



# Full wwPDB X-ray Structure Validation Report ⓘ

May 13, 2020 – 12:53 pm BST

PDB ID : 3MJK  
Title : Structure of a growth factor precursor  
Authors : Liu, H.; He, X.  
Deposited on : 2010-04-12  
Resolution : 2.40 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](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

---

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

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

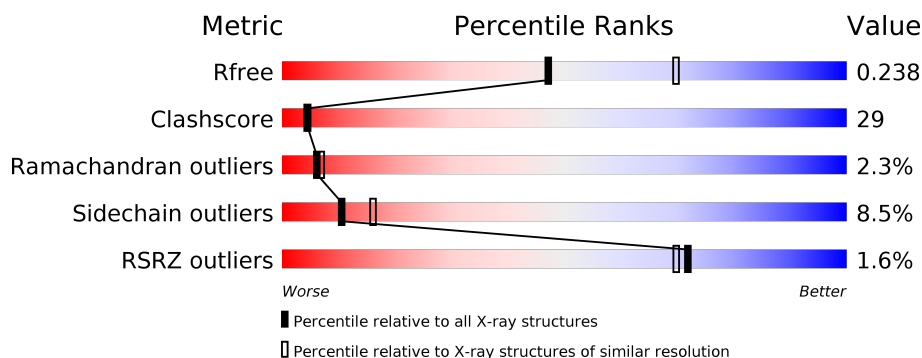
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.40 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	169	<div> <div>3%</div> <div> <div>40%</div> <div>29%</div> <div>7%</div> <div>24%</div> </div> </div>
1	B	169	<div> <div>%</div> <div> <div>44%</div> <div>23%</div> <div>5%</div> <div>27%</div> </div> </div>
1	E	169	<div> <div>%</div> <div> <div>41%</div> <div>27%</div> <div>.</div> <div>28%</div> </div> </div>
1	F	169	<div> <div>40%</div> <div>31%</div> <div>.</div> <div>26%</div> </div>
1	X	169	<div> <div>%</div> <div> <div>44%</div> <div>22%</div> <div>5%</div> <div>28%</div> </div> </div>
1	Y	169	<div> <div>2%</div> <div> <div>42%</div> <div>30%</div> <div>.</div> <div>24%</div> </div> </div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6732 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 Platelet-derived growth factor subunit A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	129	Total	C	N	O	S	0	0	0
			1040	646	200	186	8			
1	B	124	Total	C	N	O	S	0	0	0
			986	615	185	178	8			
1	E	122	Total	C	N	O	S	0	0	0
			974	608	183	175	8			
1	F	125	Total	C	N	O	S	0	0	0
			991	618	186	179	8			
1	X	121	Total	C	N	O	S	0	0	0
			967	603	182	174	8			
1	Y	129	Total	C	N	O	S	0	0	0
			1017	632	190	187	8			

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	182	THR	-	EXPRESSION TAG	UNP P04085
A	183	SER	-	EXPRESSION TAG	UNP P04085
A	184	HIS	-	EXPRESSION TAG	UNP P04085
A	185	HIS	-	EXPRESSION TAG	UNP P04085
A	186	HIS	-	EXPRESSION TAG	UNP P04085
A	187	HIS	-	EXPRESSION TAG	UNP P04085
A	188	HIS	-	EXPRESSION TAG	UNP P04085
A	189	HIS	-	EXPRESSION TAG	UNP P04085
B	182	THR	-	EXPRESSION TAG	UNP P04085
B	183	SER	-	EXPRESSION TAG	UNP P04085
B	184	HIS	-	EXPRESSION TAG	UNP P04085
B	185	HIS	-	EXPRESSION TAG	UNP P04085
B	186	HIS	-	EXPRESSION TAG	UNP P04085
B	187	HIS	-	EXPRESSION TAG	UNP P04085
B	188	HIS	-	EXPRESSION TAG	UNP P04085
B	189	HIS	-	EXPRESSION TAG	UNP P04085
E	182	THR	-	EXPRESSION TAG	UNP P04085

*Continued on next page...*

*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
E	183	SER	-	EXPRESSION TAG	UNP P04085
E	184	HIS	-	EXPRESSION TAG	UNP P04085
E	185	HIS	-	EXPRESSION TAG	UNP P04085
E	186	HIS	-	EXPRESSION TAG	UNP P04085
E	187	HIS	-	EXPRESSION TAG	UNP P04085
E	188	HIS	-	EXPRESSION TAG	UNP P04085
E	189	HIS	-	EXPRESSION TAG	UNP P04085
F	182	THR	-	EXPRESSION TAG	UNP P04085
F	183	SER	-	EXPRESSION TAG	UNP P04085
F	184	HIS	-	EXPRESSION TAG	UNP P04085
F	185	HIS	-	EXPRESSION TAG	UNP P04085
F	186	HIS	-	EXPRESSION TAG	UNP P04085
F	187	HIS	-	EXPRESSION TAG	UNP P04085
F	188	HIS	-	EXPRESSION TAG	UNP P04085
F	189	HIS	-	EXPRESSION TAG	UNP P04085
X	182	THR	-	EXPRESSION TAG	UNP P04085
X	183	SER	-	EXPRESSION TAG	UNP P04085
X	184	HIS	-	EXPRESSION TAG	UNP P04085
X	185	HIS	-	EXPRESSION TAG	UNP P04085
X	186	HIS	-	EXPRESSION TAG	UNP P04085
X	187	HIS	-	EXPRESSION TAG	UNP P04085
X	188	HIS	-	EXPRESSION TAG	UNP P04085
X	189	HIS	-	EXPRESSION TAG	UNP P04085
Y	182	THR	-	EXPRESSION TAG	UNP P04085
Y	183	SER	-	EXPRESSION TAG	UNP P04085
Y	184	HIS	-	EXPRESSION TAG	UNP P04085
Y	185	HIS	-	EXPRESSION TAG	UNP P04085
Y	186	HIS	-	EXPRESSION TAG	UNP P04085
Y	187	HIS	-	EXPRESSION TAG	UNP P04085
Y	188	HIS	-	EXPRESSION TAG	UNP P04085
Y	189	HIS	-	EXPRESSION TAG	UNP P04085

- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	124	Total O 124 124	0	0
2	B	134	Total O 134 134	0	0
2	E	105	Total O 105 105	0	0
2	F	123	Total O 123 123	0	0

