



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 03:40 PM GMT

PDB ID : 4D28
Title : Crystal structure of the kinase domain of SnRK3.11 At5g35410
Authors : Gonzalez-Rubio, J.M.; Chaves-Sanjuan, A.; Sanchez-Barrena, M.J.; Albert, A.
Deposited on : 2014-05-08
Resolution : 3.30 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

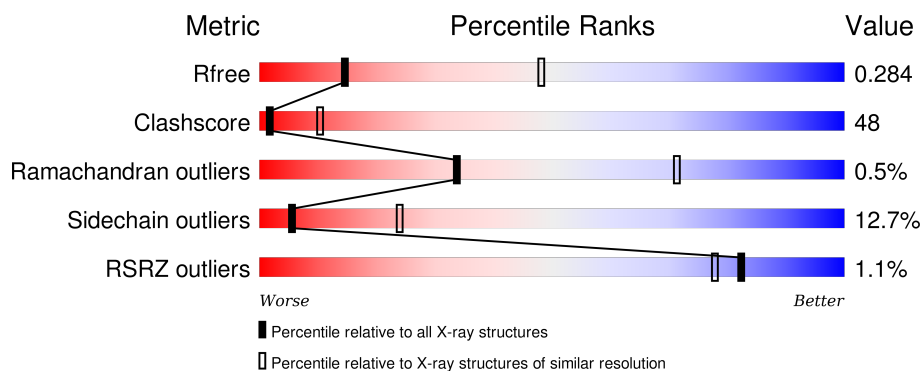
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.30 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	2060 (3.40-3.20)
Clashscore	102246	1058 (3.38-3.22)
Ramachandran outliers	100387	1038 (3.38-3.22)
Sidechain outliers	100360	1037 (3.38-3.22)
RSRZ outliers	91569	2070 (3.40-3.20)

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	446	<div> <div>%</div> <div> <div></div> <div>27%</div> <div>31%</div> <div>•</div> <div>39%</div> </div> </div>
1	B	446	<div> <div>25%</div> <div>31%</div> <div>7%</div> <div>38%</div> </div>
1	C	446	<div> <div>%</div> <div> <div></div> <div>24%</div> <div>33%</div> <div>5%</div> <div>37%</div> </div> </div>
1	D	446	<div> <div>%</div> <div> <div></div> <div>21%</div> <div>35%</div> <div>5%</div> <div>39%</div> </div> </div>

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 8821 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 CBL-INTERACTING SERINE/THREONINE-PROTEIN KINASE 24.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	274	Total	C	N	O	S	0	0	0
			2192	1404	382	399	7			
1	B	277	Total	C	N	O	S	0	0	0
			2217	1419	388	403	7			
1	C	279	Total	C	N	O	S	0	0	0
			2234	1430	390	407	7			
1	D	271	Total	C	N	O	S	0	0	0
			2178	1397	379	395	7			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	81	LYS	PRO	ENGINEERED MUTATION	UNP Q9LDI3
A	107	LYS	GLU	ENGINEERED MUTATION	UNP Q9LDI3
A	109	ASP	SER	ENGINEERED MUTATION	UNP Q9LDI3
A	127	SER	CYS	ENGINEERED MUTATION	UNP Q9LDI3
A	167	ASN	ARG	CONFLICT	UNP Q9LDI3
A	168	ASP	THR	ENGINEERED MUTATION	UNP Q9LDI3
A	228	ASP	SER	ENGINEERED MUTATION	UNP Q9LDI3
A	266	LYS	LEU	ENGINEERED MUTATION	UNP Q9LDI3
B	81	LYS	PRO	ENGINEERED MUTATION	UNP Q9LDI3
B	107	LYS	GLU	ENGINEERED MUTATION	UNP Q9LDI3
B	109	ASP	SER	ENGINEERED MUTATION	UNP Q9LDI3
B	127	SER	CYS	ENGINEERED MUTATION	UNP Q9LDI3
B	167	ASN	ARG	CONFLICT	UNP Q9LDI3
B	168	ASP	THR	ENGINEERED MUTATION	UNP Q9LDI3
B	228	ASP	SER	ENGINEERED MUTATION	UNP Q9LDI3
B	266	LYS	LEU	ENGINEERED MUTATION	UNP Q9LDI3
C	81	LYS	PRO	ENGINEERED MUTATION	UNP Q9LDI3
C	107	LYS	GLU	ENGINEERED MUTATION	UNP Q9LDI3
C	109	ASP	SER	ENGINEERED MUTATION	UNP Q9LDI3
C	127	SER	CYS	ENGINEERED MUTATION	UNP Q9LDI3

Continued on next page...

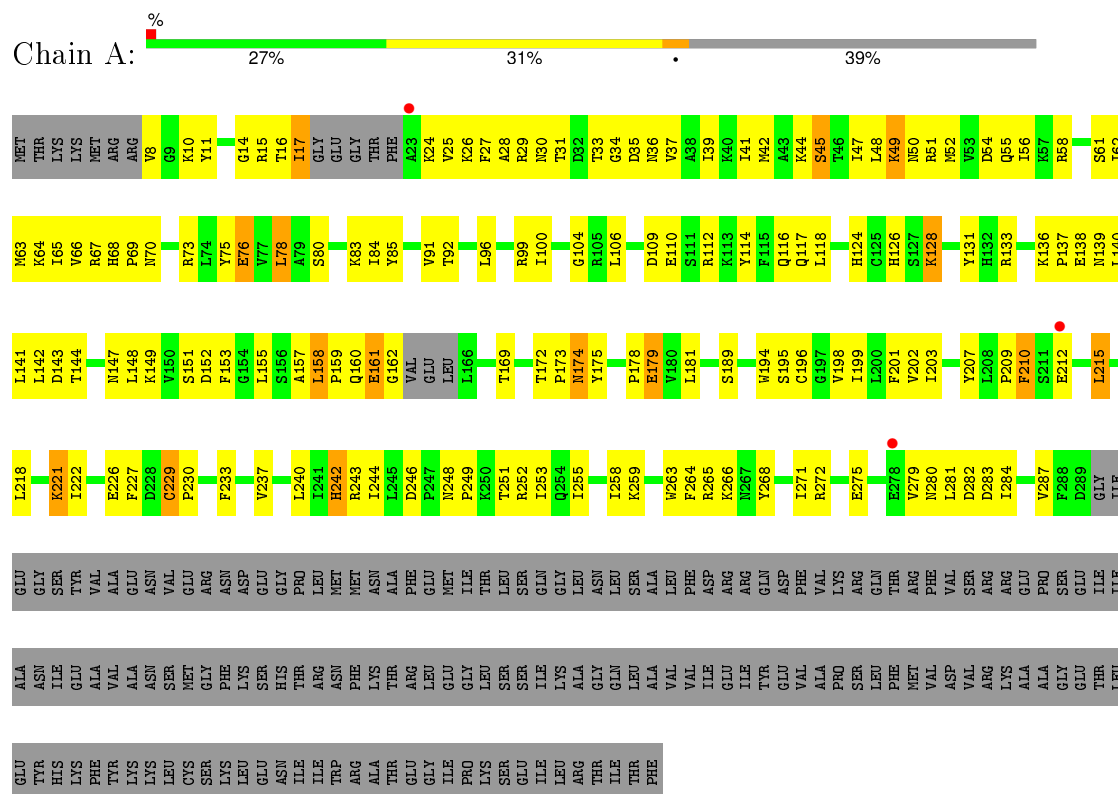
Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
C	167	ASN	ARG	CONFLICT	UNP Q9LDI3
C	168	ASP	THR	ENGINEERED MUTATION	UNP Q9LDI3
C	228	ASP	SER	ENGINEERED MUTATION	UNP Q9LDI3
C	266	LYS	LEU	ENGINEERED MUTATION	UNP Q9LDI3
D	81	LYS	PRO	ENGINEERED MUTATION	UNP Q9LDI3
D	107	LYS	GLU	ENGINEERED MUTATION	UNP Q9LDI3
D	109	ASP	SER	ENGINEERED MUTATION	UNP Q9LDI3
D	127	SER	CYS	ENGINEERED MUTATION	UNP Q9LDI3
D	167	ASN	ARG	CONFLICT	UNP Q9LDI3
D	168	ASP	THR	ENGINEERED MUTATION	UNP Q9LDI3
D	228	ASP	SER	ENGINEERED MUTATION	UNP Q9LDI3
D	266	LYS	LEU	ENGINEERED MUTATION	UNP Q9LDI3

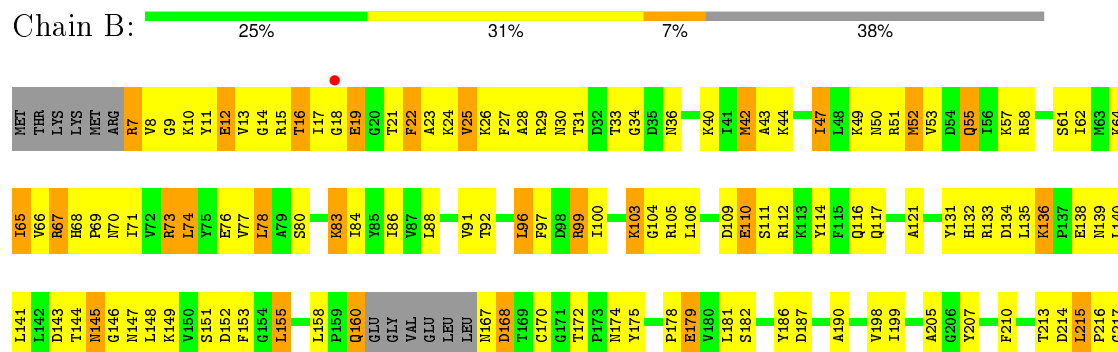
3 Residue-property plots

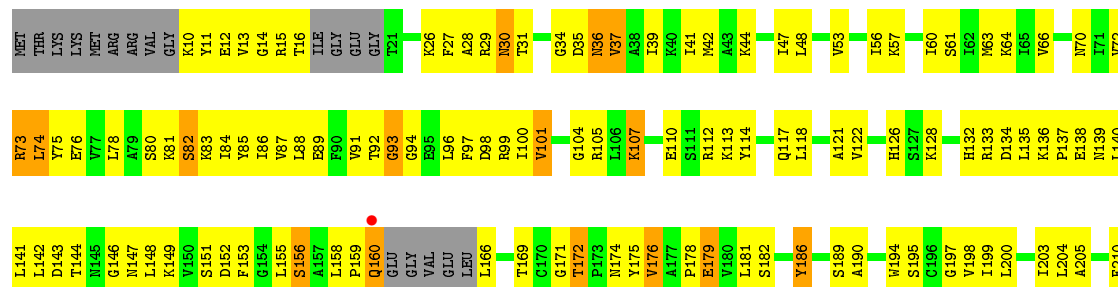
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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: CBL-INTERACTING SERINE/THREONINE-PROTEIN KINASE 24



• Molecule 1: CBL-INTERACTING SERINE/THREONINE-PROTEIN KINASE 24





LEU	PHE	MET	ASP	VAL	ARG	LYS	ALA	GLY	PRO	GLY	THR	ILE	GLN	ILE	ALA	ASN	GLY	ILE	GLU	TYR	HIS	LYS	PHE	TYR	LYS	LYS	LEU	GLU	ILE	ILE	TRP	ARG	ALA	THR	GLU	GLY	ILE	PRO	LYS	THR	ARG	LEU	ASN	GLY	GLN	ILE	THR	PHE																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--

4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	69.11Å 71.35Å 77.83Å 104.85° 100.32° 118.96°	Depositor
Resolution (Å)	70.23 – 3.30 70.23 – 3.30	Depositor EDS
% Data completeness (in resolution range)	90.8 (70.23-3.30) 76.9 (70.23-3.30)	Depositor EDS
R_{merge}	0.27	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.73 (at 3.33Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.271 , 0.283 0.275 , 0.284	Depositor DCC
R_{free} test set	810 reflections (5.31%)	DCC
Wilson B-factor (Å ²)	72.5	Xtriage
Anisotropy	0.128	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 21.5	EDS
Estimated twinning fraction	0.045 for k,h,-h-k-l 0.043 for -k,-h,-l 0.069 for -h,-k,h+k+l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.26$	Xtriage
Outliers	0 of 16052 reflections	Xtriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	8821	wwPDB-VP
Average B, all atoms (Å ²)	70.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.13% 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	0.30	0/2236	0.56	0/3020
1	B	0.31	0/2263	0.56	0/3057
1	C	0.29	0/2280	0.54	0/3080
1	D	0.30	0/2223	0.54	0/3003
All	All	0.30	0/9002	0.55	0/12160

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	2192	0	2222	171	0
1	B	2217	0	2244	202	0
1	C	2234	0	2261	241	0
1	D	2178	0	2206	254	0
All	All	8821	0	8933	860	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 48.

