



# Full wwPDB X-ray Structure Validation Report ⓘ

May 16, 2020 – 01:03 am BST

PDB ID : 4WD5  
Title : Crystal structure of EGFR 696-1022 T790M in complex with QL-X138  
Authors : Yun, C.H.; Eck, M.J.  
Deposited on : 2014-09-07  
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](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  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.11  
buster-report : 1.1.7 (2018)  
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

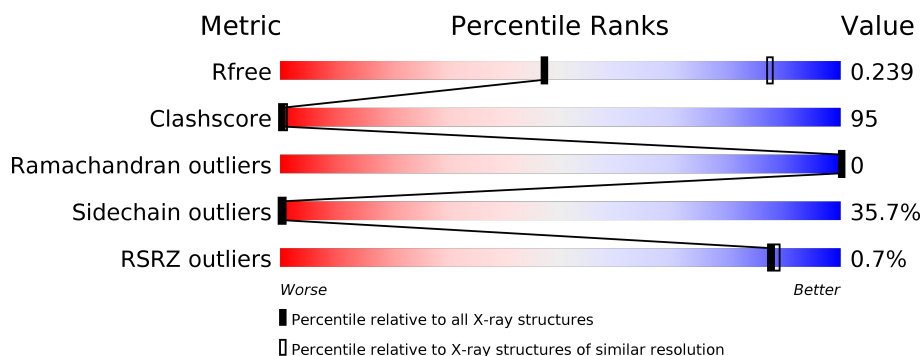
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 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))
$R_{free}$	130704	1149 (3.34-3.26)
Clashscore	141614	1205 (3.34-3.26)
Ramachandran outliers	138981	1183 (3.34-3.26)
Sidechain outliers	138945	1182 (3.34-3.26)
RSRZ outliers	127900	1115 (3.34-3.26)

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	331	<div> <div></div> <div>28%</div> <div>39%</div> <div>26%</div> <div>7%</div> </div>
1	B	331	<div> <div></div> <div>24%</div> <div>48%</div> <div>20%</div> <div>8%</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	3LH	A	1101	-	-	X	-



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.

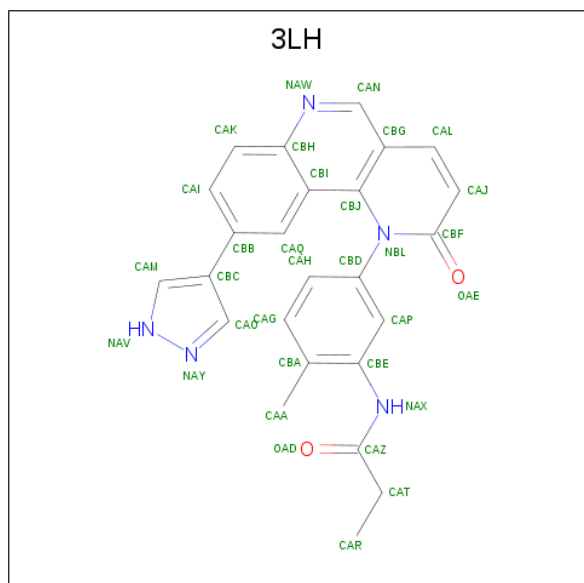
- Molecule 1 is a protein called Epidermal growth factor receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	307	Total 2384	C 1538	N 400	O 429	S 17	0	0	0
1	B	304	Total 2368	C 1521	N 407	O 422	S 18	0	0	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	692	GLY	-	expression tag	UNP P00533
A	693	SER	-	expression tag	UNP P00533
A	790	MET	THR	engineered mutation	UNP P00533
B	692	GLY	-	expression tag	UNP P00533
B	693	SER	-	expression tag	UNP P00533
B	790	MET	THR	engineered mutation	UNP P00533

- Molecule 2 is N-{2-methyl-5-[2-oxo-9-(1H-pyrazol-4-yl)benzo[h][1,6]naphthyridin-1(2H)-yl]phenyl}propanamide (three-letter code: 3LH) (formula: C<sub>25</sub>H<sub>21</sub>N<sub>5</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			32	25	5	2		