*Continued on next page...*

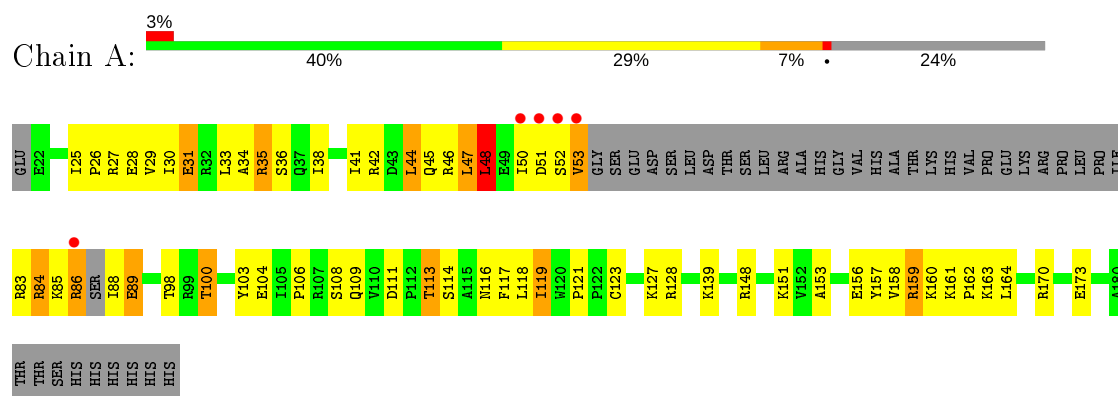
*Continued from previous page...*

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	X	122	Total 122	O 122	0	0
2	Y	149	Total 149	O 149	0	0

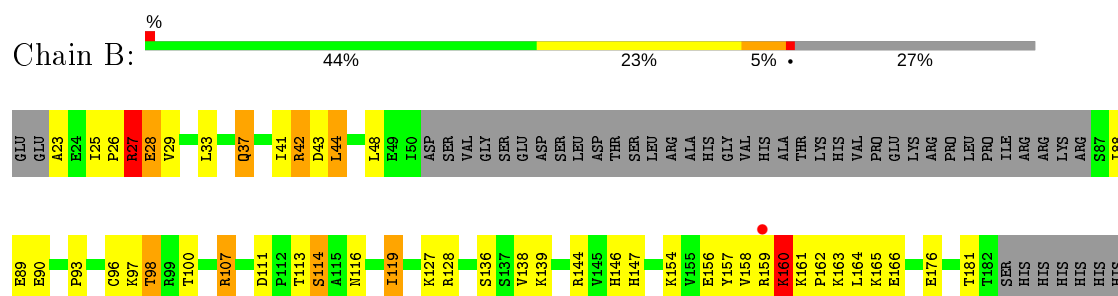
### 3 Residue-property plots [i](#)

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

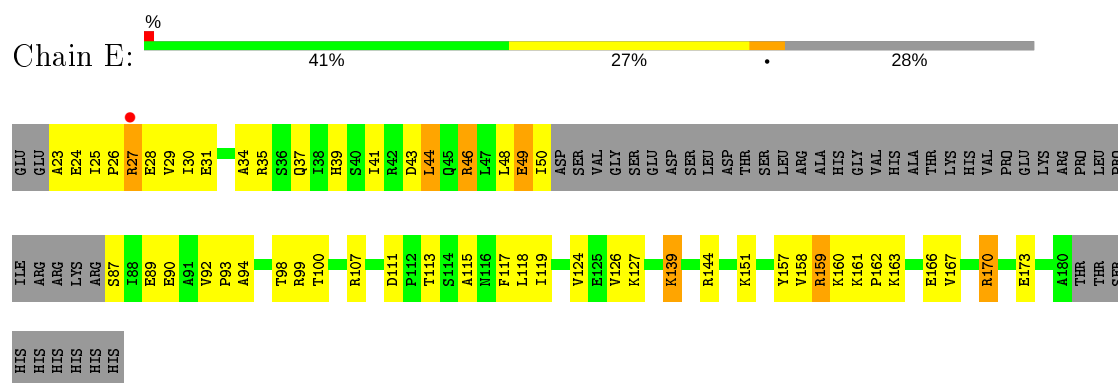
- Molecule 1: Platelet-derived growth factor subunit A



- Molecule 1: Platelet-derived growth factor subunit A

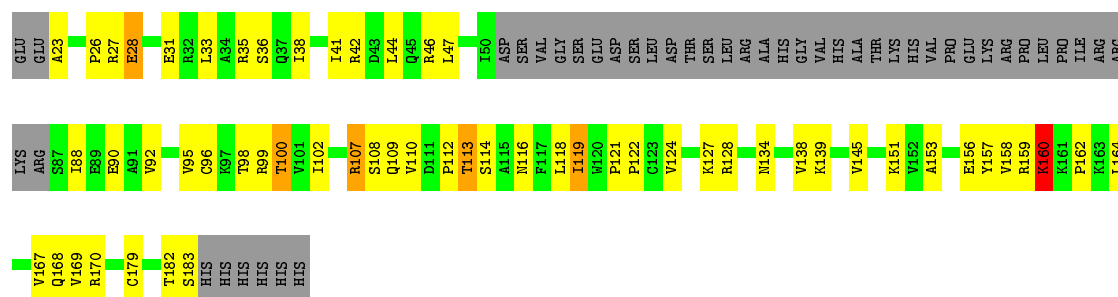


- Molecule 1: Platelet-derived growth factor subunit A




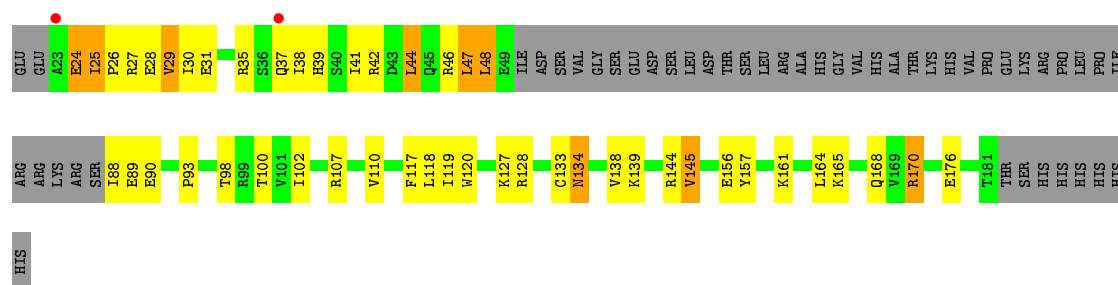
- Molecule 1: Platelet-derived growth factor subunit A