All (860) 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:C:174:ASN:OD1	1:C:212:GLU:OE2	1.60	1.15
1:D:86:ILE:HG22	1:D:88:LEU:HD11	1.17	1.14
1:B:92:THR:OG1	1:B:144:THR:HG23	1.49	1.12
1:B:7:ARG:HD2	1:B:12:GLU:OE2	1.48	1.11
1:D:175:TYR:O	1:D:194:TRP:NE1	1.83	1.10
1:B:99:ARG:NH2	1:B:110:GLU:CD	2.04	1.10
1:C:243:ARG:CG	1:C:253:ILE:HD11	1.82	1.09
1:A:179:GLU:OE2	1:A:252:ARG:NH2	1.86	1.08
1:D:16:THR:HA	1:D:26:LYS:HG2	1.36	1.05
1:C:243:ARG:HG3	1:C:253:ILE:CG1	1.86	1.05
1:B:112:ARG:O	1:B:116:GLN:HG3	1.54	1.05
1:B:99:ARG:NH2	1:B:110:GLU:OE1	1.90	1.04
1:C:136:LYS:H	1:C:139:ASN:ND2	1.56	1.03
1:C:143:ASP:OD1	1:C:147:ASN:N	1.92	1.02
1:C:210:PHE:CD2	1:C:222:ILE:HG12	1.95	1.01
1:C:243:ARG:HG3	1:C:253:ILE:HD11	1.42	1.00
1:D:255:ILE:H	1:D:255:ILE:HD12	1.26	1.00
1:B:7:ARG:HD2	1:B:12:GLU:CD	1.81	0.99
1:C:243:ARG:HG3	1:C:253:ILE:CD1	1.92	0.99
1:C:281:LEU:O	1:C:284:ILE:N	1.96	0.99
1:B:281:LEU:O	1:B:284:ILE:N	1.96	0.98
1:B:99:ARG:NH2	1:B:110:GLU:OE2	1.96	0.97
1:C:179:GLU:OE2	1:C:252:ARG:NH1	1.96	0.97
1:C:210:PHE:HD2	1:C:222:ILE:HG12	1.28	0.97
1:D:281:LEU:O	1:D:284:ILE:N	1.96	0.97
1:D:86:ILE:HG22	1:D:88:LEU:CD1	1.95	0.97
1:B:7:ARG:CD	1:B:12:GLU:OE2	2.12	0.96
1:C:173:PRO:HD2	1:C:212:GLU:OE2	1.66	0.96
1:A:281:LEU:O	1:A:284:ILE:N	1.98	0.95
1:D:73:ARG:NH1	1:D:75:TYR:HA	1.81	0.95
1:A:41:ILE:HG12	1:A:85:TYR:HD1	1.29	0.95
1:D:248:ASN:ND2	1:D:251:THR:HG23	1.80	0.94
1:A:51:ARG:HB3	1:A:52:MET:HE3	1.50	0.94
1:C:255:ILE:HD12	1:C:255:ILE:H	1.30	0.94
1:D:44:LYS:HD2	1:D:80:SER:O	1.67	0.94
1:B:99:ARG:HH11	1:B:103:LYS:HZ2	1.15	0.94
1:A:155:LEU:O	1:A:158:LEU:HB2	1.65	0.94
1:D:29:ARG:HA	1:D:36:ASN:HA	1.47	0.93
1:B:17:ILE:HB	1:B:25:VAL:HB	1.50	0.93
1:C:212:GLU:O	1:C:215:LEU:CD2	2.17	0.93
1:C:248:ASN:ND2	1:C:251:THR:HG23	1.84	0.93
1:A:118:LEU:HD21	1:A:196:CYS:SG	2.10	0.92

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:7:ARG:HG3	1:B:7:ARG:HH11	1.35	0.91
1:A:243:ARG:HG2	1:A:253:ILE:HD12	1.53	0.91
1:D:15:ARG:HG2	1:D:26:LYS:CE	2.00	0.91
1:D:105:ARG:NH2	1:D:232:TRP:CG	2.39	0.90
1:C:99:ARG:CZ	1:C:110:GLU:OE2	2.20	0.90
1:D:64:LYS:HA	1:D:74:LEU:HD13	1.53	0.90
1:B:136:LYS:H	1:B:139:ASN:ND2	1.69	0.89
1:D:37:VAL:HG13	1:D:88:LEU:O	1.72	0.89
1:D:86:ILE:CG2	1:D:88:LEU:HD11	2.01	0.89
1:A:158:LEU:CD1	1:A:159:PRO:HD2	2.02	0.89
1:B:136:LYS:H	1:B:139:ASN:HD22	1.11	0.88
1:D:155:LEU:HA	1:D:158:LEU:HD23	1.54	0.88
1:C:133:ARG:HH11	1:C:133:ARG:HG2	1.38	0.88
1:A:8:VAL:N	1:A:11:TYR:O	2.07	0.88
1:C:243:ARG:NE	1:C:253:ILE:HD11	1.89	0.87
1:B:42:MET:CE	1:B:158:LEU:HD23	2.05	0.87
1:C:67:ARG:HE	1:C:73:ARG:HH21	1.20	0.87
1:B:100:ILE:CD1	1:B:106:LEU:HG	2.05	0.86
1:B:99:ARG:NH1	1:B:103:LYS:NZ	2.22	0.86
1:C:99:ARG:NH2	1:C:110:GLU:OE2	2.08	0.86
1:D:256:GLN:HG3	1:D:260:LYS:NZ	1.91	0.86
1:D:100:ILE:HG23	1:D:104:GLY:O	1.75	0.86
1:A:51:ARG:C	1:A:52:MET:HE3	1.97	0.85
1:B:43:ALA:HA	1:B:83:LYS:HG3	1.57	0.84
1:D:15:ARG:HA	1:D:26:LYS:HG2	1.59	0.84
1:A:158:LEU:HD13	1:A:159:PRO:HD2	1.58	0.84
1:D:15:ARG:HB3	1:D:16:THR:HG23	1.58	0.84
1:D:29:ARG:HB3	1:D:36:ASN:HB3	1.60	0.84
1:D:96:LEU:HD11	1:D:114:TYR:CD1	2.13	0.84
1:A:99:ARG:NH1	1:A:114:TYR:OH	2.10	0.84
1:B:51:ARG:HB3	1:B:52:MET:HE3	1.60	0.84
1:C:116:GLN:HG2	1:C:268:TYR:HD1	1.44	0.83
1:B:7:ARG:NH1	1:B:11:TYR:O	2.11	0.83
1:C:136:LYS:H	1:C:139:ASN:HD22	1.26	0.83
1:D:136:LYS:HB2	1:D:137:PRO:HD2	1.60	0.83
1:B:99:ARG:HH11	1:B:103:LYS:NZ	1.77	0.82
1:A:172:THR:HG22	1:D:169:THR:OG1	1.78	0.82
1:D:64:LYS:HA	1:D:74:LEU:CD1	2.09	0.82
1:C:40:LYS:HB3	1:C:86:ILE:HB	1.60	0.82
1:D:76:GLU:OE1	1:D:78:LEU:HD21	1.78	0.82
1:B:40:LYS:NZ	1:B:152:ASP:OD1	2.12	0.82

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:42:MET:SD	1:B:158:LEU:HD23	2.20	0.82
1:C:80:SER:OG	1:C:83:LYS:N	2.13	0.81
1:A:237:VAL:HG22	1:A:263:TRP:CE2	2.16	0.81
1:C:136:LYS:N	1:C:139:ASN:ND2	2.29	0.81
1:B:96:LEU:O	1:B:96:LEU:HD12	1.81	0.81
1:B:275:GLU:N	1:B:275:GLU:OE1	2.13	0.81
1:C:227:PHE:CZ	1:C:242:HIS:CD2	2.69	0.80
1:A:112:ARG:O	1:A:116:GLN:HG3	1.81	0.80
1:D:175:TYR:O	1:D:194:TRP:CD1	2.34	0.80
1:C:70:ASN:O	1:C:149:LYS:HA	1.82	0.79
1:B:243:ARG:HG2	1:B:253:ILE:HB	1.63	0.79
1:B:15:ARG:HB3	1:B:16:THR:HG22	1.63	0.79
1:D:197:GLY:CA	1:D:244:ILE:HG21	2.12	0.79
1:A:237:VAL:HG22	1:A:263:TRP:NE1	1.97	0.79
1:D:256:GLN:O	1:D:260:LYS:HD2	1.81	0.79
1:D:155:LEU:CA	1:D:158:LEU:HD23	2.12	0.78
1:C:212:GLU:O	1:C:215:LEU:HD23	1.82	0.78
1:D:74:LEU:H	1:D:74:LEU:HD12	1.47	0.78
1:B:7:ARG:NH1	1:B:7:ARG:HG3	1.96	0.78
1:B:136:LYS:HD3	1:B:139:ASN:HD21	1.47	0.78
1:C:155:LEU:O	1:C:158:LEU:HB2	1.84	0.78
1:C:243:ARG:CZ	1:C:253:ILE:HD11	2.14	0.78
1:C:246:ASP:O	1:C:252:ARG:NE	2.14	0.78
1:D:87:VAL:C	1:D:88:LEU:HD12	2.05	0.77
1:C:25:VAL:HG12	1:C:40:LYS:HA	1.67	0.77
1:C:7:ARG:HD3	1:C:12:GLU:HA	1.67	0.77
1:A:16:THR:HA	1:A:26:LYS:HG2	1.64	0.77
1:C:29:ARG:HB3	1:C:36:ASN:OD1	1.83	0.77
1:A:41:ILE:HG12	1:A:85:TYR:CD1	2.15	0.77
1:A:116:GLN:NE2	1:A:268:TYR:HB2	2.00	0.77
1:D:212:GLU:OE1	1:D:215:LEU:HD11	1.84	0.77
1:C:133:ARG:NH1	1:C:133:ARG:HG2	1.98	0.77
1:C:44:LYS:O	1:C:47:ILE:HG22	1.85	0.76
1:D:30:ASN:OD1	1:D:30:ASN:O	2.03	0.76
1:C:80:SER:HB3	1:C:85:TYR:HE1	1.48	0.76
1:B:237:VAL:HG22	1:B:263:TRP:CE2	2.21	0.76
1:B:281:LEU:HA	1:B:284:ILE:HG13	1.68	0.76
1:B:210:PHE:CE1	1:B:227:PHE:HB3	2.21	0.76
1:D:14:GLY:O	1:D:26:LYS:HD3	1.86	0.76
1:D:143:ASP:OD1	1:D:147:ASN:N	2.18	0.76
1:B:29:ARG:HA	1:B:36:ASN:HA	1.67	0.76

