN:HA	1:B:300:GLU:HG2	2.01	0.43
1:D:103:ARG:NH2	1:D:133:THR:HG21	2.25	0.43
3:I:296:THR:HG22	3:I:296:THR:O	2.19	0.43
1:A:300:GLU:HG3	1:B:227:SER:HB2	1.99	0.43
1:D:223:ILE:HB	1:D:226:ILE:HG13	2.01	0.43
1:C:112:ILE:HG22	1:C:116:TYR:HE2	1.83	0.42
1:B:62:LEU:O	1:B:67:MSE:HG2	2.19	0.42
1:A:130:PHE:O	1:A:134:ILE:HG13	2.19	0.42
1:D:85:ILE:HD12	1:D:116:TYR:HE1	1.84	0.42
1:A:12:ARG:NH1	1:A:36:GLU:OE1	2.52	0.42
1:D:12:ARG:HG2	1:D:17:TYR:O	2.19	0.42
1:A:139:LYS:O	1:A:143:ASP:HB2	2.19	0.42
1:D:100:GLU:N	1:D:101:PRO:HD2	2.35	0.42
1:A:272:ILE:O	1:A:276:LEU:HD22	2.19	0.42
1:A:300:GLU:HG2	1:B:225:ASN:CA	2.46	0.42
1:C:224:LYS:HZ3	1:C:224:LYS:HB2	1.84	0.42
1:C:148:PHE:CD2	1:C:175:MSE:HG2	2.55	0.42
1:C:12:ARG:HG2	1:C:17:TYR:O	2.19	0.42
1:D:68:ASN:OD1	1:D:69:THR:N	2.51	0.42
1:A:250:ASN:HD22	1:A:251:ILE:N	2.17	0.42
1:C:186:TYR:O	1:C:190:ILE:HG23	2.19	0.42
1:C:245:PHE:CD1	1:C:254:TYR:HB2	2.54	0.42
1:D:139:LYS:HA	1:D:143:ASP:OD2	2.19	0.42
1:C:205:ARG:NH2	1:C:283:ILE:HG23	2.34	0.42
1:C:22:LEU:HD22	1:C:32:TYR:OH	2.19	0.42
1:D:22:LEU:HD22	1:D:32:TYR:OH	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:200:ILE:HG22	1:C:204:ASN:ND2	2.34	0.42
1:A:27:MSE:HE3	1:A:50:PHE:CZ	2.55	0.42
1:C:64:ARG:HH11	1:C:64:ARG:HG2	1.85	0.42
1:D:62:LEU:O	1:D:67:MSE:HG2	2.19	0.42
1:C:265:LYS:HD2	1:C:265:LYS:C	2.40	0.42
1:A:57:ASN:OD1	1:A:59:PHE:N	2.53	0.42
1:A:185:ASP:HB3	2:E:7:VAL:HG11	2.00	0.42
1:A:297:MSE:HE2	2:E:6:PHE:HE1	1.84	0.42
1:B:23:TYR:CD2	1:B:23:TYR:C	2.92	0.42
1:A:261:ILE:HG23	1:A:276:LEU:HB3	2.02	0.42
1:B:227:SER:O	1:B:227:SER:OG	2.34	0.42
1:A:290:THR:O	1:A:291:PRO:C	2.58	0.42
1:D:20:ILE:O	1:D:24:SER:HB3	2.20	0.42
1:C:112:ILE:CG2	1:C:116:TYR:HE2	2.33	0.42
1:B:251:ILE:HD11	3:I:290:THR:O	2.19	0.42
1:D:198:LEU:HG	1:D:239:LEU:HD13	2.01	0.42
1:D:86:PHE:CE2	1:D:119:ILE:HA	2.55	0.42
1:C:144:LYS:HD2	1:C:144:LYS:C	2.40	0.42
1:D:27:MSE:HE3	1:D:50:PHE:CZ	2.55	0.42
1:A:20:ILE:O	1:A:24:SER:HB3	2.20	0.42
1:A:289:PHE:CZ	2:E:2:VAL:HG21	2.55	0.42
1:D:233:ASP:O	1:D:237:ASN:HB2	2.19	0.42
1:C:57:ASN:HB3	1:C:60:GLU:HB2	2.02	0.42
1:B:81:LEU:CD1	1:B:85:ILE:HG13	2.50	0.42
1:A:128:PRO:O	1:A:132:LYS:HG3	2.20	0.42
1:B:95:ASN:O	1:B:98:ARG:HB3	2.20	0.42
1:B:23:TYR:OH	1:B:29:LYS:HD2	2.20	0.41
1:B:69:THR:CG2	1:B:73:ASN:ND2	2.82	0.41
1:B:69:THR:HG22	1:B:73:ASN:HD21	1.84	0.41
1:C:261:ILE:HG12	1:C:276:LEU:HD12	2.01	0.41
1:B:259:ASN:O	1:B:263:ILE:HD13	2.20	0.41
1:B:2:PHE:CD1	1:B:2:PHE:N	2.88	0.41
1:B:20:ILE:O	1:B:24:SER:HB3	2.20	0.41
1:A:79:LYS:HZ1	1:A:108:GLN:HE22	1.65	0.41
1:A:305:ILE:O	1:A:306:GLU:CB	2.68	0.41
1:A:139:LYS:HD2	1:A:143:ASP:OD1	2.20	0.41
1:D:64:ARG:HG2	1:D:64:ARG:HH11	1.84	0.41
1:C:23:TYR:OH	1:C:29:LYS:HD2	2.20	0.41
1:C:45:GLU:HB3	1:D:1:MSE:HE3	2.01	0.41
1:A:157:SER:OG	1:A:192:THR:HG22	2.20	0.41