Chain F: 




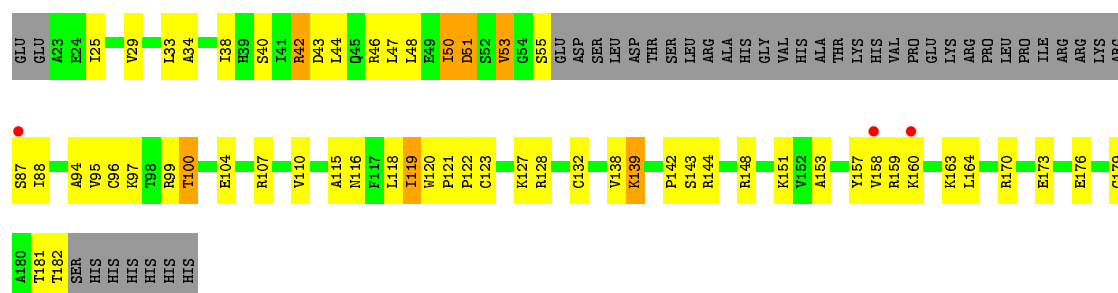
• Molecule 1: Platelet-derived growth factor subunit A

Chain X: 



• Molecule 1: Platelet-derived growth factor subunit A

Chain Y: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	50.84Å 119.21Å 146.71Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.04 – 2.40 48.04 – 2.20	Depositor EDS
% Data completeness (in resolution range)	98.6 (48.04-2.40) 98.1 (48.04-2.20)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.61 (at 2.20Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.225 , 0.276 0.230 , 0.238	Depositor DCC
$R_{free}$ test set	2284 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	36.3	Xtriage
Anisotropy	0.249	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 73.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	6732	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	65.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 19.80 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 9.9951e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<sup>1</sup>Intensities estimated from amplitudes.

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



## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	A	0.50	0/1054	0.79	3/1419 (0.2%)
1	B	0.44	0/1001	0.73	0/1353
1	E	0.43	0/989	0.68	0/1336
1	F	0.46	0/1006	0.67	0/1360
1	X	0.44	0/982	0.67	0/1327
1	Y	0.46	0/1032	0.77	2/1395 (0.1%)
All	All	0.46	0/6064	0.72	5/8190 (0.1%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	48	LEU	N-CA-C	-7.09	91.86	111.00
1	A	48	LEU	CA-CB-CG	6.23	129.64	115.30
1	Y	51	ASP	N-CA-C	6.17	127.67	111.00
1	A	159	ARG	N-CA-C	-5.43	96.32	111.00
1	Y	50	ILE	N-CA-C	-5.17	97.03	111.00

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	1040	0	1077	75	0
1	B	986	0	1016	69	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	974	0	1007	62	0
1	F	991	0	1018	66	0
1	X	967	0	998	72	0
1	Y	1017	0	1042	54	0
2	A	124	0	0	5	0
2	B	134	0	0	4	0
2	E	105	0	0	3	0
2	F	123	0	0	2	0
2	X	122	0	0	5	0
2	Y	149	0	0	6	0
All	All	6732	0	6158	346	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 29.

All (346) 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:Y:100:THR:HG22	1:Y:127:LYS:HE2	1.35	1.05
1:A:45:GLN:O	1:A:48:LEU:O	1.74	1.05
1:B:119:ILE:H	1:B:119:ILE:HD13	1.20	1.04
1:F:31:GLU:HB3	1:F:35:ARG:HH12	1.17	1.03
1:Y:132:CYS:HB3	2:Y:254:HOH:O	1.59	1.00
1:X:88:ILE:HG23	1:X:89:GLU:H	1.27	1.00
1:B:98:THR:HG23	1:B:127:LYS:HD2	1.47	0.97
1:A:119:ILE:H	1:A:119:ILE:HD13	1.30	0.95
1:B:160:LYS:HA	1:B:160:LYS:HZ2	1.28	0.95
1:Y:40:SER:HB2	1:Y:42:ARG:HH12	1.32	0.94
1:A:158:VAL:HG23	1:A:163:LYS:HG3	1.51	0.90
1:Y:42:ARG:H	1:Y:42:ARG:HH11	1.21	0.87
1:X:42:ARG:HE	1:X:46:ARG:HH22	1.22	0.86
1:B:42:ARG:HD2	1:B:42:ARG:H	1.40	0.86
1:A:31:GLU:HB3	1:A:35:ARG:HH12	1.42	0.85
1:F:107:ARG:HB2	1:F:107:ARG:HH11	1.41	0.85
1:B:160:LYS:HA	1:B:160:LYS:NZ	1.93	0.84
1:F:119:ILE:HD13	1:F:119:ILE:H	1.42	0.84
1:A:100:THR:HG22	1:A:127:LYS:NZ	1.93	0.83
1:X:42:ARG:HE	1:X:46:ARG:NH2	1.76	0.82
1:B:27:ARG:O	1:B:27:ARG:HG2	1.78	0.82
1:A:83:ARG:HD3	2:F:691:HOH:O	1.80	0.81
1:F:31:GLU:HB3	1:F:35:ARG:NH1	1.94	0.81