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:106:LEU:HD12	1:A:203:ILE:HG23	1.68	0.76
1:A:281:LEU:HD12	1:A:282:ASP:N	2.00	0.75
1:B:80:SER:OG	1:B:83:LYS:N	2.20	0.75
1:B:19:GLU:N	1:B:19:GLU:OE1	2.20	0.75
1:A:47:ILE:HG21	1:A:84:ILE:HD12	1.68	0.75
1:C:174:ASN:ND2	1:C:210:PHE:O	2.20	0.75
1:A:173:PRO:HB3	1:D:219:TYR:OH	1.87	0.74
1:D:30:ASN:N	1:D:35:ASP:O	2.18	0.74
1:A:237:VAL:CG2	1:A:263:TRP:NE1	2.50	0.74
1:D:281:LEU:HA	1:D:284:ILE:HG13	1.69	0.74
1:C:243:ARG:CG	1:C:253:ILE:CD1	2.56	0.74
1:A:175:TYR:O	1:A:194:TRP:CD1	2.41	0.74
1:C:25:VAL:HG12	1:C:40:LYS:CA	2.18	0.74
1:A:221:LYS:HE2	1:A:226:GLU:OE2	1.88	0.73
1:B:136:LYS:HG2	1:B:139:ASN:ND2	2.02	0.73
1:C:116:GLN:HG2	1:C:268:TYR:CD1	2.22	0.73
1:B:237:VAL:CG2	1:B:263:TRP:NE1	2.52	0.73
1:D:15:ARG:HB3	1:D:16:THR:CG2	2.18	0.73
1:D:256:GLN:HG3	1:D:260:LYS:HZ3	1.53	0.73
1:C:136:LYS:O	1:C:139:ASN:ND2	2.20	0.73
1:C:44:LYS:H	1:C:83:LYS:HA	1.53	0.73
1:D:195:SER:O	1:D:199:ILE:HD12	1.89	0.73
1:B:99:ARG:NH1	1:B:103:LYS:HZ3	1.86	0.72
1:B:138:GLU:OE1	1:B:138:GLU:N	2.16	0.72
1:D:261:ASP:OD1	1:D:263:TRP:N	2.23	0.72
1:C:193:ILE:O	1:C:197:GLY:N	2.20	0.72
1:D:190:ALA:O	1:D:252:ARG:NH1	2.22	0.72
1:A:69:PRO:HG3	1:A:271:ILE:HG21	1.69	0.72
1:D:155:LEU:HA	1:D:158:LEU:CD2	2.19	0.72
1:D:155:LEU:C	1:D:158:LEU:HD23	2.10	0.72
1:C:74:LEU:HD13	1:C:87:VAL:O	1.90	0.72
1:B:27:PHE:CD1	1:B:28:ALA:N	2.57	0.72
1:B:31:THR:O	1:B:34:GLY:N	2.21	0.72
1:B:92:THR:OG1	1:B:144:THR:CG2	2.36	0.72
1:C:25:VAL:HG12	1:C:40:LYS:N	2.05	0.72
1:C:25:VAL:CG1	1:C:40:LYS:HD2	2.19	0.71
1:B:175:TYR:CE1	1:B:198:VAL:HG12	2.25	0.71
1:B:77:VAL:C	1:B:78:LEU:HD23	2.10	0.71
1:C:243:ARG:CD	1:C:253:ILE:HD11	2.19	0.71
1:D:210:PHE:HB2	1:D:218:LEU:CD2	2.20	0.71
1:C:212:GLU:O	1:C:215:LEU:HD22	1.91	0.70

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:136:LYS:N	1:B:139:ASN:ND2	2.38	0.70
1:B:237:VAL:CG2	1:B:263:TRP:CD1	2.74	0.70
1:A:96:LEU:HA	1:A:142:LEU:HD11	1.72	0.70
1:C:29:ARG:HG3	1:C:29:ARG:O	1.90	0.70
1:B:7:ARG:NH2	1:B:9:GLY:O	2.24	0.70
1:A:281:LEU:HA	1:A:284:ILE:HG13	1.72	0.70
1:D:53:VAL:O	1:D:57:LYS:HG3	1.92	0.70
1:D:15:ARG:HG2	1:D:26:LYS:CD	2.21	0.70
1:A:152:ASP:HA	1:A:155:LEU:HD22	1.74	0.70
1:A:158:LEU:HD12	1:A:159:PRO:HD2	1.74	0.69
1:A:67:ARG:N	1:A:275:GLU:OE1	2.24	0.69
1:C:25:VAL:CG1	1:C:40:LYS:HA	2.22	0.69
1:C:25:VAL:HG13	1:C:40:LYS:HD2	1.75	0.69
1:D:15:ARG:HG2	1:D:26:LYS:HD3	1.73	0.69
1:C:97:PHE:CE2	1:C:202:VAL:HG11	2.27	0.69
1:C:247:PRO:O	1:C:252:ARG:NH2	2.25	0.69
1:C:47:ILE:HG21	1:C:84:ILE:CD1	2.22	0.69
1:A:39:ILE:HG22	1:A:41:ILE:HG13	1.75	0.69
1:B:42:MET:HE1	1:B:158:LEU:HD23	1.75	0.69
1:B:15:ARG:CB	1:B:16:THR:HG22	2.23	0.69
1:A:143:ASP:OD1	1:A:147:ASN:N	2.26	0.69
1:A:17:ILE:N	1:A:25:VAL:O	2.25	0.69
1:B:42:MET:O	1:B:83:LYS:HG2	1.93	0.69
1:A:141:LEU:O	1:A:148:LEU:HD12	1.92	0.69
1:B:7:ARG:NH1	1:B:8:VAL:O	2.23	0.68
1:A:51:ARG:HB3	1:A:52:MET:CE	2.22	0.68
1:D:76:GLU:OE1	1:D:78:LEU:CD2	2.40	0.68
1:C:243:ARG:CG	1:C:253:ILE:CG1	2.69	0.68
1:C:133:ARG:HH11	1:C:133:ARG:CG	2.06	0.68
1:A:100:ILE:CD1	1:A:106:LEU:HG	2.24	0.68
1:A:259:LYS:HA	1:A:264:PHE:CD2	2.28	0.68
1:C:67:ARG:HE	1:C:73:ARG:NH2	1.90	0.68
1:B:27:PHE:CD1	1:B:27:PHE:C	2.67	0.68
1:C:281:LEU:HA	1:C:284:ILE:HG13	1.76	0.68
1:D:155:LEU:O	1:D:158:LEU:HD23	1.94	0.68
1:D:64:LYS:O	1:D:73:ARG:NH2	2.27	0.67
1:D:88:LEU:HD12	1:D:88:LEU:N	2.09	0.67
1:D:92:THR:O	1:D:94:GLY:N	2.27	0.67
1:A:215:LEU:HA	1:A:218:LEU:HB3	1.76	0.67
1:C:137:PRO:HG2	1:C:138:GLU:OE2	1.94	0.67
1:B:134:ASP:OD2	1:B:136:LYS:NZ	2.19	0.67