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Cl	0	0
			1	1		

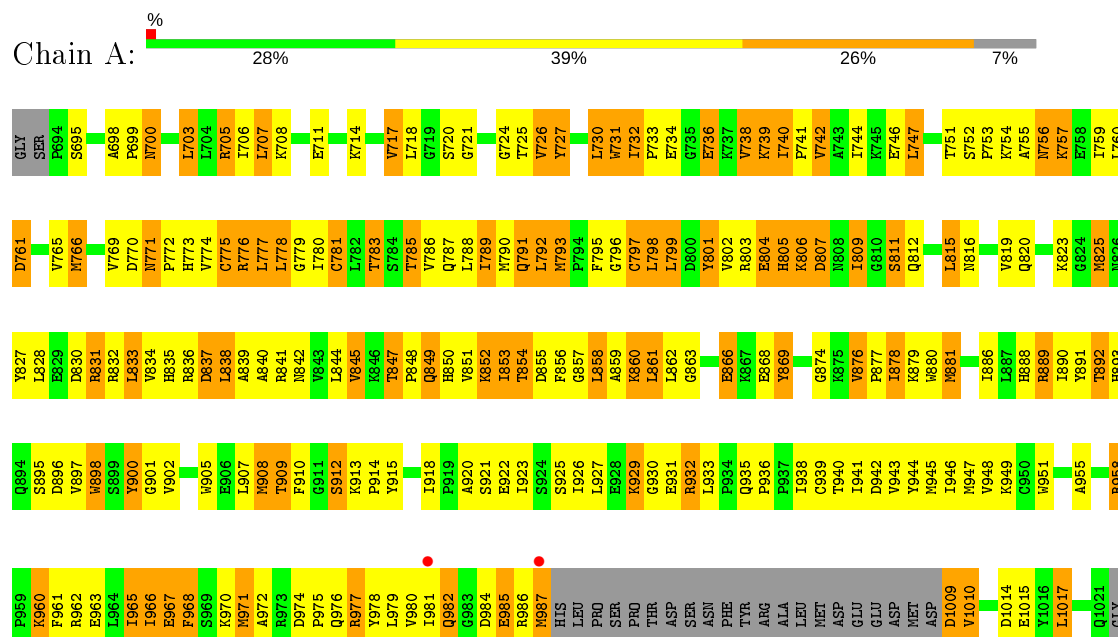
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	16	Total	O	0	0
			16	16		
4	B	6	Total	O	0	0
			6	6		

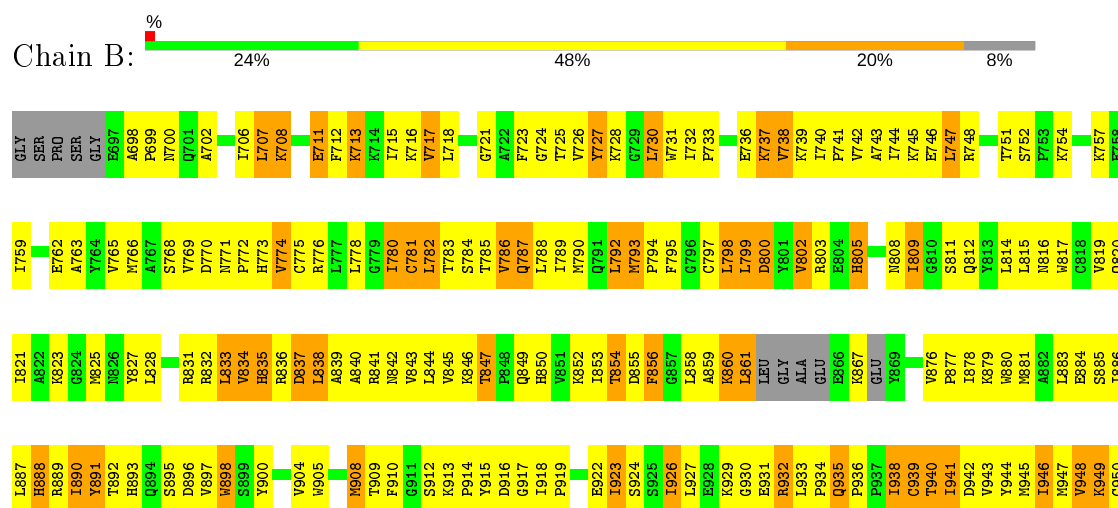
### 3 Residue-property plots

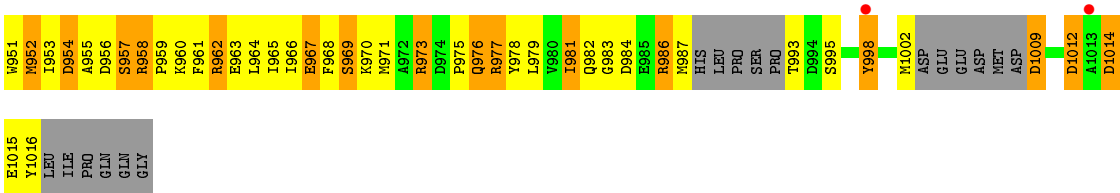
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are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

#### • Molecule 1: Epidermal growth factor receptor



#### • Molecule 1: Epidermal growth factor receptor





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	47.58Å 93.29Å 163.86Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	37.64 – 3.30 47.14 – 3.22	Depositor EDS
% Data completeness (in resolution range)	96.9 (37.64-3.30) 97.0 (47.14-3.22)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	0.97 (at 3.19Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.4_1496)	Depositor
R, $R_{free}$	0.210 , 0.239 0.222 , 0.239	Depositor DCC
$R_{free}$ test set	594 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	87.7	Xtriage
Anisotropy	0.769	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 49.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	4807	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	79.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.63% of the height of the origin peak. No significant pseudotranslation is detected.*

<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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 3LH, CL

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	0.61	0/2434	0.68	0/3297
1	B	0.61	0/2415	0.64	0/3268
All	All	0.61	0/4849	0.66	0/6565

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

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	2384	0	2388	481	0
1	B	2368	0	2370	432	0
2	A	32	0	0	15	0
3	B	1	0	0	1	0
4	A	16	0	0	0	0
4	B	6	0	0	0	0
All	All	4807	0	4758	909	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 95.