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:163:LYS:NZ	1:B:165:LYS:HE3	1.96	0.81
1:F:100:THR:HG22	1:F:127:LYS:NZ	1.94	0.81
1:E:98:THR:HG23	1:E:127:LYS:HB3	1.64	0.78
1:E:100:THR:HG22	1:E:127:LYS:HD3	1.66	0.78
1:F:160:LYS:HD2	1:F:160:LYS:N	1.99	0.76
1:B:119:ILE:H	1:B:119:ILE:CD1	1.99	0.76
1:A:26:PRO:HB2	1:A:29:VAL:HG23	1.68	0.75
1:E:151:LYS:HD2	1:E:166:GLU:OE1	1.86	0.75
1:X:31:GLU:HB3	1:X:35:ARG:HH12	1.52	0.75
1:Y:42:ARG:H	1:Y:42:ARG:NH1	1.85	0.74
1:A:52:SER:O	1:A:53:VAL:HB	1.85	0.74
1:F:116:ASN:HB3	2:F:296:HOH:O	1.87	0.74
1:A:31:GLU:HB3	1:A:35:ARG:NH1	2.02	0.74
1:B:157:TYR:OH	1:B:162:PRO:HG3	1.88	0.73
1:F:99:ARG:HG3	1:F:99:ARG:HH11	1.51	0.73
1:X:26:PRO:HB2	1:X:29:VAL:HG23	1.69	0.73
1:Y:40:SER:CB	1:Y:42:ARG:HH12	2.01	0.73
1:E:26:PRO:HG2	1:E:29:VAL:HG23	1.72	0.72
1:B:42:ARG:N	1:B:42:ARG:HD2	2.05	0.70
1:Y:116:ASN:HB2	2:Y:442:HOH:O	1.92	0.70
1:E:28:GLU:OE1	2:E:508:HOH:O	2.10	0.69
1:X:156:GLU:HA	1:Y:25:ILE:HD11	1.74	0.69
1:X:139:LYS:N	1:X:139:LYS:HD3	2.08	0.68
1:A:103:TYR:HA	2:A:17:HOH:O	1.94	0.68
1:B:119:ILE:HD13	1:B:119:ILE:N	2.02	0.68
1:A:26:PRO:O	1:A:30:ILE:HG12	1.94	0.67
1:A:83:ARG:O	1:A:84:ARG:HB2	1.94	0.67
1:B:139:LYS:N	1:B:139:LYS:HD3	2.11	0.66
1:Y:163:LYS:HD3	1:Y:164:LEU:N	2.10	0.66
1:F:100:THR:HG22	1:F:127:LYS:HZ3	1.61	0.66
1:F:99:ARG:HG3	1:F:99:ARG:NH1	2.10	0.66
1:X:98:THR:HG22	1:X:127:LYS:HD2	1.78	0.66
1:A:100:THR:HG22	1:A:127:LYS:HZ3	1.59	0.66
1:X:88:ILE:HG23	1:X:89:GLU:N	2.05	0.65
1:B:113:THR:HG22	1:B:114:SER:N	2.11	0.65
1:F:118:LEU:HD23	1:F:119:ILE:N	2.12	0.65
1:B:157:TYR:CZ	1:B:162:PRO:HG3	2.32	0.65
1:A:119:ILE:HD13	1:A:119:ILE:N	2.09	0.64
1:E:139:LYS:HD3	1:E:139:LYS:N	2.12	0.64
1:A:86:ARG:HA	1:A:88:ILE:N	2.11	0.64
1:X:44:LEU:O	1:X:48:LEU:HB2	1.97	0.64

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:157:TYR:CZ	1:F:162:PRO:HG3	2.34	0.63
1:X:28:GLU:HG3	1:X:29:VAL:N	2.14	0.63
1:B:156:GLU:HG3	1:B:163:LYS:HD3	1.80	0.63
1:X:98:THR:CG2	1:X:127:LYS:HD2	2.29	0.63
1:Y:144:ARG:HD3	2:Y:193:HOH:O	1.99	0.62
1:A:104:GLU:HG2	1:A:123:CYS:SG	2.40	0.62
1:A:38:ILE:CD1	1:A:47:LEU:HD12	2.30	0.62
1:X:38:ILE:HD12	1:X:134:ASN:HB3	1.82	0.61
1:A:41:ILE:O	1:A:45:GLN:HG3	2.00	0.61
1:X:41:ILE:HG12	1:X:90:GLU:OE1	2.00	0.61
1:X:41:ILE:HD12	1:Y:153:ALA:HB2	1.81	0.61
1:E:107:ARG:HG3	1:E:117:PHE:CZ	2.36	0.61
1:A:111:ASP:OD2	1:A:114:SER:HB3	2.01	0.61
1:B:26:PRO:C	1:B:28:GLU:H	2.04	0.60
1:B:163:LYS:HZ1	1:B:165:LYS:HE3	1.64	0.60
1:F:157:TYR:CE1	1:F:162:PRO:HG3	2.36	0.60
1:F:41:ILE:HG12	1:F:90:GLU:OE1	2.00	0.60
1:B:159:ARG:O	1:B:161:LYS:N	2.35	0.60
1:E:29:VAL:HG21	1:F:157:TYR:CE2	2.36	0.60
1:F:110:VAL:HG13	1:F:167:VAL:HG11	1.84	0.59
1:B:33:LEU:HD21	1:B:48:LEU:HD21	1.84	0.59
1:F:138:VAL:C	1:F:139:LYS:HD3	2.22	0.59
1:X:102:ILE:HD12	1:Y:94:ALA:HB1	1.83	0.59
1:B:25:ILE:HD12	1:B:25:ILE:N	2.18	0.59
1:E:124:VAL:HG12	1:F:92:VAL:O	2.03	0.59
1:A:159:ARG:C	1:A:161:LYS:H	2.07	0.59
1:E:27:ARG:O	1:E:31:GLU:HG3	2.03	0.59
1:F:31:GLU:CB	1:F:35:ARG:HH12	2.05	0.59
1:X:31:GLU:O	1:X:35:ARG:HG2	2.03	0.58
1:X:42:ARG:NE	1:X:46:ARG:NH2	2.48	0.58
1:A:38:ILE:HD11	1:A:47:LEU:HD12	1.83	0.58
1:B:98:THR:CG2	1:B:127:LYS:HD2	2.27	0.58
1:X:100:THR:HG22	1:X:127:LYS:HD3	1.85	0.58
1:X:24:GLU:O	1:X:25:ILE:C	2.41	0.58
1:A:119:ILE:CD1	1:A:119:ILE:H	2.11	0.58
1:B:138:VAL:HG22	1:B:181:THR:HB	1.86	0.58
1:X:144:ARG:HD3	1:X:176:GLU:CD	2.24	0.58
1:E:162:PRO:O	1:E:163:LYS:HD2	2.03	0.58
1:F:159:ARG:C	1:F:160:LYS:HD2	2.24	0.58
1:E:89:GLU:HA	1:X:127:LYS:HZ1	1.69	0.57
1:X:164:LEU:HD23	1:X:164:LEU:C	2.24	0.57