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:62:ILE:O	1:A:66:VAL:HG23	1.94	0.67
1:A:55:GLN:HE21	1:A:157:ALA:HB2	1.59	0.67
1:B:143:ASP:OD1	1:B:147:ASN:N	2.28	0.67
1:D:105:ARG:NH2	1:D:232:TRP:CD2	2.62	0.67
1:D:230:PRO:HB3	1:D:232:TRP:CZ2	2.29	0.67
1:D:248:ASN:ND2	1:D:251:THR:CG2	2.56	0.67
1:C:193:ILE:HG22	1:C:244:ILE:HG23	1.77	0.67
1:D:197:GLY:HA3	1:D:244:ILE:HG21	1.75	0.67
1:D:217:GLY:O	1:D:220:ARG:HG2	1.95	0.67
1:C:19:GLU:HG3	1:C:24:LYS:HB3	1.76	0.66
1:B:248:ASN:OD1	1:B:249:PRO:N	2.29	0.66
1:D:136:LYS:HD2	1:D:138:GLU:OE1	1.94	0.66
1:B:47:ILE:HG21	1:B:84:ILE:HD12	1.78	0.66
1:D:210:PHE:HB2	1:D:218:LEU:HD21	1.78	0.66
1:B:179:GLU:OE2	1:B:252:ARG:NH1	2.28	0.66
1:D:118:LEU:O	1:D:122:VAL:HG23	1.95	0.66
1:A:237:VAL:HG22	1:A:263:TRP:CD1	2.30	0.66
1:C:237:VAL:HG22	1:C:263:TRP:CE2	2.30	0.66
1:A:64:LYS:HE3	1:A:76:GLU:HA	1.77	0.66
1:B:70:ASN:HD21	1:B:117:GLN:CD	1.99	0.66
1:D:72:VAL:CG2	1:D:149:LYS:HB3	2.26	0.66
1:C:68:HIS:CE1	1:C:70:ASN:HB2	2.31	0.66
1:D:80:SER:OG	1:D:83:LYS:N	2.25	0.66
1:A:17:ILE:HG12	1:A:25:VAL:HG12	1.76	0.66
1:D:39:ILE:HG22	1:D:41:ILE:HG13	1.78	0.66
1:A:179:GLU:HG2	1:A:249:PRO:HG3	1.78	0.66
1:D:236:GLU:OE2	1:D:262:PRO:HG2	1.94	0.65
1:A:78:LEU:HB3	1:A:85:TYR:HB2	1.77	0.65
1:C:25:VAL:HG12	1:C:39:ILE:C	2.17	0.65
1:C:235:ALA:HA	1:C:238:LYS:HE2	1.78	0.65
1:C:143:ASP:OD1	1:C:146:GLY:N	2.30	0.65
1:D:253:ILE:HG12	1:D:258:ILE:CG2	2.27	0.65
1:D:15:ARG:HG2	1:D:26:LYS:HE2	1.78	0.65
1:C:141:LEU:O	1:C:148:LEU:HD12	1.96	0.65
1:B:136:LYS:CD	1:B:139:ASN:HD21	2.10	0.65
1:B:65:ILE:HD11	1:B:279:VAL:HB	1.79	0.65
1:A:70:ASN:O	1:A:149:LYS:HA	1.96	0.65
1:A:30:ASN:N	1:A:35:ASP:O	2.30	0.65
1:C:243:ARG:HG3	1:C:253:ILE:HG12	1.74	0.64
1:C:193:ILE:HA	1:C:196:CYS:HB2	1.77	0.64
1:D:16:THR:HG22	1:D:26:LYS:HE2	1.80	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:17:ILE:HB	1:C:25:VAL:O	1.97	0.64
1:C:25:VAL:HA	1:C:39:ILE:O	1.97	0.64
1:C:227:PHE:HZ	1:C:242:HIS:CD2	2.13	0.64
1:D:199:ILE:O	1:D:203:ILE:HG13	1.97	0.64
1:C:44:LYS:N	1:C:83:LYS:HA	2.12	0.64
1:C:91:VAL:HG21	1:C:141:LEU:HB3	1.80	0.64
1:A:51:ARG:CB	1:A:52:MET:HE3	2.26	0.64
1:D:241:ILE:CG2	1:D:245:LEU:HD12	2.27	0.63
1:C:116:GLN:CG	1:C:268:TYR:HD1	2.10	0.63
1:A:15:ARG:HB3	1:A:16:THR:CG2	2.28	0.63
1:D:44:LYS:N	1:D:82:SER:O	2.25	0.63
1:B:15:ARG:HB3	1:B:16:THR:CG2	2.27	0.63
1:D:212:GLU:OE1	1:D:215:LEU:CD1	2.46	0.63
1:D:253:ILE:HG12	1:D:258:ILE:HG22	1.79	0.63
1:A:201:PHE:CD1	1:A:209:PRO:HG3	2.33	0.63
1:C:27:PHE:HE1	1:C:90:PHE:CE2	2.16	0.63
1:B:237:VAL:HG23	1:B:263:TRP:CD1	2.31	0.63
1:A:178:PRO:O	1:A:181:LEU:HB2	1.98	0.63
1:C:243:ARG:CZ	1:C:253:ILE:CD1	2.75	0.63
1:D:255:ILE:CD1	1:D:255:ILE:H	2.05	0.63
1:D:107:LYS:CD	1:D:110:GLU:HB2	2.28	0.63
1:D:134:ASP:O	1:D:136:LYS:HG2	1.99	0.63
1:B:237:VAL:HG22	1:B:263:TRP:NE1	2.12	0.63
1:A:195:SER:O	1:A:199:ILE:HG13	1.98	0.63
1:C:19:GLU:HB2	1:C:23:ALA:O	1.99	0.63
1:D:197:GLY:HA3	1:D:244:ILE:CG2	2.29	0.63
1:C:202:VAL:CG2	1:C:208:LEU:HD23	2.29	0.62
1:C:7:ARG:NH1	1:C:9:GLY:O	2.32	0.62
1:D:99:ARG:CZ	1:D:110:GLU:OE2	2.47	0.62
1:A:68:HIS:CG	1:A:69:PRO:HD2	2.34	0.62
1:B:61:SER:CB	1:B:284:ILE:HG12	2.29	0.62
1:D:28:ALA:O	1:D:36:ASN:HB2	1.99	0.62
1:A:106:LEU:HD12	1:A:203:ILE:CG2	2.30	0.62
1:D:113:LYS:HE2	1:D:117:GLN:HE22	1.63	0.62
1:B:139:ASN:HA	1:B:151:SER:OG	2.00	0.62
1:D:72:VAL:HG23	1:D:149:LYS:HB3	1.81	0.62
1:C:40:LYS:CB	1:C:86:ILE:HB	2.29	0.62
1:B:256:GLN:HG2	1:B:260:LYS:HE3	1.81	0.62
1:B:7:ARG:CG	1:B:7:ARG:HH11	2.10	0.61
1:D:15:ARG:HG2	1:D:26:LYS:NZ	2.14	0.61
1:D:261:ASP:HB3	1:D:264:PHE:HB3	1.81	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:133:ARG:NH1	1:D:186:TYR:CZ	2.69	0.61
1:C:50:ASN:OD1	1:C:51:ARG:N	2.33	0.61
1:D:105:ARG:CZ	1:D:232:TRP:CD2	2.84	0.61
1:A:237:VAL:CG2	1:A:263:TRP:CD1	2.82	0.61
1:C:216:PRO:O	1:C:220:ARG:HG3	2.01	0.61
1:C:248:ASN:HD22	1:C:251:THR:HG23	1.64	0.61
1:D:107:LYS:HD3	1:D:110:GLU:HB2	1.82	0.61
1:C:29:ARG:HA	1:C:36:ASN:HA	1.81	0.61
1:B:58:ARG:O	1:B:62:ILE:HG13	2.01	0.61
1:B:136:LYS:N	1:B:139:ASN:HD22	1.92	0.60
1:B:274:ARG:HA	1:B:275:GLU:OE1	2.01	0.60
1:B:246:ASP:OD2	1:B:251:THR:OG1	2.19	0.60
1:A:172:THR:HB	1:A:174:ASN:OD1	2.01	0.60
1:D:105:ARG:CZ	1:D:232:TRP:CE2	2.84	0.60
1:D:158:LEU:N	1:D:158:LEU:HD22	2.16	0.60
1:C:246:ASP:OD2	1:C:251:THR:OG1	2.17	0.60
1:D:92:THR:OG1	1:D:144:THR:HG22	2.02	0.60
1:D:75:TYR:HE1	1:D:89:GLU:HB2	1.66	0.60
1:D:15:ARG:HA	1:D:26:LYS:CG	2.29	0.60
1:D:30:ASN:C	1:D:30:ASN:OD1	2.40	0.60
1:C:19:GLU:HB3	1:C:24:LYS:CB	2.31	0.60
1:A:80:SER:OG	1:A:83:LYS:N	2.31	0.60
1:B:100:ILE:HG23	1:B:104:GLY:O	2.02	0.60
1:B:61:SER:HB3	1:B:284:ILE:HG12	1.83	0.60
1:D:12:GLU:HB2	1:D:31:THR:HG22	1.82	0.60
1:C:202:VAL:HG21	1:C:208:LEU:HD23	1.81	0.59
1:C:243:ARG:HG3	1:C:253:ILE:HG13	1.81	0.59
1:D:246:ASP:OD2	1:D:251:THR:OG1	2.18	0.59
1:B:175:TYR:CE1	1:B:198:VAL:CG1	2.85	0.59
1:C:136:LYS:N	1:C:139:ASN:HD21	1.98	0.59
1:C:137:PRO:HA	1:C:140:LEU:HD12	1.83	0.59
1:C:15:ARG:HB3	1:C:16:THR:HG23	1.85	0.59
1:A:30:ASN:C	1:A:30:ASN:OD1	2.40	0.59
1:C:80:SER:HB3	1:C:85:TYR:CE1	2.35	0.59
1:A:37:VAL:HG12	1:A:75:TYR:HE2	1.67	0.59
1:A:29:ARG:NH1	1:A:34:GLY:HA2	2.17	0.59
1:B:237:VAL:HG22	1:B:263:TRP:CD1	2.38	0.59
1:C:92:THR:OG1	1:C:144:THR:HG22	2.03	0.59
1:C:187:ASP:OD1	1:C:189:SER:N	2.35	0.59
1:C:67:ARG:NE	1:C:73:ARG:HH21	1.96	0.59
1:A:15:ARG:HB3	1:A:16:THR:HG23	1.84	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:30:ASN:OD1	1:C:33:THR:N	2.31	0.59
1:A:136:LYS:HG3	1:A:138:GLU:OE1	2.02	0.59
1:B:214:ASP:OD1	1:B:217:GLY:N	2.30	0.59
1:C:247:PRO:C	1:C:252:ARG:HH21	2.06	0.59
1:D:284:ILE:O	1:D:287:VAL:HG12	2.03	0.59
1:C:15:ARG:HB3	1:C:16:THR:CG2	2.33	0.59
1:B:7:ARG:HD3	1:B:12:GLU:OE2	2.00	0.59
1:D:41:ILE:HG12	1:D:85:TYR:HD1	1.68	0.59
1:C:72:VAL:HG23	1:C:149:LYS:HB3	1.83	0.59
1:A:54:ASP:O	1:A:58:ARG:HG3	2.03	0.59
1:C:86:ILE:HG22	1:C:88:LEU:HD21	1.85	0.58
1:C:10:LYS:O	1:C:31:THR:HG23	2.04	0.58
1:C:97:PHE:O	1:C:101:VAL:HG23	2.02	0.58
1:A:99:ARG:NH2	1:A:110:GLU:OE1	2.36	0.58
1:D:91:VAL:HG21	1:D:141:LEU:HB3	1.85	0.58
1:C:210:PHE:HD2	1:C:222:ILE:CG1	2.09	0.58
1:A:52:MET:O	1:A:56:ILE:HG13	2.02	0.58
1:C:67:ARG:HG2	1:C:73:ARG:HE	1.67	0.58
1:A:136:LYS:H	1:A:139:ASN:ND2	2.02	0.58
1:C:186:TYR:HD1	1:C:186:TYR:H	1.52	0.58
1:B:155:LEU:O	1:B:158:LEU:HB2	2.04	0.58
1:C:112:ARG:HH21	1:C:266:LYS:CD	2.17	0.58
1:D:230:PRO:HG2	1:D:233:PHE:CE1	2.38	0.58
1:C:30:ASN:C	1:C:30:ASN:OD1	2.41	0.58
1:D:100:ILE:CG2	1:D:104:GLY:O	2.51	0.57
1:B:22:PHE:CE1	1:B:160:GLN:OE1	2.57	0.57
1:B:68:HIS:CG	1:B:69:PRO:HD2	2.39	0.57
1:A:172:THR:CG2	1:D:169:THR:OG1	2.49	0.57
1:C:236:GLU:OE2	1:C:262:PRO:HG2	2.03	0.57
1:B:256:GLN:CG	1:B:260:LYS:HE3	2.34	0.57
1:B:62:ILE:O	1:B:66:VAL:HG23	2.04	0.57
1:B:99:ARG:O	1:B:103:LYS:HG3	2.05	0.57
1:D:237:VAL:HG22	1:D:263:TRP:NE1	2.19	0.57
1:C:74:LEU:CD1	1:C:87:VAL:O	2.52	0.57
1:D:128:LYS:NZ	1:D:275:GLU:HG2	2.20	0.57
1:B:281:LEU:HD12	1:B:282:ASP:N	2.19	0.57
1:D:205:ALA:HB2	1:D:233:PHE:CZ	2.39	0.57
1:C:47:ILE:HG21	1:C:84:ILE:HD11	1.87	0.57
1:B:284:ILE:O	1:B:287:VAL:HG12	2.05	0.57
1:C:199:ILE:O	1:C:203:ILE:HG13	2.04	0.57