All (909) 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:B:838:LEU:HD12	1:B:839:ALA:N	1.16	1.46
1:A:936:PRO:HG2	1:A:939:CYS:SG	1.60	1.41
1:B:725:THR:HG22	1:B:727:TYR:CE1	1.52	1.41
1:A:706:ILE:C	1:A:707:LEU:HD23	1.37	1.41
1:B:706:ILE:C	1:B:707:LEU:HD23	1.37	1.41
1:A:861:LEU:HD12	1:A:862:LEU:N	1.35	1.40
1:A:792:LEU:HD12	1:A:793:MET:N	1.34	1.39
1:B:723:PHE:CE1	1:B:836:ARG:HD2	1.60	1.34
1:A:777:LEU:C	1:A:777:LEU:HD12	1.51	1.28
1:A:838:LEU:HD12	1:A:839:ALA:N	1.48	1.25
1:A:804:GLU:HG2	1:A:805:HIS:ND1	1.53	1.23
1:B:838:LEU:C	1:B:838:LEU:HD12	1.51	1.22
1:A:777:LEU:HD12	1:A:778:LEU:N	1.53	1.22
1:A:781:CYS:SG	1:A:783:THR:HG22	1.80	1.21
1:B:838:LEU:CD1	1:B:839:ALA:N	2.03	1.21
1:B:798:LEU:HD12	1:B:798:LEU:O	1.37	1.20
1:A:936:PRO:CG	1:A:939:CYS:SG	2.30	1.18
1:A:1017:LEU:HD22	1:A:1017:LEU:O	1.40	1.17
1:A:809:ILE:HG21	1:A:910:PHE:CE1	1.78	1.17
1:B:771:ASN:HB3	1:B:774:VAL:CG2	1.75	1.17
1:A:725:THR:HG22	1:A:727:TYR:CE2	1.80	1.16
1:A:936:PRO:HB2	1:A:939:CYS:SG	1.84	1.16
1:A:946:ILE:HD11	1:A:967:GLU:OE1	1.42	1.16
1:B:935:GLN:HB2	1:B:944:TYR:CD2	1.80	1.16
1:B:707:LEU:HD23	1:B:707:LEU:N	1.51	1.16
1:A:707:LEU:O	1:A:781:CYS:HB2	1.43	1.16
1:B:932:ARG:HH11	1:B:932:ARG:CG	1.60	1.15
1:A:861:LEU:CD1	1:A:862:LEU:H	1.59	1.14
1:B:932:ARG:HH11	1:B:932:ARG:HG3	1.05	1.13
1:B:782:LEU:N	1:B:782:LEU:HD12	1.56	1.13
1:B:725:THR:CG2	1:B:727:TYR:CE1	2.33	1.12
1:A:809:ILE:HG21	1:A:910:PHE:HE1	1.03	1.11
1:B:771:ASN:CB	1:B:774:VAL:HG23	1.79	1.11
1:B:747:LEU:N	1:B:747:LEU:HD12	1.60	1.11
1:A:792:LEU:C	1:A:792:LEU:HD12	1.63	1.10
1:B:847:THR:HG23	1:B:850:HIS:HB3	1.30	1.10
2:A:1101:3LH:CAQ	2:A:1101:3LH:CAH	2.29	1.10
1:A:847:THR:OG1	1:A:848:PRO:HD2	1.52	1.09
1:A:938:ILE:HG22	1:A:979:LEU:HD23	1.22	1.09
1:A:854:THR:HG23	1:A:855:ASP:N	1.62	1.09
1:A:936:PRO:CB	1:A:939:CYS:SG	2.40	1.09