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:46:ARG:HB2	2:X:4:HOH:O	2.04	0.57
1:B:41:ILE:HG13	1:B:90:GLU:OE1	2.05	0.57
1:X:93:PRO:HB3	1:Y:121:PRO:HB3	1.87	0.57
1:A:25:ILE:HG22	1:A:30:ILE:HD11	1.86	0.57
1:A:36:SER:CB	1:A:47:LEU:HD11	2.35	0.56
1:X:98:THR:HG23	1:X:127:LYS:HB3	1.87	0.56
1:E:158:VAL:HG12	1:E:163:LYS:HD3	1.87	0.56
1:F:119:ILE:H	1:F:119:ILE:CD1	2.18	0.56
1:E:93:PRO:HB3	1:F:121:PRO:HB3	1.88	0.56
1:X:107:ARG:HH11	1:X:107:ARG:HG2	1.71	0.56
1:X:26:PRO:HD2	1:X:29:VAL:HG21	1.86	0.56
1:E:37:GLN:HB3	1:E:39:HIS:CE1	2.41	0.56
1:A:106:PRO:O	1:A:109:GLN:HB3	2.05	0.56
1:F:27:ARG:O	1:F:31:GLU:HG3	2.06	0.56
1:B:164:LEU:HD23	1:B:165:LYS:N	2.21	0.56
1:B:42:ARG:CD	1:B:42:ARG:H	2.15	0.56
1:B:160:LYS:H	1:B:160:LYS:HZ3	1.54	0.55
1:F:158:VAL:O	1:F:159:ARG:HB2	2.06	0.55
1:E:139:LYS:CD	1:E:139:LYS:N	2.69	0.55
1:A:27:ARG:HG3	1:A:28:GLU:OE1	2.06	0.55
1:X:100:THR:HG22	1:X:127:LYS:CE	2.37	0.55
1:X:31:GLU:CB	1:X:35:ARG:HH12	2.20	0.55
1:B:147:HIS:HB2	1:X:145:VAL:HG13	1.90	0.54
1:E:25:ILE:HD13	1:F:157:TYR:HB2	1.88	0.54
1:F:109:GLN:HE21	1:F:169:VAL:HG13	1.72	0.54
1:F:100:THR:HG22	1:F:127:LYS:HZ1	1.68	0.54
1:Y:148:ARG:NH1	1:Y:173:GLU:OE2	2.40	0.54
1:E:90:GLU:HG3	1:F:151:LYS:HE3	1.90	0.54
1:F:107:ARG:HB2	1:F:107:ARG:NH1	2.18	0.54
1:Y:119:ILE:HD13	1:Y:119:ILE:H	1.71	0.53
1:A:28:GLU:OE1	1:A:28:GLU:N	2.40	0.53
1:X:107:ARG:NH1	1:X:107:ARG:HG2	2.23	0.53
1:A:111:ASP:OD2	1:A:114:SER:CB	2.57	0.53
1:A:52:SER:O	1:A:53:VAL:CB	2.56	0.53
1:X:27:ARG:HD2	2:X:211:HOH:O	2.08	0.53
1:X:164:LEU:HB2	1:Y:50:ILE:HD13	1.88	0.53
1:E:29:VAL:HG21	1:F:157:TYR:CZ	2.43	0.53
1:A:151:LYS:HE3	1:B:90:GLU:HB2	1.89	0.53
1:Y:157:TYR:HE1	1:Y:160:LYS:HA	1.74	0.53
1:A:160:LYS:HD2	2:A:209:HOH:O	2.08	0.53
1:B:119:ILE:N	1:B:119:ILE:CD1	2.66	0.53

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Y:164:LEU:C	1:Y:164:LEU:HD23	2.29	0.53
1:B:146:HIS:CE1	1:X:144:ARG:HE	2.26	0.53
1:E:170:ARG:HD2	1:E:170:ARG:N	2.23	0.52
1:A:44:LEU:HD13	1:B:164:LEU:HD11	1.91	0.52
1:F:113:THR:OG1	1:F:114:SER:N	2.41	0.52
1:B:158:VAL:HG13	1:B:158:VAL:O	2.09	0.52
1:A:157:TYR:O	1:B:23:ALA:N	2.43	0.52
1:X:31:GLU:HB3	1:X:35:ARG:NH1	2.22	0.52
1:B:26:PRO:C	1:B:28:GLU:N	2.61	0.52
1:B:157:TYR:CE1	1:B:162:PRO:HA	2.45	0.51
1:B:96:CYS:O	1:B:97:LYS:HB3	2.09	0.51
1:F:182:THR:O	1:F:183:SER:CB	2.59	0.51
1:A:139:LYS:N	1:A:139:LYS:HD3	2.26	0.51
1:Y:55:SER:HB3	2:Y:714:HOH:O	2.10	0.51
1:E:94:ALA:HB1	1:F:102:ILE:HD12	1.92	0.51
1:E:31:GLU:O	1:E:35:ARG:HG2	2.11	0.51
1:Y:53:VAL:HG13	1:Y:53:VAL:O	2.09	0.51
1:X:138:VAL:C	1:X:139:LYS:HD3	2.32	0.51
1:A:25:ILE:CG2	1:A:30:ILE:HD11	2.40	0.51
1:X:164:LEU:CB	1:Y:50:ILE:HD13	2.41	0.50
1:Y:138:VAL:HG11	1:Y:179:CYS:HB3	1.91	0.50
1:B:146:HIS:HE1	1:X:144:ARG:HE	1.58	0.50
1:E:89:GLU:HA	1:X:127:LYS:NZ	2.26	0.50
1:Y:119:ILE:HG12	1:Y:122:PRO:HA	1.94	0.50
1:B:107:ARG:HH12	1:B:119:ILE:HD12	1.77	0.50
1:X:46:ARG:C	1:X:48:LEU:H	2.14	0.50
1:E:98:THR:CG2	1:E:127:LYS:HB3	2.38	0.50
1:F:31:GLU:O	1:F:35:ARG:HG2	2.10	0.50
1:Y:97:LYS:HE3	1:Y:99:ARG:CZ	2.42	0.50
1:X:37:GLN:HB3	1:X:39:HIS:NE2	2.27	0.50
1:A:83:ARG:HH21	1:A:85:LYS:HA	1.76	0.49
1:X:25:ILE:HD13	1:Y:157:TYR:HB2	1.93	0.49
1:E:89:GLU:CB	1:X:127:LYS:HZ2	2.25	0.49
1:Y:38:ILE:HG12	1:Y:47:LEU:HD12	1.93	0.49
1:A:36:SER:OG	1:A:47:LEU:HD11	2.12	0.49
1:B:98:THR:HG22	1:B:98:THR:O	2.11	0.49
1:E:90:GLU:HA	1:F:151:LYS:HG3	1.94	0.49
1:X:164:LEU:HD23	1:X:164:LEU:O	2.13	0.49
1:A:127:LYS:O	1:A:128:ARG:HD3	2.12	0.49
1:A:161:LYS:HB3	1:A:162:PRO:HD2	1.93	0.49
1:E:25:ILE:HG23	1:F:157:TYR:CD2	2.47	0.49