1:C:41:ILE:HG12	1:C:85:TYR:CD2	2.40	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:61:SER:HB3	1:A:284:ILE:HG12	1.87	0.57
1:D:100:ILE:O	1:D:104:GLY:N	2.38	0.57
1:C:19:GLU:CG	1:C:24:LYS:HB3	2.34	0.57
1:A:66:VAL:O	1:A:67:ARG:HG2	2.04	0.57
1:A:31:THR:O	1:A:34:GLY:N	2.38	0.57
1:D:281:LEU:HD12	1:D:282:ASP:N	2.20	0.56
1:C:112:ARG:CB	1:C:112:ARG:HH11	2.18	0.56
1:A:131:TYR:HE2	1:A:189:SER:HB3	1.69	0.56
1:C:215:LEU:N	1:C:216:PRO:HD2	2.20	0.56
1:C:10:LYS:O	1:C:31:THR:CG2	2.53	0.56
1:B:44:LYS:O	1:B:47:ILE:HG22	2.05	0.56
1:A:138:GLU:CD	1:A:138:GLU:H	2.09	0.56
1:C:207:TYR:OH	1:C:230:PRO:HG3	2.04	0.56
1:C:211:SER:O	1:C:218:LEU:HD13	2.05	0.56
1:D:70:ASN:O	1:D:149:LYS:HA	2.04	0.56
1:B:70:ASN:O	1:B:149:LYS:HA	2.04	0.56
1:B:116:GLN:NE2	1:B:268:TYR:HB2	2.19	0.56
1:D:210:PHE:CD2	1:D:222:ILE:HG12	2.40	0.56
1:C:100:ILE:HG23	1:C:104:GLY:O	2.05	0.56
1:D:210:PHE:CB	1:D:218:LEU:HD23	2.35	0.56
1:B:96:LEU:C	1:B:96:LEU:HD12	2.25	0.56
1:A:201:PHE:CG	1:A:209:PRO:HG3	2.41	0.56
1:C:227:PHE:CE1	1:C:242:HIS:CE1	2.93	0.56
1:C:247:PRO:C	1:C:252:ARG:NH2	2.59	0.56
1:D:28:ALA:O	1:D:36:ASN:CB	2.54	0.56
1:D:139:ASN:O	1:D:151:SER:OG	2.21	0.56
1:D:175:TYR:CD2	1:D:198:VAL:HG11	2.41	0.56
1:B:31:THR:C	1:B:34:GLY:H	2.08	0.56
1:D:98:ASP:O	1:D:101:VAL:HG12	2.05	0.56
1:C:227:PHE:CZ	1:C:242:HIS:NE2	2.74	0.55
1:B:136:LYS:CG	1:B:139:ASN:HD21	2.19	0.55
1:C:143:ASP:OD2	1:C:147:ASN:HB2	2.05	0.55
1:A:221:LYS:HG3	1:A:226:GLU:OE2	2.05	0.55
1:D:179:GLU:OE2	1:D:252:ARG:NH2	2.34	0.55
1:A:161:GLU:O	1:D:214:ASP:HB2	2.06	0.55
1:A:37:VAL:CG1	1:A:75:TYR:HE2	2.19	0.55
1:D:178:PRO:HA	1:D:181:LEU:HD12	1.89	0.55
1:D:256:GLN:HG3	1:D:260:LYS:HZ2	1.68	0.55
1:A:109:ASP:HA	1:A:112:ARG:NH1	2.22	0.55
1:D:15:ARG:HE	1:D:26:LYS:NZ	2.04	0.54
1:D:137:PRO:HA	1:D:140:LEU:HG	1.88	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:210:PHE:CE2	1:C:222:ILE:HG12	2.42	0.54
1:A:281:LEU:C	1:A:281:LEU:HD12	2.27	0.54
1:B:70:ASN:ND2	1:B:117:GLN:CD	2.60	0.54
1:C:105:ARG:HB2	1:C:204:LEU:O	2.07	0.54
1:C:112:ARG:HH21	1:C:266:LYS:HB2	1.73	0.54
1:C:19:GLU:HB3	1:C:24:LYS:HB2	1.89	0.54
1:C:227:PHE:HZ	1:C:242:HIS:CG	2.25	0.54
1:D:175:TYR:CD2	1:D:198:VAL:CG1	2.90	0.54
1:A:243:ARG:HG3	1:A:253:ILE:HB	1.90	0.54
1:D:136:LYS:HB2	1:D:137:PRO:CD	2.34	0.54
1:C:284:ILE:O	1:C:287:VAL:HG12	2.08	0.54
1:B:281:LEU:HD12	1:B:281:LEU:C	2.27	0.54
1:C:8:VAL:HG12	1:C:13:VAL:CG2	2.38	0.54
1:A:100:ILE:HD13	1:A:106:LEU:HG	1.90	0.54
1:A:27:PHE:CD1	1:A:27:PHE:C	2.81	0.54
1:D:255:ILE:N	1:D:255:ILE:HD12	2.10	0.54
1:B:136:LYS:CG	1:B:139:ASN:ND2	2.71	0.54
1:C:246:ASP:O	1:C:252:ARG:NH2	2.42	0.53
1:A:10:LYS:HE3	1:A:11:TYR:CE1	2.43	0.53
1:A:175:TYR:O	1:A:194:TRP:HD1	1.88	0.53
1:C:87:VAL:C	1:C:88:LEU:HD23	2.28	0.53
1:B:246:ASP:O	1:B:252:ARG:NH2	2.38	0.53
1:D:15:ARG:HG2	1:D:26:LYS:HZ3	1.72	0.53
1:B:76:GLU:HG2	1:B:77:VAL:N	2.24	0.53
1:B:30:ASN:OD1	1:B:31:THR:N	2.42	0.53
1:A:41:ILE:HG23	1:A:85:TYR:CE1	2.43	0.53
1:D:91:VAL:HG23	1:D:91:VAL:O	2.09	0.53
1:C:46:THR:HG22	1:C:159:PRO:HG2	1.91	0.53
1:A:14:GLY:O	1:A:26:LYS:HD3	2.09	0.53
1:B:33:THR:O	1:B:34:GLY:C	2.47	0.53
1:D:210:PHE:HB2	1:D:218:LEU:HD23	1.89	0.53
1:C:187:ASP:OD1	1:C:190:ALA:N	2.29	0.53
1:B:178:PRO:O	1:B:181:LEU:HB2	2.08	0.53
1:B:141:LEU:O	1:B:148:LEU:HD12	2.09	0.53
1:D:280:ASN:O	1:D:283:ASP:HB3	2.09	0.53
1:D:15:ARG:NE	1:D:26:LYS:NZ	2.57	0.53
1:C:8:VAL:HG12	1:C:13:VAL:HG21	1.91	0.53
1:A:96:LEU:HA	1:A:142:LEU:CD1	2.37	0.53
1:D:227:PHE:CZ	1:D:242:HIS:CE1	2.96	0.53
1:C:243:ARG:CG	1:C:253:ILE:HG13	2.39	0.53
1:D:261:ASP:O	1:D:265:ARG:HG3	2.09	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:215:LEU:O	1:A:218:LEU:HB3	2.09	0.53
1:A:15:ARG:HG2	1:A:26:LYS:CE	2.39	0.52
1:D:75:TYR:CE1	1:D:89:GLU:HB2	2.44	0.52
1:A:116:GLN:HE21	1:A:268:TYR:HB2	1.74	0.52
1:B:44:LYS:O	1:B:47:ILE:N	2.35	0.52
1:A:37:VAL:CG1	1:A:75:TYR:CE2	2.93	0.52
1:D:227:PHE:CD1	1:D:227:PHE:N	2.76	0.52
1:A:198:VAL:O	1:A:202:VAL:HG23	2.09	0.52
1:A:44:LYS:HD2	1:A:80:SER:O	2.10	0.52
1:D:44:LYS:HD3	1:D:81:LYS:O	2.09	0.52
1:A:126:HIS:CE1	1:A:189:SER:HA	2.45	0.52
1:A:284:ILE:O	1:A:287:VAL:HG12	2.09	0.52
1:D:155:LEU:O	1:D:158:LEU:HB2	2.09	0.52
1:A:143:ASP:OD2	1:A:147:ASN:HB2	2.10	0.52
1:A:248:ASN:HB3	1:A:251:THR:OG1	2.09	0.52
1:A:42:MET:CE	1:A:158:LEU:HD12	2.39	0.52
1:D:159:PRO:C	1:D:160:GLN:HG3	2.29	0.52
1:C:52:MET:O	1:C:56:ILE:HG13	2.10	0.52
1:D:16:THR:HA	1:D:26:LYS:CG	2.25	0.52
1:A:15:ARG:HA	1:A:26:LYS:HD3	1.91	0.52
1:D:243:ARG:CZ	1:D:253:ILE:HD12	2.40	0.52
1:B:99:ARG:CG	1:B:99:ARG:HH11	2.23	0.52
1:B:7:ARG:HH22	1:B:10:LYS:CA	2.23	0.52
1:B:78:LEU:HD23	1:B:78:LEU:N	2.25	0.52
1:A:117:GLN:OE1	1:A:148:LEU:HB3	2.10	0.51
1:A:259:LYS:HA	1:A:264:PHE:CE2	2.44	0.51
1:A:136:LYS:H	1:A:139:ASN:HD22	1.57	0.51
1:B:43:ALA:HA	1:B:83:LYS:CG	2.35	0.51
1:D:186:TYR:CD1	1:D:186:TYR:N	2.79	0.51
1:D:175:TYR:HD2	1:D:198:VAL:HB	1.75	0.51
1:B:19:GLU:HG3	1:B:24:LYS:HG3	1.91	0.51
1:D:237:VAL:HG22	1:D:263:TRP:CE2	2.45	0.51
1:C:108:GLU:HA	1:C:204:LEU:HD21	1.91	0.51
1:A:61:SER:CB	1:A:284:ILE:HG12	2.41	0.51
1:D:44:LYS:HB2	1:D:82:SER:C	2.30	0.51
1:D:227:PHE:HZ	1:D:242:HIS:CE1	2.28	0.51
1:B:281:LEU:O	1:B:282:ASP:C	2.49	0.51
1:D:97:PHE:CD1	1:D:100:ILE:HD12	2.45	0.51
1:D:230:PRO:HB3	1:D:232:TRP:CE2	2.45	0.51
1:A:148:LEU:HG	1:A:149:LYS:N	2.26	0.51
1:B:230:PRO:HD2	1:B:233:PHE:CD1	2.46	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:265:ARG:HG2	1:C:265:ARG:HH11	1.76	0.51
1:A:178:PRO:O	1:A:181:LEU:N	2.44	0.51
1:D:241:ILE:HG22	1:D:245:LEU:HD12	1.92	0.51
1:C:209:PRO:HB2	1:C:210:PHE:CE1	2.46	0.50
1:D:70:ASN:HB2	1:D:121:ALA:HB2	1.92	0.50
1:C:234:SER:O	1:C:238:LYS:CG	2.60	0.50
1:C:138:GLU:H	1:C:138:GLU:CD	2.14	0.50
1:B:205:ALA:HB2	1:B:230:PRO:HG2	1.93	0.50
1:A:280:ASN:O	1:A:283:ASP:HB3	2.11	0.50
1:C:247:PRO:CA	1:C:252:ARG:HH21	2.24	0.50
1:A:174:ASN:OD1	1:A:174:ASN:N	2.38	0.50
1:A:29:ARG:HH12	1:A:34:GLY:HA2	1.74	0.50
1:B:64:LYS:O	1:B:73:ARG:NH2	2.44	0.50
1:A:179:GLU:OE2	1:A:252:ARG:CZ	2.56	0.50
1:B:17:ILE:HG22	1:B:18:GLY:N	2.27	0.50
1:B:210:PHE:HE1	1:B:227:PHE:HB3	1.73	0.50
1:A:230:PRO:HD2	1:A:233:PHE:CE1	2.47	0.50
1:B:179:GLU:OE2	1:B:252:ARG:NH2	2.45	0.50
1:C:43:ALA:HA	1:C:83:LYS:HB3	1.94	0.50
1:C:112:ARG:NH2	1:C:266:LYS:HB2	2.25	0.50
1:B:214:ASP:OD1	1:B:216:PRO:HG2	2.12	0.50
1:C:11:TYR:CD1	1:C:11:TYR:N	2.79	0.50
1:C:227:PHE:CE1	1:C:242:HIS:NE2	2.80	0.50
1:D:236:GLU:O	1:D:239:PHE:N	2.44	0.50
1:D:96:LEU:HD11	1:D:114:TYR:CE1	2.45	0.50
1:C:85:TYR:N	1:C:85:TYR:CD1	2.79	0.50
1:B:248:ASN:OD1	1:B:248:ASN:C	2.50	0.50
1:C:230:PRO:O	1:C:233:PHE:HB2	2.11	0.50
1:B:7:ARG:HH22	1:B:10:LYS:C	2.15	0.49
1:D:231:PRO:HD2	1:D:232:TRP:CZ3	2.47	0.49
1:D:261:ASP:HB3	1:D:264:PHE:CB	2.41	0.49
1:D:281:LEU:O	1:D:282:ASP:C	2.49	0.49
1:B:97:PHE:HA	1:B:100:ILE:HG12	1.93	0.49
1:C:234:SER:O	1:C:238:LYS:HG3	2.12	0.49
1:B:55:GLN:HA	1:B:58:ARG:HG2	1.95	0.49
1:B:167:ASN:OD1	1:B:168:ASP:N	2.46	0.49
1:D:237:VAL:O	1:D:241:ILE:HG13	2.12	0.49
1:D:204:LEU:CD1	1:D:237:VAL:HG11	2.43	0.49
1:D:158:LEU:CD2	1:D:158:LEU:H	2.25	0.49
1:A:112:ARG:HH21	1:A:266:LYS:HD2	1.77	0.49
1:B:261:ASP:O	1:B:265:ARG:HB2	2.13	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:143:ASP:OD1	1:B:146:GLY:N	2.46	0.49