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:837:ASP:OD1	1:A:842:ASN:ND2	1.86	1.08
1:B:833:LEU:HD12	1:B:833:LEU:N	1.62	1.08
1:B:842:ASN:O	1:B:854:THR:HG23	1.52	1.08
1:A:935:GLN:HA	1:A:944:TYR:CD2	1.88	1.08
1:B:772:PRO:O	1:B:852:LYS:HE3	1.53	1.08
1:A:766:MET:HG2	1:A:777:LEU:HB2	1.29	1.07
1:A:781:CYS:SG	1:A:783:THR:CG2	2.44	1.06
1:A:943:VAL:HG22	1:A:971:MET:CE	1.84	1.06
1:B:965:ILE:O	1:B:969:SER:HB2	1.56	1.05
1:A:766:MET:HG2	1:A:777:LEU:CB	1.87	1.03
1:B:707:LEU:O	1:B:781:CYS:HB2	1.56	1.03
1:A:831:ARG:HH21	1:A:831:ARG:HG3	1.22	1.02
1:A:725:THR:CG2	1:A:727:TYR:CE2	2.41	1.02
1:A:801:TYR:HE1	1:A:805:HIS:HB2	1.23	1.02
1:A:801:TYR:CE1	1:A:805:HIS:HB2	1.95	1.01
1:A:909:THR:OG1	1:A:912:SER:HB2	1.59	1.01
1:B:723:PHE:HE1	1:B:836:ARG:CD	1.73	1.01
1:B:837:ASP:OD1	1:B:842:ASN:ND2	1.93	1.01
1:B:723:PHE:HE1	1:B:836:ARG:HD2	0.86	1.01
1:A:783:THR:HG21	1:A:787:GLN:HE21	1.18	1.01
1:A:936:PRO:CG	1:A:939:CYS:HG	1.71	1.00
1:B:771:ASN:HB3	1:B:774:VAL:HG23	1.02	1.00
1:B:723:PHE:CE1	1:B:836:ARG:CD	2.44	1.00
1:A:706:ILE:C	1:A:707:LEU:CD2	2.30	1.00
1:A:707:LEU:HD23	1:A:707:LEU:N	1.55	1.00
1:B:935:GLN:HA	1:B:944:TYR:CE2	1.96	1.00
1:A:740:ILE:N	1:A:740:ILE:HD12	1.73	1.00
1:A:900:TYR:C	1:A:900:TYR:CD1	2.32	1.00
1:A:943:VAL:HG22	1:A:971:MET:HE1	1.44	1.00
1:A:777:LEU:HD11	1:A:779:GLY:H	1.27	0.99
1:B:706:ILE:C	1:B:707:LEU:CD2	2.30	0.99
1:A:806:LYS:HA	1:A:809:ILE:HB	1.43	0.99
1:A:926:ILE:O	1:A:929:LYS:HB2	1.62	0.99
1:A:938:ILE:CG2	1:A:979:LEU:HD23	1.91	0.99
1:A:747:LEU:H	1:A:747:LEU:HD12	1.28	0.99
1:A:801:TYR:HD1	1:A:801:TYR:O	1.43	0.99
1:A:777:LEU:CD1	1:A:779:GLY:H	1.75	0.98
1:A:926:ILE:HG13	1:A:927:LEU:HD12	1.43	0.98
1:B:935:GLN:CA	1:B:944:TYR:CE2	2.46	0.98
1:A:809:ILE:HG22	1:A:809:ILE:O	1.62	0.97
1:B:952:MET:HG3	1:B:957:SER:OG	1.63	0.97

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:900:TYR:HD1	1:A:900:TYR:C	1.68	0.96
1:B:725:THR:HG21	1:B:727:TYR:OH	1.65	0.96
1:A:777:LEU:CD1	1:A:777:LEU:C	2.30	0.96
1:B:798:LEU:C	1:B:798:LEU:HD12	1.80	0.96
1:B:815:LEU:O	1:B:819:VAL:HG23	1.66	0.96
1:B:936:PRO:HB2	1:B:939:CYS:HB2	1.45	0.96
1:B:831:ARG:HB2	1:B:833:LEU:HD13	1.47	0.96
1:B:940:THR:HB	1:B:978:TYR:O	1.65	0.96
1:B:782:LEU:N	1:B:782:LEU:CD1	2.30	0.95
1:A:831:ARG:HH21	1:A:831:ARG:CG	1.79	0.95
1:A:860:LYS:HD2	1:A:869:TYR:OH	1.67	0.95
1:B:790:MET:CE	1:B:854:THR:HB	1.95	0.95
1:A:775:CYS:SG	1:A:853:ILE:O	2.25	0.94
1:B:926:ILE:HG12	1:B:927:LEU:N	1.80	0.94
1:A:804:GLU:CG	1:A:805:HIS:ND1	2.30	0.94
1:A:806:LYS:O	1:A:809:ILE:HB	1.67	0.94
1:A:935:GLN:HA	1:A:944:TYR:CE2	2.03	0.93
1:A:769:VAL:O	1:A:776:ARG:HG3	1.66	0.93
1:B:747:LEU:HD12	1:B:747:LEU:H	1.32	0.93
1:A:820:GLN:OE1	1:A:851:VAL:HG22	1.69	0.93
1:A:831:ARG:NH2	1:A:831:ARG:HG3	1.79	0.93
1:B:833:LEU:CD1	1:B:833:LEU:N	2.30	0.93
1:A:740:ILE:CD1	1:A:740:ILE:N	2.30	0.93
1:A:792:LEU:CD1	1:A:793:MET:N	2.30	0.93
1:A:838:LEU:CD1	1:A:839:ALA:N	2.30	0.93
1:A:940:THR:HG23	1:A:978:TYR:O	1.69	0.93
1:B:725:THR:HB	1:B:746:GLU:O	1.69	0.93
1:B:790:MET:HE1	1:B:854:THR:HB	1.49	0.93
1:B:831:ARG:C	1:B:833:LEU:CD1	2.38	0.92
1:B:716:LYS:HG3	1:B:717:VAL:N	1.81	0.92
1:B:918:ILE:HG23	1:B:919:PRO:HD2	1.52	0.92
1:A:798:LEU:O	1:A:798:LEU:HD22	1.70	0.92
1:A:854:THR:CG2	1:A:855:ASP:N	2.31	0.92
1:A:777:LEU:HD11	1:A:779:GLY:N	1.86	0.91
1:B:799:LEU:HB2	1:B:840:ALA:HB1	1.53	0.91
1:B:931:GLU:O	1:B:932:ARG:HD2	1.67	0.91
1:A:946:ILE:CD1	1:A:967:GLU:OE1	2.19	0.91
1:A:801:TYR:HE1	1:A:805:HIS:CB	1.84	0.90
1:A:801:TYR:HD1	1:A:801:TYR:C	1.74	0.90
1:A:706:ILE:HA	1:A:780:ILE:O	1.72	0.90
1:A:804:GLU:CG	1:A:805:HIS:CE1	2.55	0.90