1:D:113:TYR:CZ	1:D:117:ILE:HD11	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:245:PHE:O	1:D:249:LYS:HA	2.20	0.41
1:A:12:ARG:HG2	1:A:17:TYR:O	2.19	0.41
1:A:245:PHE:O	1:A:249:LYS:HA	2.20	0.41
1:C:129:THR:HG23	1:C:130:PHE:N	2.35	0.41
1:B:203:MSE:HE3	1:B:289:PHE:HD1	1.85	0.41
1:A:227:SER:CB	1:B:300:GLU:HG3	2.27	0.41
1:C:247:THR:OG1	1:C:248:ASP:N	2.54	0.41
1:A:229:ASN:ND2	1:A:232:TYR:N	2.59	0.41
1:C:158:ASN:ND2	1:C:158:ASN:C	2.64	0.41
3:I:292:PRO:HA	3:I:295:VAL:CG2	2.50	0.41
1:B:279:GLU:OE1	2:F:1:LEU:HA	2.20	0.41
1:B:99:ILE:HG13	1:B:116:TYR:CE2	2.56	0.41
1:B:12:ARG:HG2	1:B:17:TYR:O	2.21	0.41
1:A:68:ASN:O	1:A:69:THR:O	2.39	0.41
1:C:95:ASN:ND2	1:C:116:TYR:CZ	2.89	0.41
3:I:290:THR:HG23	3:I:291:PRO:HD2	2.02	0.41
1:A:221:LYS:HE2	1:A:228:ILE:HD13	2.02	0.41
1:D:93:ASP:CG	1:D:94:LYS:H	2.24	0.41
1:D:57:ASN:OD1	1:D:59:PHE:N	2.53	0.41
1:C:240:LYS:O	1:C:244:GLN:HG3	2.20	0.41
1:B:191:GLN:HE22	1:B:228:ILE:HA	1.86	0.41
1:C:210:ALA:O	1:C:214:ILE:HG12	2.21	0.41
1:C:20:ILE:O	1:C:24:SER:HB3	2.21	0.41
1:A:23:TYR:CE1	1:A:29:LYS:HG3	2.56	0.41
1:C:260:ILE:HG12	1:D:263:ILE:CD1	2.50	0.41
1:B:79:LYS:NZ	1:B:108:GLN:NE2	2.60	0.41
1:C:267:ILE:HG22	1:D:237:ASN:ND2	2.36	0.41
1:A:288:LYS:NZ	1:A:288:LYS:CB	2.84	0.41
1:C:211:GLN:HG3	1:C:215:ASN:HD21	1.84	0.41
1:D:103:ARG:HG2	1:D:103:ARG:NH1	2.36	0.41
1:D:114:LEU:HA	1:D:117:ILE:HD12	2.03	0.41
1:A:35:VAL:CG2	1:A:40:ARG:HE	2.34	0.41
1:C:245:PHE:O	1:C:249:LYS:HA	2.22	0.40
1:D:99:ILE:HG13	1:D:116:TYR:HE2	1.83	0.40
1:D:178:ILE:O	1:D:223:ILE:HD11	2.21	0.40
1:C:27:MSE:HE3	1:C:50:PHE:CZ	2.56	0.40
1:A:78:GLU:CD	1:A:98:ARG:HH12	2.25	0.40
1:C:11:ILE:HG13	1:D:149:PHE:CE2	2.55	0.40
1:C:12:ARG:NH1	1:C:36:GLU:OE1	2.54	0.40
1:B:288:LYS:CB	1:B:288:LYS:NZ	2.84	0.40
1:B:89:PRO:HB3	1:B:123:TYR:CE2	2.55	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:180:ASP:OD2	1:B:181:SER:N	2.53	0.40
1:C:81:LEU:HD21	1:C:85:ILE:HD11	2.03	0.40
1:B:238:TYR:HA	1:B:260:ILE:HD12	2.04	0.40
1:C:11:ILE:HD12	1:C:11:ILE:N	2.36	0.40
1:A:286:LYS:HB3	1:D:286:LYS:HE3	2.04	0.40
1:D:187:ASP:HA	1:D:190:ILE:CD1	2.52	0.40
1:B:27:MSE:HE3	1:B:50:PHE:CZ	2.56	0.40
1:B:290:THR:O	1:B:291:PRO:C	2.59	0.40
1:C:158:ASN:O	1:C:161:ASN:OD1	2.40	0.40
1:D:92:PHE:O	1:D:93:ASP:C	2.60	0.40
1:B:178:ILE:O	1:B:223:ILE:HD11	2.22	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	304/317 (96%)	273 (90%)	24 (8%)	7 (2%)	8	36
1	B	303/317 (96%)	276 (91%)	22 (7%)	5 (2%)	11	46
1	C	275/317 (87%)	252 (92%)	16 (6%)	7 (2%)	7	34
1	D	303/317 (96%)	276 (91%)	22 (7%)	5 (2%)	11	46
2	E	5/7 (71%)	5 (100%)	0	0	100	100
2	F	5/7 (71%)	5 (100%)	0	0	100	100
2	H	5/7 (71%)	5 (100%)	0	0	100	100
3	I	6/8 (75%)	4 (67%)	2 (33%)	0	100	100
All	All	1206/1297 (93%)	1096 (91%)	86 (7%)	24 (2%)	9	41