1:B:230:PRO:O	1:B:233:PHE:HB2	2.13	0.49
1:D:63:MET:O	1:D:66:VAL:N	2.42	0.49
1:D:30:ASN:O	1:D:34:GLY:N	2.46	0.49
1:C:27:PHE:CE1	1:C:90:PHE:CE2	3.00	0.49
1:B:53:VAL:O	1:B:57:LYS:HG3	2.12	0.49
1:B:7:ARG:NH1	1:B:11:TYR:C	2.66	0.49
1:C:19:GLU:OE1	1:C:19:GLU:N	2.46	0.49
1:C:187:ASP:HB3	1:C:190:ALA:HB3	1.94	0.49
1:D:88:LEU:CD1	1:D:88:LEU:N	2.76	0.49
1:C:281:LEU:HD12	1:C:282:ASP:N	2.27	0.49
1:D:36:ASN:O	1:D:36:ASN:ND2	2.39	0.49
1:D:158:LEU:HD22	1:D:158:LEU:H	1.76	0.49
1:A:91:VAL:HG21	1:A:141:LEU:HB3	1.94	0.49
1:C:280:ASN:O	1:C:283:ASP:HB3	2.12	0.49
1:B:7:ARG:HA	1:B:13:VAL:H	1.78	0.49
1:D:175:TYR:O	1:D:176:VAL:C	2.51	0.49
1:D:205:ALA:HB2	1:D:233:PHE:HZ	1.77	0.49
1:D:197:GLY:HA2	1:D:244:ILE:HG21	1.93	0.49
1:A:30:ASN:ND2	1:A:33:THR:OG1	2.46	0.49
1:D:132:HIS:O	1:D:156:SER:OG	2.24	0.49
1:A:255:ILE:O	1:A:258:ILE:HG12	2.13	0.49
1:D:74:LEU:HD12	1:D:74:LEU:N	2.23	0.49
1:C:67:ARG:CG	1:C:73:ARG:HE	2.26	0.49
1:D:141:LEU:O	1:D:148:LEU:HD12	2.12	0.49
1:C:253:ILE:HG22	1:C:254:GLN:O	2.12	0.48
1:A:281:LEU:O	1:A:282:ASP:C	2.50	0.48
1:A:51:ARG:O	1:A:52:MET:CE	2.61	0.48
1:B:51:ARG:CB	1:B:52:MET:HE3	2.39	0.48
1:D:72:VAL:HG22	1:D:149:LYS:HB3	1.94	0.48
1:B:240:LEU:HD12	1:B:240:LEU:O	2.14	0.48
1:C:155:LEU:HA	1:C:158:LEU:HD13	1.94	0.48
1:B:138:GLU:H	1:B:138:GLU:CD	2.13	0.48
1:B:67:ARG:O	1:B:273:ALA:HB1	2.13	0.48
1:C:178:PRO:O	1:C:181:LEU:HB2	2.12	0.48
1:D:74:LEU:O	1:D:74:LEU:HD13	2.13	0.48
1:C:63:MET:HG3	1:C:153:PHE:O	2.13	0.48
1:D:15:ARG:NE	1:D:26:LYS:HZ1	2.11	0.48
1:C:248:ASN:OD1	1:C:249:PRO:HD2	2.14	0.48
1:D:114:TYR:HE1	1:D:142:LEU:HD21	1.78	0.48
1:D:92:THR:C	1:D:94:GLY:H	2.17	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:266:LYS:O	1:D:268:TYR:N	2.47	0.48
1:B:7:ARG:HG3	1:B:8:VAL:N	2.28	0.48
1:D:210:PHE:CE2	1:D:222:ILE:HG12	2.49	0.48
1:A:66:VAL:HA	1:A:275:GLU:OE1	2.14	0.48
1:D:113:LYS:HE2	1:D:117:GLN:NE2	2.28	0.48
1:D:10:LYS:HE2	1:D:11:TYR:HE1	1.78	0.48
1:D:15:ARG:HE	1:D:26:LYS:HZ3	1.62	0.48
1:C:281:LEU:O	1:C:282:ASP:C	2.50	0.48
1:D:61:SER:CB	1:D:284:ILE:HG12	2.43	0.48
1:A:15:ARG:HG2	1:A:26:LYS:HE2	1.95	0.48
1:C:97:PHE:HE2	1:C:202:VAL:HG11	1.78	0.48
1:A:50:ASN:OD1	1:A:51:ARG:N	2.46	0.48
1:C:39:ILE:HG22	1:C:41:ILE:HG13	1.95	0.48
1:B:280:ASN:O	1:B:283:ASP:HB3	2.13	0.48
1:A:131:TYR:CE2	1:A:189:SER:HB3	2.49	0.48
1:D:266:LYS:HB3	1:D:267:ASN:HD22	1.79	0.48
1:C:96:LEU:HD13	1:C:142:LEU:HD21	1.96	0.48
1:B:99:ARG:HH22	1:B:110:GLU:CD	1.89	0.47
1:C:246:ASP:O	1:C:252:ARG:CZ	2.61	0.47
1:D:28:ALA:O	1:D:36:ASN:CA	2.62	0.47
1:D:230:PRO:HD2	1:D:233:PHE:CD2	2.49	0.47
1:A:221:LYS:CG	1:A:226:GLU:OE2	2.62	0.47
1:B:100:ILE:HD12	1:B:106:LEU:HG	1.93	0.47
1:C:281:LEU:HD12	1:C:281:LEU:C	2.35	0.47
1:D:44:LYS:CD	1:D:80:SER:O	2.53	0.47
1:B:47:ILE:HG21	1:B:84:ILE:CD1	2.43	0.47
1:A:51:ARG:O	1:A:52:MET:HE3	2.14	0.47
1:C:67:ARG:NE	1:C:73:ARG:NH2	2.59	0.47
1:A:15:ARG:HB3	1:A:16:THR:HG22	1.96	0.47
1:C:127:SER:OG	1:C:128:LYS:HE3	2.13	0.47
1:C:210:PHE:CD1	1:C:210:PHE:N	2.75	0.47
1:C:210:PHE:HE1	1:C:227:PHE:HB3	1.80	0.47
1:A:44:LYS:O	1:A:47:ILE:HG22	2.14	0.47
1:C:112:ARG:HG3	1:C:263:TRP:CH2	2.49	0.47
1:C:19:GLU:CB	1:C:24:LYS:CB	2.92	0.47
1:B:76:GLU:HG2	1:B:77:VAL:H	1.80	0.47
1:D:178:PRO:O	1:D:181:LEU:HB2	2.13	0.47
1:A:27:PHE:CD1	1:A:28:ALA:N	2.83	0.47
1:C:57:LYS:HG2	1:C:287:VAL:HG11	1.97	0.47
1:D:56:ILE:O	1:D:60:ILE:HG12	2.15	0.47
1:C:281:LEU:O	1:C:284:ILE:CA	2.63	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:78:LEU:CB	1:A:85:TYR:HB2	2.43	0.47
1:B:100:ILE:O	1:B:104:GLY:N	2.48	0.47
1:D:78:LEU:HB2	1:D:85:TYR:HB2	1.97	0.47
1:A:64:LYS:HE3	1:A:76:GLU:HG2	1.97	0.47
1:B:237:VAL:HG22	1:B:263:TRP:CD2	2.50	0.47
1:C:174:ASN:CG	1:C:208:LEU:HD13	2.35	0.47
1:B:42:MET:SD	1:B:158:LEU:CD2	3.00	0.47
1:A:229:CYS:SG	1:A:242:HIS:HE1	2.38	0.47
1:C:227:PHE:HD1	1:C:227:PHE:O	1.97	0.46
1:C:132:HIS:C	1:C:133:ARG:HG3	2.36	0.46
1:D:142:LEU:HD22	1:D:146:GLY:O	2.14	0.46
1:D:64:LYS:HA	1:D:74:LEU:HD11	1.93	0.46
1:B:112:ARG:O	1:B:116:GLN:CG	2.45	0.46
1:B:16:THR:HA	1:B:26:LYS:HA	1.97	0.46
1:C:236:GLU:CD	1:C:262:PRO:HG2	2.36	0.46
1:B:175:TYR:CD1	1:B:198:VAL:HB	2.50	0.46
1:C:230:PRO:HB3	1:C:232:TRP:CH2	2.50	0.46
1:D:96:LEU:CD1	1:D:114:TYR:CD1	2.93	0.46
1:A:230:PRO:HD2	1:A:233:PHE:CD1	2.51	0.46
1:B:234:SER:OG	1:B:237:VAL:HG23	2.16	0.46
1:C:100:ILE:O	1:C:104:GLY:N	2.48	0.46
1:B:270:PRO:HG2	1:B:272:ARG:CZ	2.45	0.46
1:D:236:GLU:OE1	1:D:239:PHE:HB3	2.15	0.46
1:B:27:PHE:CG	1:B:28:ALA:N	2.83	0.46
1:A:246:ASP:OD2	1:A:251:THR:OG1	2.30	0.46
1:C:269:VAL:HA	1:C:270:PRO:HD2	1.77	0.46
1:B:132:HIS:O	1:B:133:ARG:HB2	2.15	0.46
1:D:281:LEU:C	1:D:281:LEU:HD12	2.36	0.46
1:B:114:TYR:O	1:B:117:GLN:N	2.49	0.46
1:C:105:ARG:NH1	1:C:232:TRP:CD2	2.84	0.46
1:A:161:GLU:HA	1:A:162:GLY:HA2	1.76	0.46
1:D:236:GLU:OE1	1:D:236:GLU:HA	2.15	0.46
1:D:158:LEU:N	1:D:158:LEU:CD2	2.78	0.46
1:A:17:ILE:N	1:A:17:ILE:HD13	2.31	0.46
1:D:10:LYS:HG3	1:D:11:TYR:HD1	1.81	0.46
1:C:128:LYS:HA	1:C:128:LYS:HD3	1.73	0.46
1:D:171:GLY:HA3	1:D:172:THR:HA	1.64	0.46
1:B:140:LEU:HD11	1:B:199:ILE:HD13	1.98	0.46
1:C:209:PRO:HB2	1:C:210:PHE:CD1	2.50	0.46
1:D:44:LYS:HB2	1:D:83:LYS:N	2.31	0.46
1:C:186:TYR:CD1	1:C:186:TYR:N	2.84	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:51:ARG:C	1:B:52:MET:HE3	2.37	0.46
1:C:80:SER:HG	1:C:83:LYS:H	1.55	0.46
1:D:266:LYS:HB3	1:D:267:ASN:ND2	2.31	0.46
1:D:268:TYR:O	1:D:269:VAL:HG23	2.16	0.46
1:C:221:LYS:O	1:C:225:ALA:N	2.49	0.46
1:B:99:ARG:HG3	1:B:99:ARG:HH11	1.80	0.45
1:D:241:ILE:HG23	1:D:245:LEU:HD12	1.98	0.45
1:C:112:ARG:HH21	1:C:266:LYS:HD2	1.79	0.45
1:C:237:VAL:CG2	1:C:263:TRP:NE1	2.79	0.45
1:A:68:HIS:CE1	1:A:70:ASN:HB2	2.50	0.45
1:C:230:PRO:HB3	1:C:232:TRP:CZ2	2.51	0.45
1:A:139:ASN:HA	1:A:151:SER:OG	2.15	0.45
1:C:112:ARG:HE	1:C:266:LYS:HB2	1.81	0.45
1:A:160:GLN:NE2	1:D:211:SER:HB2	2.32	0.45
1:D:99:ARG:NH2	1:D:110:GLU:OE2	2.50	0.45
1:A:29:ARG:HA	1:A:36:ASN:HA	1.98	0.45
1:D:237:VAL:CG2	1:D:263:TRP:NE1	2.79	0.45
1:D:39:ILE:HG22	1:D:41:ILE:CG1	2.46	0.45
1:C:19:GLU:CB	1:C:24:LYS:HB3	2.46	0.45
1:B:178:PRO:O	1:B:181:LEU:N	2.47	0.45
1:A:118:LEU:CD2	1:A:196:CYS:SG	2.94	0.45
1:B:50:ASN:OD1	1:B:51:ARG:N	2.49	0.45
1:C:240:LEU:HD13	1:C:261:ASP:CG	2.37	0.45
1:A:210:PHE:CD2	1:A:222:ILE:HG12	2.51	0.45
1:B:175:TYR:CD1	1:B:198:VAL:CG1	3.00	0.45
1:A:131:TYR:HB2	1:A:133:ARG:CZ	2.47	0.45
1:C:279:VAL:HG12	1:C:280:ASN:OD1	2.17	0.45
1:C:71:ILE:HD13	1:C:125:CYS:SG	2.57	0.45
1:D:237:VAL:HG22	1:D:263:TRP:CD1	2.52	0.45
1:A:207:TYR:OH	1:A:230:PRO:HG3	2.17	0.45
1:C:243:ARG:HG2	1:C:253:ILE:HD11	1.88	0.45
1:D:13:VAL:HA	1:D:28:ALA:CB	2.47	0.45
1:B:65:ILE:HD13	1:B:279:VAL:H	1.81	0.45
1:A:42:MET:O	1:A:83:LYS:HB3	2.17	0.44
1:D:93:GLY:HA3	1:D:142:LEU:O	2.17	0.44
1:C:25:VAL:HG13	1:C:40:LYS:CD	2.46	0.44
1:B:258:ILE:O	1:B:261:ASP:HB3	2.17	0.44
1:D:227:PHE:HZ	1:D:242:HIS:ND1	2.15	0.44
1:B:134:ASP:O	1:B:135:LEU:C	2.55	0.44
1:A:100:ILE:HG23	1:A:104:GLY:O	2.17	0.44
1:B:19:GLU:CB	1:B:24:LYS:HG3	2.47	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:187:ASP:HB2	1:B:190:ALA:HB3	1.99	0.44
1:C:62:ILE:O	1:C:66:VAL:HG23	2.18	0.44
1:B:80:SER:HG	1:B:83:LYS:H	1.56	0.44