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:918:ILE:CG2	1:B:919:PRO:HD2	2.02	0.90
1:A:797:CYS:SG	2:A:1101:3LH:OAD	2.30	0.90
1:B:799:LEU:HB2	1:B:840:ALA:CB	2.02	0.89
1:A:845:VAL:CG1	1:A:851:VAL:HG12	2.02	0.89
1:B:959:PRO:HB2	1:B:964:LEU:HD11	1.54	0.88
1:A:806:LYS:CA	1:A:809:ILE:HB	2.02	0.88
1:B:970:LYS:O	1:B:973:ARG:HB2	1.73	0.88
1:B:935:GLN:CB	1:B:944:TYR:CD2	2.57	0.87
1:B:935:GLN:HA	1:B:944:TYR:CD2	2.10	0.87
1:B:809:ILE:O	1:B:987:MET:CE	2.23	0.87
1:B:838:LEU:CD1	1:B:839:ALA:H	1.76	0.86
1:A:860:LYS:HD2	1:A:869:TYR:CZ	2.09	0.86
1:A:815:LEU:HD13	1:A:971:MET:HB2	1.55	0.86
1:B:838:LEU:HD12	1:B:839:ALA:H	1.26	0.86
1:B:935:GLN:CA	1:B:944:TYR:HE2	1.87	0.86
1:A:725:THR:HG22	1:A:727:TYR:HE2	1.36	0.85
1:A:777:LEU:CD1	1:A:779:GLY:N	2.37	0.85
1:A:777:LEU:CD1	1:A:778:LEU:N	2.37	0.85
1:A:835:HIS:CE1	1:A:837:ASP:O	2.29	0.85
1:B:932:ARG:HH12	1:B:951:TRP:HB3	1.42	0.85
1:B:944:TYR:O	1:B:948:VAL:HG22	1.76	0.85
1:A:898:TRP:HE3	1:A:958:ARG:NH2	1.75	0.84
1:A:854:THR:HG23	1:A:855:ASP:H	1.41	0.84
1:B:835:HIS:CE1	1:B:837:ASP:O	2.30	0.84
1:B:998:TYR:HD2	1:B:998:TYR:O	1.59	0.84
1:B:832:ARG:C	1:B:833:LEU:HD12	1.98	0.84
1:B:945:MET:O	1:B:948:VAL:HG23	1.78	0.84
1:B:926:ILE:O	1:B:929:LYS:HB2	1.78	0.84
1:A:804:GLU:OE1	1:A:805:HIS:CE1	2.30	0.83
1:A:936:PRO:HD2	1:A:944:TYR:HD2	1.43	0.83
1:B:747:LEU:N	1:B:747:LEU:CD1	2.35	0.83
1:A:801:TYR:CD1	1:A:801:TYR:O	2.30	0.83
1:B:707:LEU:CD2	1:B:707:LEU:N	2.30	0.83
1:A:838:LEU:C	1:A:838:LEU:HD12	1.89	0.83
1:A:789:ILE:N	1:A:789:ILE:CD1	2.41	0.83
1:B:725:THR:HG22	1:B:727:TYR:HE1	0.98	0.83
1:A:781:CYS:O	1:A:781:CYS:SG	2.35	0.83
1:B:831:ARG:O	1:B:832:ARG:HB2	1.78	0.82
1:A:1017:LEU:C	1:A:1017:LEU:HD22	1.98	0.82
1:B:717:VAL:O	1:B:717:VAL:HG12	1.80	0.82
1:B:795:PHE:CD1	1:B:998:TYR:HD1	1.98	0.81