All (24) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	69	THR
1	B	69	THR
1	C	74	GLU
1	D	68	ASN
1	A	68	ASN
1	C	3	LYS
1	C	282	LYS
1	A	93	ASP
1	A	249	LYS
1	B	93	ASP
1	C	93	ASP
1	C	130	PHE
1	D	249	LYS
1	A	72	VAL
1	A	73	ASN
1	A	130	PHE
1	B	68	ASN
1	B	130	PHE
1	B	249	LYS
1	C	249	LYS
1	D	93	ASP
1	D	130	PHE
1	C	67	MSE
1	D	227	SER

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	288/293 (98%)	268 (93%)	20 (7%)	19	56
1	B	287/293 (98%)	272 (95%)	15 (5%)	29	68
1	C	263/293 (90%)	242 (92%)	21 (8%)	15	47
1	D	287/293 (98%)	273 (95%)	14 (5%)	31	71
2	E	7/7 (100%)	6 (86%)	1 (14%)	4	19
2	F	7/7 (100%)	6 (86%)	1 (14%)	4	19

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	H	7/7 (100%)	6 (86%)	1 (14%)	4	19
3	I	8/7 (114%)	7 (88%)	1 (12%)	6	24
All	All	1154/1200 (96%)	1080 (94%)	74 (6%)	22	59

All (74) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MSE
1	A	23	TYR
1	A	45	GLU
1	A	81	LEU
1	A	86	PHE
1	A	93	ASP
1	A	129	THR
1	A	134	ILE
1	A	136	SER
1	A	157	SER
1	A	188	LEU
1	A	226	ILE
1	A	229	ASN
1	A	238	TYR
1	A	249	LYS
1	A	250	ASN
1	A	263	ILE
1	A	276	LEU
1	A	302	TYR
1	A	306	GLU
1	B	3	LYS
1	B	23	TYR
1	B	45	GLU
1	B	68	ASN
1	B	86	PHE
1	B	129	THR
1	B	134	ILE
1	B	166	GLU
1	B	188	LEU
1	B	227	SER
1	B	238	TYR
1	B	250	ASN
1	B	251	ILE
1	B	276	LEU