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:153:ALA:HB1	1:F:164:LEU:HD11	1.94	0.49
1:Y:139:LYS:HD2	2:Y:211:HOH:O	2.12	0.49
1:B:159:ARG:C	1:B:161:LYS:H	2.15	0.49
1:F:138:VAL:HG11	1:F:179:CYS:HB3	1.94	0.49
1:Y:104:GLU:HG2	1:Y:123:CYS:SG	2.52	0.49
1:A:50:ILE:O	1:A:51:ASP:HB2	2.13	0.49
1:Y:43:ASP:HA	1:Y:46:ARG:NH1	2.28	0.48
1:A:29:VAL:O	1:A:33:LEU:HG	2.13	0.48
1:X:25:ILE:HG22	1:X:30:ILE:HG13	1.95	0.48
1:E:46:ARG:NH2	1:Y:87:SER:O	2.46	0.48
1:X:100:THR:HG22	1:X:127:LYS:CD	2.43	0.48
1:X:25:ILE:HD13	1:Y:157:TYR:CB	2.44	0.48
1:A:117:PHE:CD1	1:A:117:PHE:C	2.86	0.48
1:A:50:ILE:CG2	1:B:162:PRO:HB2	2.43	0.48
1:B:136:SER:HB2	2:B:672:HOH:O	2.12	0.48
1:E:158:VAL:O	1:E:159:ARG:HB2	2.13	0.48
1:Y:142:PRO:HA	1:Y:176:GLU:O	2.13	0.48
1:A:121:PRO:HB3	1:B:93:PRO:HB3	1.96	0.48
1:A:42:ARG:HA	1:A:45:GLN:OE1	2.13	0.48
1:E:100:THR:HG22	1:E:127:LYS:CD	2.41	0.48
1:Y:119:ILE:H	1:Y:119:ILE:CD1	2.27	0.48
1:B:89:GLU:HG2	1:B:90:GLU:N	2.29	0.48
1:Y:158:VAL:O	1:Y:159:ARG:HB2	2.13	0.47
1:X:127:LYS:O	1:X:128:ARG:HD3	2.14	0.47
1:E:126:VAL:HA	1:E:173:GLU:OE2	2.14	0.47
1:E:159:ARG:HG2	1:E:159:ARG:HH11	1.80	0.47
1:B:160:LYS:NZ	1:B:160:LYS:CA	2.71	0.47
1:E:25:ILE:O	1:E:26:PRO:C	2.50	0.47
1:A:25:ILE:HD11	1:B:116:ASN:C	2.35	0.47
1:E:49:GLU:O	1:E:50:ILE:C	2.53	0.47
1:A:26:PRO:HB2	1:A:29:VAL:CG2	2.41	0.47
1:B:144:ARG:HD2	1:B:176:GLU:OE2	2.14	0.47
1:F:139:LYS:HD3	1:F:139:LYS:N	2.30	0.47
1:A:83:ARG:HH21	1:A:85:LYS:CA	2.28	0.47
1:A:89:GLU:HB2	2:A:689:HOH:O	2.15	0.46
1:E:158:VAL:HG11	2:E:190:HOH:O	2.15	0.46
1:E:160:LYS:NZ	1:F:26:PRO:HG3	2.30	0.46
1:F:95:VAL:HG12	1:F:96:CYS:N	2.30	0.46
1:F:108:SER:O	1:F:112:PRO:HG3	2.14	0.46
1:X:28:GLU:HG3	1:X:29:VAL:H	1.80	0.46
1:Y:181:THR:O	1:Y:182:THR:CB	2.63	0.46

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:41:ILE:HG12	1:F:90:GLU:CD	2.36	0.46
1:X:107:ARG:NH2	1:X:117:PHE:O	2.48	0.46
1:A:100:THR:HG22	1:A:127:LYS:CE	2.45	0.46
1:A:83:ARG:HA	1:A:83:ARG:NE	2.30	0.46
1:B:25:ILE:N	1:B:25:ILE:CD1	2.79	0.46
1:Y:95:VAL:CG1	1:Y:96:CYS:N	2.79	0.46
1:B:107:ARG:HG3	1:B:107:ARG:HH11	1.81	0.45
1:F:158:VAL:HG23	1:F:158:VAL:O	2.16	0.45
1:E:159:ARG:HG2	1:E:159:ARG:NH1	2.32	0.45
1:E:87:SER:OG	1:Y:99:ARG:HG2	2.17	0.45
1:X:27:ARG:O	1:X:31:GLU:HG3	2.15	0.45
1:X:48:LEU:HA	1:X:48:LEU:HD22	1.80	0.45
1:E:158:VAL:O	1:E:158:VAL:HG13	2.15	0.45
1:E:43:ASP:O	1:E:46:ARG:HB3	2.17	0.45
1:E:111:ASP:OD2	1:E:113:THR:HB	2.17	0.45
1:F:95:VAL:CG1	1:F:96:CYS:N	2.79	0.45
1:X:157:TYR:HA	1:X:161:LYS:O	2.17	0.45
1:B:42:ARG:HG2	1:B:42:ARG:HH11	1.82	0.44
1:Y:138:VAL:CG1	1:Y:179:CYS:HB3	2.46	0.44
1:A:157:TYR:CE1	1:B:26:PRO:CD	2.99	0.44
1:B:154:LYS:O	1:B:164:LEU:HA	2.17	0.44
1:A:116:ASN:ND2	1:B:23:ALA:O	2.50	0.44
1:Y:42:ARG:HB2	1:Y:42:ARG:CZ	2.47	0.44
1:X:44:LEU:O	1:X:44:LEU:HD22	2.16	0.44
1:E:151:LYS:HA	1:E:167:VAL:O	2.18	0.44
1:F:28:GLU:OE1	1:F:28:GLU:N	2.51	0.44
1:B:107:ARG:HH12	1:B:119:ILE:CD1	2.30	0.44
1:X:110:VAL:HG21	1:X:119:ILE:CD1	2.47	0.44
1:Y:34:ALA:HB1	1:Y:138:VAL:HG21	2.00	0.44
1:Y:120:TRP:HA	1:Y:121:PRO:C	2.39	0.44
1:Y:95:VAL:HG12	1:Y:96:CYS:N	2.32	0.44
1:A:148:ARG:NH1	1:A:173:GLU:OE2	2.51	0.43
1:B:111:ASP:OD2	1:B:113:THR:HB	2.18	0.43
1:B:26:PRO:O	1:B:28:GLU:N	2.51	0.43
1:F:99:ARG:CG	1:F:99:ARG:HH11	2.26	0.43
1:B:107:ARG:NH1	1:B:119:ILE:HD12	2.32	0.43
1:B:127:LYS:O	1:B:128:ARG:HD3	2.18	0.43
1:F:33:LEU:HA	1:F:33:LEU:HD23	1.86	0.43
1:X:26:PRO:O	1:X:29:VAL:HB	2.17	0.43
1:A:159:ARG:HH11	1:A:159:ARG:HG3	1.83	0.43
1:E:157:TYR:O	1:F:23:ALA:HA	2.17	0.43