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:926:ILE:HA	1:B:929:LYS:HG2	1.62	0.81
1:B:725:THR:CG2	1:B:727:TYR:HE1	1.78	0.81
2:A:1101:3LH:CAG	2:A:1101:3LH:CAM	2.58	0.81
1:B:775:CYS:SG	1:B:844:LEU:HD12	2.20	0.81
1:A:898:TRP:CE3	1:A:958:ARG:NH2	2.48	0.81
1:A:809:ILE:CG2	1:A:910:PHE:HE1	1.91	0.81
1:B:718:LEU:CD1	1:B:728:LYS:HB2	2.11	0.81
1:A:806:LYS:C	1:A:809:ILE:HB	2.01	0.81
1:A:806:LYS:HA	1:A:809:ILE:CB	2.09	0.80
1:A:905:TRP:O	1:A:909:THR:CG2	2.30	0.80
1:A:938:ILE:CG2	1:A:979:LEU:CD2	2.59	0.80
1:A:825:MET:HE3	1:A:825:MET:HA	1.64	0.80
1:A:845:VAL:HG12	1:A:851:VAL:HG12	1.63	0.80
1:A:926:ILE:O	1:A:929:LYS:CB	2.30	0.80
1:A:793:MET:O	2:A:1101:3LH:CAN	2.29	0.80
1:A:900:TYR:O	1:A:900:TYR:CD1	2.34	0.80
1:B:932:ARG:CG	1:B:932:ARG:NH1	2.30	0.80
1:A:801:TYR:CE1	1:A:805:HIS:CB	2.62	0.80
1:A:809:ILE:O	1:A:809:ILE:CG2	2.30	0.80
1:B:717:VAL:O	1:B:717:VAL:CG1	2.30	0.80
1:B:935:GLN:CB	1:B:944:TYR:CE2	2.65	0.80
1:B:931:GLU:O	1:B:932:ARG:CD	2.30	0.79
1:A:909:THR:HG1	1:A:912:SER:HB2	1.41	0.79
1:A:940:THR:CG2	1:A:978:TYR:O	2.31	0.79
1:A:785:THR:O	1:A:785:THR:CG2	2.31	0.79
1:B:771:ASN:CB	1:B:774:VAL:CG2	2.50	0.79
1:B:932:ARG:HG3	1:B:932:ARG:NH1	1.87	0.79
1:B:831:ARG:O	1:B:833:LEU:CD1	2.30	0.79
1:A:807:ASP:O	1:A:987:MET:SD	2.40	0.79
1:A:861:LEU:CD1	1:A:862:LEU:N	2.30	0.79
1:A:798:LEU:O	1:A:798:LEU:CD2	2.30	0.79
1:A:905:TRP:O	1:A:909:THR:HG23	1.83	0.79
1:B:808:ASN:O	1:B:987:MET:SD	2.41	0.79
1:B:781:CYS:C	1:B:782:LEU:HD12	2.02	0.79
1:B:876:VAL:HB	1:B:877:PRO:HD2	1.65	0.79
1:B:962:ARG:O	1:B:966:ILE:HD13	1.81	0.79
1:B:995:SER:OG	1:B:998:TYR:CB	2.32	0.78
1:A:783:THR:HG21	1:A:787:GLN:NE2	1.97	0.78
1:A:968:PHE:HA	1:A:971:MET:HG3	1.65	0.78
2:A:1101:3LH:CAQ	2:A:1101:3LH:CBD	2.57	0.78
1:A:706:ILE:O	1:A:707:LEU:HD23	1.83	0.78

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:739:LYS:C	1:A:740:ILE:HD12	2.04	0.78
1:A:847:THR:CB	1:A:848:PRO:HD2	2.14	0.78
1:B:725:THR:CG2	1:B:727:TYR:CZ	2.67	0.78
1:A:730:LEU:HD23	1:A:739:LYS:HB3	1.63	0.78
1:B:935:GLN:HB2	1:B:944:TYR:CE2	2.18	0.78
1:A:847:THR:OG1	1:A:848:PRO:CD	2.30	0.77
1:A:804:GLU:HG2	1:A:805:HIS:CE1	2.17	0.77
1:B:727:TYR:N	1:B:727:TYR:CD1	2.51	0.77
1:A:858:LEU:HD23	1:A:858:LEU:N	1.99	0.77
1:B:727:TYR:HD1	1:B:727:TYR:N	1.83	0.77
1:A:731:TRP:C	1:A:731:TRP:CD1	2.54	0.77
1:B:831:ARG:O	1:B:833:LEU:HD11	1.83	0.77
1:A:799:LEU:HD11	1:A:803:ARG:NH2	1.99	0.77
1:B:793:MET:HG3	1:B:846:LYS:HA	1.67	0.77
1:A:1017:LEU:O	1:A:1017:LEU:CD2	2.30	0.76
1:B:827:TYR:O	1:B:831:ARG:HG2	1.85	0.76
1:B:940:THR:CB	1:B:978:TYR:O	2.32	0.76
1:B:795:PHE:CE1	1:B:998:TYR:CD1	2.74	0.76
1:A:980:VAL:O	1:A:980:VAL:HG12	1.85	0.76
1:B:790:MET:SD	1:B:855:ASP:OD1	2.43	0.76
1:B:847:THR:CG2	1:B:850:HIS:HB3	2.14	0.76
1:A:838:LEU:HD12	1:A:839:ALA:H	1.47	0.75
1:B:707:LEU:O	1:B:781:CYS:CB	2.34	0.75
1:B:944:TYR:O	1:B:948:VAL:CG2	2.33	0.75
1:A:801:TYR:CD1	1:A:801:TYR:C	2.49	0.75
1:A:982:GLN:CD	1:A:982:GLN:H	1.89	0.75
1:B:789:ILE:N	1:B:789:ILE:HD12	2.02	0.75
1:A:747:LEU:HD12	1:A:786:VAL:O	1.85	0.75
1:A:725:THR:CG2	1:A:727:TYR:HE2	1.89	0.75
1:A:863:GLY:O	1:A:866:GLU:HG3	1.87	0.75
1:A:966:ILE:HG12	1:A:967:GLU:N	2.01	0.75
1:B:708:LYS:HG3	1:B:711:GLU:OE1	1.87	0.75
1:B:995:SER:OG	1:B:998:TYR:HB2	1.87	0.74
1:A:740:ILE:O	1:A:742:VAL:HG13	1.87	0.74
1:A:798:LEU:C	1:A:798:LEU:CD2	2.56	0.74
1:A:773:HIS:O	1:A:852:LYS:HA	1.86	0.74
1:A:731:TRP:CD1	1:A:732:ILE:N	2.55	0.74
1:A:892:THR:O	1:A:895:SER:HB3	1.88	0.74
1:A:789:ILE:N	1:A:789:ILE:HD13	2.03	0.73
1:A:926:ILE:HA	1:A:929:LYS:HB2	1.68	0.73
1:B:742:VAL:HG21	1:B:789:ILE:CG2	2.18	0.73