1:A:15:ARG:CB	1:A:16:THR:HG22	2.47	0.44
1:C:16:THR:HA	1:C:26:LYS:HA	1.99	0.44
1:C:119:VAL:CG1	1:C:258:ILE:HD11	2.47	0.44
1:D:64:LYS:N	1:D:74:LEU:HD11	2.32	0.44
1:B:92:THR:CB	1:B:144:THR:HG23	2.44	0.44
1:C:74:LEU:HD12	1:C:74:LEU:C	2.37	0.44
1:B:240:LEU:HD12	1:B:244:ILE:HG13	1.99	0.44
1:A:141:LEU:HB2	1:A:149:LYS:O	2.18	0.44
1:D:210:PHE:HB3	1:D:218:LEU:HD23	1.98	0.44
1:D:253:ILE:HG21	1:D:258:ILE:HG22	2.00	0.44
1:D:48:LEU:HD23	1:D:48:LEU:HA	1.68	0.44
1:B:110:GLU:O	1:B:111:SER:C	2.56	0.44
1:A:281:LEU:O	1:A:284:ILE:CA	2.64	0.44
1:B:42:MET:C	1:B:83:LYS:HG2	2.38	0.44
1:D:236:GLU:O	1:D:237:VAL:C	2.54	0.44
1:A:8:VAL:HG12	1:A:11:TYR:O	2.17	0.44
1:B:80:SER:HG	1:B:83:LYS:N	2.13	0.44
1:C:240:LEU:O	1:C:244:ILE:HG13	2.17	0.44
1:D:253:ILE:HG21	1:D:258:ILE:CG2	2.47	0.44
1:C:99:ARG:HA	1:C:102:HIS:HD2	1.81	0.44
1:A:96:LEU:O	1:A:96:LEU:HD12	2.17	0.44
1:C:7:ARG:NH1	1:C:10:LYS:O	2.51	0.44
1:A:47:ILE:CG2	1:A:48:LEU:N	2.81	0.43
1:D:27:PHE:CE2	1:D:36:ASN:HB2	2.53	0.43
1:C:30:ASN:O	1:C:34:GLY:HA2	2.18	0.43
1:B:215:LEU:N	1:B:216:PRO:HD2	2.32	0.43
1:C:178:PRO:O	1:C:181:LEU:N	2.52	0.43
1:C:86:ILE:HG22	1:C:88:LEU:CD2	2.47	0.43
1:C:148:LEU:HG	1:C:149:LYS:N	2.34	0.43
1:D:132:HIS:CE1	1:D:152:ASP:O	2.71	0.43
1:A:128:LYS:HD3	1:A:128:LYS:HA	1.69	0.43
1:D:44:LYS:CB	1:D:82:SER:C	2.86	0.43
1:B:227:PHE:HD1	1:B:227:PHE:C	2.21	0.43
1:C:236:GLU:HB3	1:C:263:TRP:HB2	2.00	0.43
1:C:237:VAL:CG2	1:C:263:TRP:CE2	3.00	0.43
1:D:99:ARG:NH1	1:D:114:TYR:OH	2.51	0.43
1:C:40:LYS:O	1:C:85:TYR:HA	2.19	0.43
1:C:74:LEU:HD11	1:C:76:GLU:O	2.18	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:240:LEU:HD22	1:B:261:ASP:OD1	2.18	0.43
1:B:254:GLN:O	1:B:258:ILE:HG23	2.19	0.43
1:B:227:PHE:C	1:B:227:PHE:CD1	2.92	0.43
1:B:116:GLN:HA	1:B:264:PHE:CE1	2.53	0.43
1:D:126:HIS:CE1	1:D:189:SER:HA	2.54	0.43
1:B:8:VAL:HG12	1:B:13:VAL:CG2	2.49	0.43
1:A:51:ARG:C	1:A:52:MET:CE	2.77	0.43
1:C:41:ILE:CD1	1:C:85:TYR:HD2	2.31	0.43
1:C:235:ALA:HA	1:C:238:LYS:HG3	2.01	0.43
1:C:112:ARG:NE	1:C:266:LYS:HB2	2.34	0.43
1:A:39:ILE:CG2	1:A:41:ILE:HG13	2.48	0.43
1:D:158:LEU:HD13	1:D:158:LEU:HA	1.77	0.43
1:C:133:ARG:NH1	1:C:186:TYR:CZ	2.87	0.43
1:C:24:LYS:HE2	1:C:26:LYS:HE3	2.00	0.43
1:A:92:THR:OG1	1:A:144:THR:HG22	2.19	0.43
1:B:99:ARG:CG	1:B:99:ARG:NH1	2.81	0.42
1:D:253:ILE:CG2	1:D:258:ILE:CG2	2.96	0.42
1:B:205:ALA:O	1:B:207:TYR:CD2	2.72	0.42
1:B:145:ASN:O	1:B:145:ASN:ND2	2.52	0.42
1:D:136:LYS:H	1:D:139:ASN:HD22	1.67	0.42
1:D:253:ILE:HG12	1:D:258:ILE:HG23	1.97	0.42
1:B:22:PHE:N	1:B:22:PHE:CD1	2.82	0.42
1:A:240:LEU:O	1:A:244:ILE:HG13	2.18	0.42
1:D:105:ARG:HB2	1:D:204:LEU:O	2.20	0.42
1:B:174:ASN:ND2	1:B:210:PHE:O	2.52	0.42
1:D:254:GLN:O	1:D:258:ILE:HG23	2.19	0.42
1:A:201:PHE:CD1	1:A:201:PHE:C	2.91	0.42
1:C:71:ILE:HG13	1:C:121:ALA:HB1	2.02	0.42
1:B:109:ASP:HA	1:B:112:ARG:NH1	2.34	0.42
1:B:281:LEU:O	1:B:284:ILE:CA	2.63	0.42
1:C:179:GLU:HG2	1:C:249:PRO:HG3	2.01	0.42
1:D:230:PRO:CB	1:D:232:TRP:CE2	3.02	0.42
1:D:269:VAL:HA	1:D:270:PRO:HD3	1.89	0.42
1:B:71:ILE:HG13	1:B:121:ALA:HB1	2.00	0.42
1:B:116:GLN:HA	1:B:264:PHE:HE1	1.85	0.42
1:D:186:TYR:HD1	1:D:186:TYR:N	2.16	0.42
1:C:270:PRO:O	1:C:272:ARG:HG2	2.18	0.42
1:A:210:PHE:CE1	1:A:227:PHE:HB3	2.54	0.42
1:A:265:ARG:NH1	1:B:145:ASN:OD1	2.52	0.42
1:A:237:VAL:HG23	1:A:263:TRP:CD1	2.54	0.42
1:D:47:ILE:HG21	1:D:84:ILE:HD12	2.02	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:255:ILE:CD1	1:C:255:ILE:H	2.06	0.42
1:D:42:MET:HE1	1:D:158:LEU:HB3	2.01	0.42
1:D:256:GLN:CA	1:D:260:LYS:HZ2	2.32	0.42
1:B:70:ASN:ND2	1:B:117:GLN:OE1	2.52	0.42
1:B:70:ASN:HA	1:B:148:LEU:O	2.20	0.42
1:B:222:ILE:O	1:B:225:ALA:N	2.50	0.42
1:C:227:PHE:HE1	1:C:242:HIS:CE1	2.35	0.42
1:C:243:ARG:HG2	1:C:243:ARG:HH11	1.84	0.42
1:B:227:PHE:HD1	1:B:227:PHE:O	2.01	0.42
1:B:44:LYS:HG3	1:B:84:ILE:CG1	2.49	0.42
1:D:275:GLU:OE1	1:D:276:GLU:O	2.38	0.42
1:A:137:PRO:HA	1:A:140:LEU:HD12	2.00	0.42
1:B:99:ARG:HG3	1:B:103:LYS:HZ2	1.85	0.42
1:C:57:LYS:HG2	1:C:287:VAL:CG1	2.50	0.42
1:D:231:PRO:HG2	1:D:232:TRP:CE3	2.54	0.42
1:C:98:ASP:O	1:C:102:HIS:CD2	2.72	0.42
1:C:7:ARG:HA	1:C:13:VAL:HG23	2.00	0.42
1:B:279:VAL:HG12	1:B:280:ASN:OD1	2.20	0.42
1:A:210:PHE:HE1	1:A:227:PHE:HB3	1.85	0.42
1:C:47:ILE:CG2	1:C:48:LEU:N	2.83	0.42
1:B:279:VAL:O	1:B:280:ASN:C	2.58	0.42
1:D:64:LYS:CA	1:D:74:LEU:HD11	2.50	0.41
1:A:47:ILE:HD11	1:A:56:ILE:HG21	2.01	0.41
1:A:37:VAL:HG12	1:A:75:TYR:CE2	2.50	0.41
1:D:200:LEU:HD12	1:D:200:LEU:O	2.20	0.41
1:D:136:LYS:HB2	1:D:138:GLU:OE1	2.20	0.41
1:B:131:TYR:N	1:B:131:TYR:CD1	2.88	0.41
1:D:78:LEU:HD23	1:D:78:LEU:HA	1.88	0.41
1:A:173:PRO:HB3	1:D:219:TYR:HH	1.85	0.41
1:C:261:ASP:HA	1:C:262:PRO:HD2	1.82	0.41
1:B:14:GLY:N	1:B:27:PHE:O	2.40	0.41
1:B:44:LYS:HG3	1:B:84:ILE:HG13	2.02	0.41
1:D:128:LYS:HZ3	1:D:275:GLU:HG2	1.85	0.41
1:D:227:PHE:HD1	1:D:227:PHE:O	2.03	0.41
1:A:279:VAL:O	1:A:280:ASN:C	2.58	0.41
1:D:236:GLU:CD	1:D:262:PRO:HG2	2.40	0.41
1:B:181:LEU:HD12	1:B:223:ASN:ND2	2.35	0.41
1:B:74:LEU:HD21	1:B:86:ILE:HG23	2.02	0.41
1:D:138:GLU:H	1:D:138:GLU:CD	2.23	0.41
1:B:19:GLU:CG	1:B:24:LYS:HG3	2.51	0.41
1:A:136:LYS:HG2	1:A:139:ASN:HD21	1.85	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:248:ASN:C	1:C:248:ASN:OD1	2.59	0.41
1:C:72:VAL:CG2	1:C:149:LYS:HB3	2.49	0.41
1:D:215:LEU:N	1:D:216:PRO:HD2	2.35	0.41
1:C:237:VAL:HG22	1:C:263:TRP:CD2	2.56	0.41
1:A:124:HIS:CE1	1:A:275:GLU:OE2	2.74	0.41
1:C:15:ARG:CB	1:C:16:THR:HG22	2.51	0.41
1:B:70:ASN:HD21	1:B:117:GLN:NE2	2.18	0.41
1:D:70:ASN:HA	1:D:148:LEU:O	2.21	0.41
1:D:279:VAL:HG12	1:D:280:ASN:OD1	2.21	0.41
1:B:259:LYS:HA	1:B:264:PHE:CE2	2.56	0.41
1:D:248:ASN:HA	1:D:249:PRO:HD2	1.91	0.41
1:D:256:GLN:HA	1:D:260:LYS:HZ2	1.86	0.41
1:B:244:ILE:HA	1:B:253:ILE:HG22	2.03	0.41
1:A:175:TYR:O	1:A:194:TRP:NE1	2.54	0.41
1:D:210:PHE:CB	1:D:218:LEU:CD2	2.92	0.41
1:D:178:PRO:HA	1:D:181:LEU:CD1	2.51	0.41
1:A:45:SER:O	1:A:49:LYS:HD3	2.20	0.41
1:C:215:LEU:O	1:C:216:PRO:C	2.58	0.41
1:D:74:LEU:HA	1:D:87:VAL:O	2.21	0.41
1:D:227:PHE:HD1	1:D:227:PHE:H	1.68	0.41
1:C:133:ARG:NH1	1:C:186:TYR:CE2	2.89	0.40
1:B:55:GLN:HA	1:B:58:ARG:CZ	2.51	0.40
1:D:279:VAL:O	1:D:280:ASN:C	2.59	0.40
1:C:55:GLN:O	1:C:59:GLU:HG3	2.21	0.40
1:A:169:THR:HB	1:D:212:GLU:HG2	2.02	0.40
1:C:119:VAL:HG11	1:C:258:ILE:HD11	2.03	0.40
1:B:100:ILE:CD1	1:B:106:LEU:CG	2.90	0.40
1:C:29:ARG:CB	1:C:36:ASN:OD1	2.60	0.40
1:C:234:SER:OG	1:C:237:VAL:HG23	2.21	0.40
1:D:47:ILE:HD11	1:D:288:PHE:CE2	2.56	0.40
1:B:8:VAL:HG22	1:B:9:GLY:N	2.37	0.40
1:D:105:ARG:NH2	1:D:232:TRP:CD1	2.85	0.40
1:D:92:THR:C	1:D:94:GLY:N	2.73	0.40
1:A:248:ASN:C	1:A:248:ASN:OD1	2.58	0.40
1:D:266:LYS:O	1:D:267:ASN:C	2.59	0.40
1:D:141:LEU:HD12	1:D:151:SER:OG	2.21	0.40
1:B:47:ILE:HG12	1:B:288:PHE:CE2	2.56	0.40
1:B:91:VAL:HG21	1:B:141:LEU:HB3	2.04	0.40
1:A:37:VAL:HG11	1:A:75:TYR:CD2	2.57	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	268/446 (60%)	254 (95%)	14 (5%)	0	100	100
1	B	273/446 (61%)	249 (91%)	23 (8%)	1 (0%)	39	76
1	C	275/446 (62%)	263 (96%)	11 (4%)	1 (0%)	39	76
1	D	265/446 (59%)	247 (93%)	15 (6%)	3 (1%)	17	57
All	All	1081/1784 (61%)	1013 (94%)	63 (6%)	5 (0%)	34	71