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:35:ARG:HD2	2:X:455:HOH:O	2.19	0.43
1:X:47:LEU:HD11	2:X:194:HOH:O	2.18	0.43
1:E:151:LYS:HD3	1:F:88:ILE:HG23	2.01	0.43
1:A:119:ILE:HD13	2:B:197:HOH:O	2.19	0.43
1:F:119:ILE:HG12	1:F:122:PRO:HA	2.00	0.43
1:A:86:ARG:NH1	2:A:689:HOH:O	2.51	0.43
1:E:87:SER:HB3	2:Y:200:HOH:O	2.19	0.43
1:X:41:ILE:CD1	1:Y:153:ALA:HB2	2.46	0.43
1:Y:38:ILE:HG12	1:Y:47:LEU:CD1	2.49	0.43
1:A:164:LEU:HD23	1:A:164:LEU:C	2.40	0.43
1:E:170:ARG:HB3	2:E:195:HOH:O	2.18	0.43
1:X:133:CYS:O	1:X:134:ASN:C	2.56	0.43
1:A:159:ARG:C	1:A:161:LYS:N	2.73	0.42
1:E:107:ARG:HD3	1:E:115:ALA:HA	2.00	0.42
1:E:27:ARG:H	1:E:27:ARG:HG3	1.61	0.42
1:F:158:VAL:O	1:F:159:ARG:CB	2.67	0.42
1:Y:143:SER:O	1:Y:144:ARG:HG3	2.18	0.42
1:A:100:THR:HG22	1:A:127:LYS:HZ1	1.81	0.42
1:E:23:ALA:HB1	1:F:116:ASN:ND2	2.34	0.42
1:X:170:ARG:HE	1:X:170:ARG:HB3	1.56	0.42
1:A:83:ARG:HH21	1:A:85:LYS:N	2.18	0.42
1:X:98:THR:CG2	1:X:127:LYS:HB3	2.49	0.42
1:B:159:ARG:O	1:B:161:LYS:HG2	2.19	0.42
1:B:44:LEU:HD22	1:B:48:LEU:HG	2.01	0.42
1:F:110:VAL:HG13	1:F:167:VAL:HG21	2.01	0.42
1:X:46:ARG:O	1:X:48:LEU:N	2.52	0.42
1:A:48:LEU:HD13	1:B:162:PRO:HB3	2.01	0.42
1:E:26:PRO:C	1:E:28:GLU:N	2.71	0.42
1:A:46:ARG:C	1:A:48:LEU:N	2.73	0.42
1:B:37:GLN:HA	1:B:37:GLN:HE21	1.84	0.42
1:X:88:ILE:O	1:Y:151:LYS:HE2	2.20	0.42
1:B:26:PRO:HB2	1:B:29:VAL:HG23	2.01	0.42
1:E:30:ILE:O	1:E:34:ALA:HB2	2.20	0.42
1:F:159:ARG:HG3	1:F:159:ARG:HH11	1.84	0.42
1:A:84:ARG:HD3	1:B:166:GLU:O	2.19	0.42
1:B:44:LEU:HD23	1:B:44:LEU:HA	1.80	0.41
1:E:118:LEU:HD23	1:E:119:ILE:N	2.35	0.41
1:F:167:VAL:HG12	1:F:168:GLN:N	2.35	0.41
1:A:34:ALA:C	1:A:36:SER:H	2.22	0.41
1:E:48:LEU:HA	1:E:48:LEU:HD23	1.88	0.41
1:A:119:ILE:O	1:A:119:ILE:HG12	2.20	0.41