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:798:LEU:C	1:A:798:LEU:HD22	2.06	0.73
1:A:773:HIS:C	1:A:852:LYS:HB3	2.08	0.73
1:B:888:HIS:N	1:B:888:HIS:ND1	2.37	0.73
1:B:945:MET:C	1:B:948:VAL:HG23	2.07	0.73
1:B:740:ILE:HG23	1:B:741:PRO:HD2	1.70	0.73
1:A:730:LEU:CD2	1:A:739:LYS:HB3	2.18	0.73
1:B:831:ARG:CB	1:B:833:LEU:HD13	2.18	0.73
1:A:792:LEU:HD12	1:A:793:MET:H	1.45	0.73
1:B:782:LEU:HD12	1:B:782:LEU:H	1.54	0.73
1:B:855:ASP:O	1:B:858:LEU:HG	1.89	0.73
1:B:831:ARG:CB	1:B:833:LEU:CD1	2.68	0.72
1:A:747:LEU:HD12	1:A:747:LEU:N	2.03	0.72
1:B:775:CYS:SG	1:B:844:LEU:CD1	2.78	0.72
1:A:878:ILE:HG21	1:A:923:ILE:HG13	1.71	0.72
1:A:717:VAL:O	1:A:717:VAL:CG2	2.37	0.72
1:B:790:MET:HE3	1:B:854:THR:HB	1.71	0.72
1:B:798:LEU:C	1:B:798:LEU:CD1	2.56	0.72
1:B:935:GLN:CA	1:B:944:TYR:CD2	2.72	0.72
1:A:936:PRO:HG2	1:A:939:CYS:HG	0.75	0.72
1:A:815:LEU:HD21	1:A:979:LEU:HD12	1.72	0.71
1:A:811:SER:CB	1:A:981:ILE:HD12	2.19	0.71
1:B:960:LYS:O	1:B:964:LEU:HD13	1.88	0.71
1:B:915:TYR:CE1	1:B:933:LEU:HD21	2.24	0.71
1:A:1014:ASP:O	1:A:1017:LEU:HB3	1.90	0.71
1:A:797:CYS:HB2	2:A:1101:3LH:OAD	1.90	0.71
1:A:838:LEU:CD1	1:A:839:ALA:H	2.01	0.71
1:A:809:ILE:CG2	1:A:910:PHE:CE1	2.67	0.71
1:B:993:THR:O	1:B:993:THR:HG22	1.88	0.71
1:A:1010:VAL:O	1:A:1010:VAL:CG2	2.38	0.71
1:A:836:ARG:HD2	1:A:860:LYS:HG3	1.71	0.71
1:A:736:GLU:HB2	1:A:738:VAL:HG13	1.72	0.71
1:B:809:ILE:O	1:B:987:MET:HE1	1.90	0.71
1:A:700:ASN:OD1	1:A:700:ASN:C	2.30	0.71
1:A:797:CYS:CB	2:A:1101:3LH:OAD	2.38	0.71
1:A:837:ASP:OD1	1:A:837:ASP:C	2.29	0.71
1:A:831:ARG:O	1:A:832:ARG:HB2	1.90	0.70
1:B:887:LEU:N	1:B:887:LEU:HD23	2.05	0.70
1:B:935:GLN:HA	1:B:944:TYR:HE2	1.45	0.70
1:B:799:LEU:CB	1:B:840:ALA:HB1	2.21	0.70
1:B:923:ILE:HA	1:B:926:ILE:HD13	1.73	0.70
1:A:698:ALA:HB1	1:A:699:PRO:HD2	1.72	0.70