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	93	GLY
1	B	23	ALA
1	D	176	VAL
1	D	267	ASN
1	C	270	PRO

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	239/388 (62%)	217 (91%)	22 (9%)	11	40
1	B	241/388 (62%)	198 (82%)	43 (18%)	2	10
1	C	243/388 (63%)	214 (88%)	29 (12%)	6	27
1	D	238/388 (61%)	210 (88%)	28 (12%)	6	27
All	All	961/1552 (62%)	839 (87%)	122 (13%)	5	24

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

Mol	Chain	Res	Type
1	A	17	ILE
1	A	24	LYS
1	A	45	SER
1	A	49	LYS
1	A	63	MET
1	A	65	ILE
1	A	73	ARG
1	A	76	GLU
1	A	78	LEU
1	A	128	LYS
1	A	153	PHE
1	A	158	LEU
1	A	161	GLU
1	A	174	ASN
1	A	179	GLU
1	A	210	PHE
1	A	212	GLU
1	A	215	LEU
1	A	221	LYS
1	A	229	CYS
1	A	242	HIS
1	A	272	ARG
1	B	7	ARG
1	B	12	GLU
1	B	16	THR
1	B	19	GLU
1	B	21	THR
1	B	22	PHE
1	B	25	VAL
1	B	42	MET
1	B	47	ILE
1	B	49	LYS
1	B	52	MET
1	B	55	GLN
1	B	65	ILE
1	B	67	ARG
1	B	73	ARG
1	B	74	LEU
1	B	78	LEU
1	B	83	LYS
1	B	88	LEU
1	B	96	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	99	ARG
1	B	103	LYS
1	B	105	ARG
1	B	110	GLU
1	B	136	LYS
1	B	145	ASN
1	B	153	PHE
1	B	155	LEU
1	B	160	GLN
1	B	168	ASP
1	B	170	CYS
1	B	172	THR
1	B	179	GLU
1	B	182	SER
1	B	186	TYR
1	B	213	THR
1	B	215	LEU
1	B	227	PHE
1	B	228	ASP
1	B	229	CYS
1	B	255	ILE
1	B	258	ILE
1	B	261	ASP
1	C	7	ARG
1	C	11	TYR
1	C	12	GLU
1	C	19	GLU
1	C	22	PHE
1	C	24	LYS
1	C	25	VAL
1	C	30	ASN
1	C	40	LYS
1	C	65	ILE
1	C	74	LEU
1	C	82	SER
1	C	85	TYR
1	C	112	ARG
1	C	116	GLN
1	C	128	LYS
1	C	133	ARG
1	C	168	ASP
1	C	172	THR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	179	GLU
1	C	186	TYR
1	C	196	CYS
1	C	210	PHE
1	C	227	PHE
1	C	255	ILE
1	C	265	ARG
1	C	271	ILE
1	C	272	ARG
1	C	275	GLU
1	D	30	ASN
1	D	36	ASN
1	D	37	VAL
1	D	73	ARG
1	D	74	LEU
1	D	82	SER
1	D	101	VAL
1	D	107	LYS
1	D	112	ARG
1	D	135	LEU
1	D	153	PHE
1	D	156	SER
1	D	160	GLN
1	D	166	LEU
1	D	172	THR
1	D	174	ASN
1	D	179	GLU
1	D	182	SER
1	D	186	TYR
1	D	213	THR
1	D	218	LEU
1	D	226	GLU
1	D	227	PHE
1	D	236	GLU
1	D	253	ILE
1	D	260	LYS
1	D	267	ASN
1	D	275	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (24) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	55	GLN
1	A	116	GLN
1	A	139	ASN
1	A	145	ASN
1	A	184	GLN
1	A	223	ASN
1	A	242	HIS
1	B	68	HIS
1	B	70	ASN
1	B	116	GLN
1	B	139	ASN
1	B	160	GLN
1	B	223	ASN
1	B	242	HIS
1	B	256	GLN
1	C	102	HIS
1	C	139	ASN
1	D	102	HIS
1	D	126	HIS
1	D	139	ASN
1	D	167	ASN
1	D	223	ASN
1	D	242	HIS
1	D	267	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

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

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

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	274/446 (61%)	-0.25	3 (1%) 82 78	40, 61, 100, 124	0
1	B	277/446 (62%)	-0.19	2 (0%) 89 86	39, 64, 125, 146	0
1	C	279/446 (62%)	-0.16	3 (1%) 82 78	44, 65, 121, 136	0
1	D	271/446 (60%)	-0.23	4 (1%) 76 71	47, 67, 109, 132	0
All	All	1101/1784 (61%)	-0.21	12 (1%) 82 78	39, 64, 116, 146	0

All (12) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	18	GLY	3.8
1	B	279	VAL	3.3
1	D	160	GLN	2.5
1	A	212	GLU	2.5
1	D	277	GLU	2.4
1	A	278	GLU	2.3
1	C	161	GLU	2.3
1	D	274	ARG	2.2
1	A	23	ALA	2.2
1	D	275	GLU	2.1
1	C	174	ASN	2.1
1	C	21	THR	2.0

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.