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Mol	Chain	Res	Type
1	B	302	TYR
1	C	23	TYR
1	C	45	GLU
1	C	86	PHE
1	C	94	LYS
1	C	100	GLU
1	C	103	ARG
1	C	124	ASN
1	C	131	ASN
1	C	138	LEU
1	C	144	LYS
1	C	151	ILE
1	C	158	ASN
1	C	161	ASN
1	C	218	GLU
1	C	224	LYS
1	C	229	ASN
1	C	237	ASN
1	C	238	TYR
1	C	251	ILE
1	C	272	ILE
1	C	276	LEU
1	D	23	TYR
1	D	45	GLU
1	D	86	PHE
1	D	134	ILE
1	D	184	LYS
1	D	237	ASN
1	D	238	TYR
1	D	250	ASN
1	D	251	ILE
1	D	259	ASN
1	D	263	ILE
1	D	276	LEU
1	D	298	TYR
1	D	302	TYR
2	E	5	VAL
2	F	5	VAL
2	H	5	VAL
3	I	294	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (68) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	16	ASN
1	A	19	GLN
1	A	73	ASN
1	A	108	GLN
1	A	124	ASN
1	A	161	ASN
1	A	196	ASN
1	A	211	GLN
1	A	215	ASN
1	A	216	GLN
1	A	229	ASN
1	A	237	ASN
1	A	241	GLN
1	A	250	ASN
1	A	256	ASN
1	A	273	HIS
1	B	16	ASN
1	B	19	GLN
1	B	63	ASN
1	B	73	ASN
1	B	108	GLN
1	B	124	ASN
1	B	196	ASN
1	B	215	ASN
1	B	216	GLN
1	B	229	ASN
1	B	237	ASN
1	B	241	GLN
1	B	250	ASN
1	B	256	ASN
1	B	273	HIS
1	C	16	ASN
1	C	19	GLN
1	C	63	ASN
1	C	73	ASN
1	C	95	ASN
1	C	108	GLN
1	C	124	ASN
1	C	131	ASN
1	C	140	HIS
1	C	158	ASN
1	C	161	ASN
1	C	196	ASN

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Mol	Chain	Res	Type
1	C	204	ASN
1	C	206	ASN
1	C	215	ASN
1	C	229	ASN
1	C	237	ASN
1	C	241	GLN
1	C	244	GLN
1	C	256	ASN
1	C	262	ASN
1	C	273	HIS
1	D	19	GLN
1	D	73	ASN
1	D	95	ASN
1	D	108	GLN
1	D	124	ASN
1	D	196	ASN
1	D	206	ASN
1	D	215	ASN
1	D	216	GLN
1	D	229	ASN
1	D	237	ASN
1	D	241	GLN
1	D	250	ASN
1	D	256	ASN
1	D	273	HIS

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 [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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	300/317 (94%)	-0.57	0 100 100	15, 40, 91, 144	0
1	B	299/317 (94%)	-0.56	1 (0%) 94 84	15, 46, 98, 165	0
1	C	275/317 (86%)	0.60	39 (14%) 4 1	41, 102, 176, 185	0
1	D	299/317 (94%)	-0.13	6 (2%) 68 39	30, 80, 145, 174	0
2	E	7/7 (100%)	-0.54	0 100 100	20, 31, 33, 61	0
2	F	7/7 (100%)	-0.45	0 100 100	35, 43, 55, 60	0
2	H	7/7 (100%)	-0.42	0 100 100	43, 50, 56, 103	0
3	I	7/8 (87%)	1.10	1 (14%) 4 1	68, 112, 161, 177	0
All	All	1201/1297 (92%)	-0.18	47 (3%) 43 18	15, 63, 146, 185	0

All (47) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	92	PHE	7.1
1	C	80	LEU	7.1
1	C	122	HIS	7.0
1	C	127	VAL	6.9
1	C	95	ASN	6.5
1	C	87	THR	6.1
1	C	130	PHE	6.1
1	C	76	GLY	5.6
1	C	123	TYR	5.1
1	C	96	PHE	5.0
1	C	79	LYS	4.6
1	C	88	ASN	4.3
3	I	294	GLU	3.8
1	C	134	ILE	3.5
1	C	125	ILE	3.5
1	D	22	LEU	3.4

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Mol	Chain	Res	Type	RSRZ
1	C	124	ASN	3.4
1	C	202	ILE	3.3
1	C	115	GLY	3.3
1	C	68	ASN	3.2
1	D	144	LYS	3.2
1	C	94	LYS	3.2
1	D	26	ILE	3.1
1	C	99	ILE	2.9
1	C	131	ASN	2.8
1	C	128	PRO	2.8
1	C	83	SER	2.8
1	C	118	SER	2.8
1	C	102	LYS	2.7
1	D	53	ARG	2.7
1	C	86	PHE	2.6
1	C	82	ILE	2.6
1	C	108	GLN	2.6
1	C	89	PRO	2.6
1	B	72	VAL	2.4
1	C	165	TYR	2.3
1	C	65	ALA	2.3
1	C	119	ILE	2.3
1	C	103	ARG	2.3
1	C	34	LYS	2.3
1	C	207	LEU	2.2
1	C	93	ASP	2.2
1	C	121	HIS	2.2
1	D	126	GLU	2.1
1	C	91	LEU	2.0
1	C	106	SER	2.0
1	D	17	TYR	2.0

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

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

6.3 Carbohydrates ⓘ

There are no 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.