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:50:ILE:HG13	1:A:51:ASP:N	2.35	0.41
1:E:23:ALA:O	1:F:116:ASN:HB2	2.20	0.41
1:X:120:TRP:CZ2	1:Y:38:ILE:HG22	2.55	0.41
1:E:92:VAL:O	1:F:124:VAL:HG12	2.20	0.41
1:E:46:ARG:NH2	1:Y:87:SER:C	2.74	0.41
1:A:38:ILE:HD13	1:A:47:LEU:HD12	2.01	0.41
1:F:157:TYR:OH	1:F:162:PRO:HG3	2.19	0.41
1:A:119:ILE:HA	1:A:153:ALA:O	2.20	0.41
1:X:102:ILE:HD12	1:Y:94:ALA:CB	2.50	0.41
1:X:165:LYS:NZ	2:X:386:HOH:O	2.53	0.41
1:A:118:LEU:HG	2:B:197:HOH:O	2.20	0.41
1:A:139:LYS:HB2	1:A:139:LYS:HE2	1.87	0.41
1:Y:127:LYS:O	1:Y:128:ARG:HD3	2.20	0.41
1:A:119:ILE:CD1	1:A:119:ILE:N	2.76	0.41
1:B:37:GLN:CA	1:B:37:GLN:HE21	2.33	0.41
1:E:157:TYR:HA	1:E:161:LYS:O	2.21	0.41
1:A:86:ARG:HH12	1:E:99:ARG:HA	1.84	0.41
1:F:139:LYS:N	1:F:139:LYS:CD	2.84	0.41
1:B:159:ARG:C	1:B:161:LYS:N	2.74	0.41
1:E:144:ARG:HH11	1:E:144:ARG:HG2	1.85	0.41
1:E:170:ARG:HH11	1:E:170:ARG:HG2	1.86	0.41
1:X:157:TYR:OH	1:Y:29:VAL:HG21	2.21	0.41
1:F:38:ILE:HD12	1:F:134:ASN:CG	2.41	0.41
1:A:103:TYR:HD1	2:A:17:HOH:O	2.03	0.40
1:E:41:ILE:HD12	1:F:153:ALA:HB2	2.03	0.40
1:F:127:LYS:O	1:F:128:ARG:HD3	2.20	0.40
1:E:44:LEU:HD13	1:F:164:LEU:CD1	2.52	0.40
1:X:24:GLU:OE1	1:Y:160:LYS:HA	2.20	0.40
1:X:168:GLN:HG3	1:Y:88:ILE:HD11	2.03	0.40
1:X:88:ILE:CG2	1:X:89:GLU:H	2.09	0.40
1:B:127:LYS:HE2	2:B:215:HOH:O	2.22	0.40
1:A:44:LEU:O	1:A:48:LEU:HG	2.22	0.40
1:B:41:ILE:HD11	1:B:90:GLU:HG3	2.04	0.40
1:F:159:ARG:NH1	1:F:159:ARG:HG3	2.36	0.40
1:F:42:ARG:HG2	1:F:46:ARG:NH2	2.36	0.40
1:Y:33:LEU:HD21	1:Y:48:LEU:HD21	2.03	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	123/169 (73%)	113 (92%)	7 (6%)	3 (2%)	6	6
1	B	120/169 (71%)	113 (94%)	5 (4%)	2 (2%)	9	11
1	E	118/169 (70%)	103 (87%)	13 (11%)	2 (2%)	9	11
1	F	121/169 (72%)	110 (91%)	9 (7%)	2 (2%)	9	11
1	X	117/169 (69%)	101 (86%)	12 (10%)	4 (3%)	3	3
1	Y	125/169 (74%)	110 (88%)	11 (9%)	4 (3%)	4	3
All	All	724/1014 (71%)	650 (90%)	57 (8%)	17 (2%)	6	7

All (17) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	84	ARG
1	B	160	LYS
1	Y	53	VAL
1	X	29	VAL
1	X	47	LEU
1	E	46	ARG
1	E	49	GLU
1	Y	51	ASP
1	Y	115	ALA
1	A	113	THR
1	F	160	LYS
1	X	134	ASN
1	B	27	ARG
1	F	113	THR
1	Y	110	VAL
1	A	35	ARG
1	X	25	ILE

### 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	120/156 (77%)	106 (88%)	14 (12%)	5	7
1	B	114/156 (73%)	101 (89%)	13 (11%)	5	7
1	E	113/156 (72%)	107 (95%)	6 (5%)	22	37
1	F	114/156 (73%)	102 (90%)	12 (10%)	7	9
1	X	112/156 (72%)	106 (95%)	6 (5%)	22	36
1	Y	118/156 (76%)	110 (93%)	8 (7%)	16	25
All	All	691/936 (74%)	632 (92%)	59 (8%)	10	16

All (59) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	31	GLU
1	A	44	LEU
1	A	47	LEU
1	A	48	LEU
1	A	53	VAL
1	A	86	ARG
1	A	89	GLU
1	A	98	THR
1	A	100	THR
1	A	108	SER
1	A	113	THR
1	A	119	ILE
1	A	156	GLU
1	A	170	ARG
1	B	27	ARG
1	B	28	GLU
1	B	37	GLN
1	B	42	ARG
1	B	43	ASP
1	B	44	LEU
1	B	88	ILE
1	B	98	THR

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	B	100	THR
1	B	107	ARG
1	B	114	SER
1	B	119	ILE
1	B	160	LYS
1	E	24	GLU
1	E	27	ARG
1	E	44	LEU
1	E	139	LYS
1	E	159	ARG
1	E	170	ARG
1	F	28	GLU
1	F	36	SER
1	F	44	LEU
1	F	47	LEU
1	F	98	THR
1	F	100	THR
1	F	107	ARG
1	F	119	ILE
1	F	145	VAL
1	F	156	GLU
1	F	160	LYS
1	F	170	ARG
1	X	24	GLU
1	X	44	LEU
1	X	48	LEU
1	X	118	LEU
1	X	145	VAL
1	X	170	ARG
1	Y	42	ARG
1	Y	44	LEU
1	Y	100	THR
1	Y	107	ARG
1	Y	118	LEU
1	Y	119	ILE
1	Y	139	LYS
1	Y	170	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	37	GLN

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	A	116	ASN
1	B	37	GLN
1	B	116	ASN
1	B	146	HIS
1	B	168	GLN
1	E	168	GLN
1	F	37	GLN
1	F	109	GLN
1	X	45	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

### 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

### 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

### 5.7 Other polymers [i](#)

There are no such residues in this entry.

### 5.8 Polymer linkage issues [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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	129/169 (76%)	-0.19	5 (3%) 39 38	22, 57, 122, 141	0
1	B	124/169 (73%)	-0.37	1 (0%) 86 84	20, 56, 113, 167	0
1	E	122/169 (72%)	-0.40	1 (0%) 86 84	23, 54, 109, 146	0
1	F	125/169 (73%)	-0.42	0 100 100	24, 53, 119, 136	0
1	X	121/169 (71%)	-0.43	2 (1%) 70 68	21, 50, 126, 148	0
1	Y	129/169 (76%)	-0.32	3 (2%) 60 58	22, 54, 124, 165	0
All	All	750/1014 (73%)	-0.35	12 (1%) 72 70	20, 55, 122, 167	0

All (12) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	53	VAL	5.5
1	A	52	SER	5.3
1	A	51	ASP	4.7
1	X	23	ALA	4.4
1	Y	87	SER	3.1
1	Y	158	VAL	2.9
1	B	159	ARG	2.9
1	E	27	ARG	2.6
1	A	50	ILE	2.5
1	X	37	GLN	2.2
1	Y	160	LYS	2.1
1	A	86	ARG	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 [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.