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:718:LEU:HD13	2:A:1101:3LH:CBG	2.22	0.70
1:B:707:LEU:HD13	1:B:731:TRP:CZ2	2.26	0.70
1:A:804:GLU:CD	1:A:805:HIS:CE1	2.65	0.70
1:A:935:GLN:CA	1:A:944:TYR:CE2	2.74	0.70
1:B:1012:ASP:C	1:B:1012:ASP:OD1	2.30	0.70
1:A:985:GLU:OE1	1:A:985:GLU:HA	1.91	0.70
1:B:837:ASP:C	1:B:837:ASP:OD1	2.30	0.70
1:A:725:THR:HG22	1:A:727:TYR:CD2	2.27	0.70
1:A:845:VAL:HG13	1:A:851:VAL:HG12	1.72	0.70
1:B:842:ASN:O	1:B:854:THR:CG2	2.38	0.69
1:A:738:VAL:CG2	1:A:740:ILE:HD11	2.22	0.69
1:B:795:PHE:CD1	1:B:998:TYR:CD1	2.81	0.69
1:B:798:LEU:O	1:B:798:LEU:CD1	2.30	0.69
1:A:765:VAL:HG22	1:A:766:MET:N	2.08	0.69
1:B:740:ILE:CG2	1:B:741:PRO:HD2	2.23	0.69
1:B:742:VAL:HG11	1:B:778:LEU:HD12	1.75	0.69
1:B:952:MET:CG	1:B:957:SER:OG	2.38	0.69
1:A:811:SER:CA	1:A:981:ILE:HD12	2.23	0.69
1:B:718:LEU:HD13	1:B:728:LYS:HB2	1.74	0.69
1:A:771:ASN:C	1:A:771:ASN:OD1	2.30	0.69
1:B:795:PHE:CE1	1:B:998:TYR:HD1	2.09	0.69
1:A:943:VAL:HG22	1:A:971:MET:HE3	1.74	0.69
1:A:834:VAL:HG12	1:A:834:VAL:O	1.93	0.68
1:A:837:ASP:OD2	1:A:841:ARG:NH1	2.26	0.68
1:B:954:ASP:C	1:B:954:ASP:OD1	2.30	0.68
1:B:932:ARG:NH1	1:B:951:TRP:HB3	2.09	0.68
1:A:792:LEU:CD1	2:A:1101:3LH:NAW	2.57	0.68
1:A:806:LYS:HA	1:A:809:ILE:CG1	2.24	0.68
1:A:909:THR:OG1	1:A:912:SER:CB	2.40	0.68
1:B:945:MET:HA	1:B:948:VAL:CG2	2.24	0.67
1:B:831:ARG:HB2	1:B:833:LEU:CD1	2.21	0.67
1:B:897:VAL:O	1:B:900:TYR:HB3	1.94	0.67
1:B:861:LEU:HD21	1:B:867:LYS:O	1.95	0.67
1:A:771:ASN:OD1	1:A:773:HIS:N	2.26	0.67
1:A:900:TYR:CD2	1:A:961:PHE:HE1	2.12	0.67
1:B:700:ASN:OD1	1:B:702:ALA:CB	2.43	0.67
1:A:799:LEU:HD11	1:A:803:ARG:HH21	1.59	0.67
1:B:986:ARG:O	1:B:987:MET:C	2.32	0.67
1:A:836:ARG:HG3	1:A:859:ALA:HA	1.75	0.67
1:A:926:ILE:C	1:A:929:LYS:HB2	2.14	0.67
1:B:815:LEU:O	1:B:819:VAL:CG2	2.39	0.67

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1010:VAL:O	1:A:1010:VAL:HG23	1.94	0.66
1:A:769:VAL:HG21	1:A:774:VAL:HG12	1.78	0.66
1:A:836:ARG:HD3	1:A:858:LEU:O	1.95	0.66
1:A:860:LYS:CD	1:A:869:TYR:CZ	2.78	0.66
1:B:706:ILE:O	1:B:707:LEU:HD23	1.91	0.66
1:B:935:GLN:N	1:B:944:TYR:HE2	1.92	0.66
1:B:698:ALA:HB1	1:B:699:PRO:HD2	1.76	0.66
1:B:905:TRP:CZ2	1:B:934:PRO:HD2	2.31	0.66
1:A:962:ARG:O	1:A:965:ILE:HG13	1.96	0.66
1:B:959:PRO:HB2	1:B:964:LEU:CD1	2.26	0.66
1:A:905:TRP:HD1	1:A:947:MET:HE1	1.61	0.66
1:B:725:THR:HG21	1:B:727:TYR:CZ	2.29	0.66
1:A:703:LEU:O	1:A:703:LEU:HG	1.95	0.66
1:B:831:ARG:C	1:B:833:LEU:HD12	2.15	0.66
1:A:815:LEU:CD1	1:A:971:MET:HB2	2.24	0.66
1:B:952:MET:O	1:B:958:ARG:NH1	2.29	0.66
1:A:837:ASP:CG	1:A:842:ASN:ND2	2.48	0.66
1:A:943:VAL:CG2	1:A:971:MET:CE	2.67	0.66
1:B:938:ILE:HD11	1:B:979:LEU:HD13	1.78	0.66
1:A:938:ILE:HG21	1:A:979:LEU:CD2	2.25	0.65
1:A:974:ASP:C	1:A:974:ASP:OD1	2.34	0.65
1:B:808:ASN:C	1:B:987:MET:SD	2.74	0.65
1:B:723:PHE:CD1	1:B:836:ARG:NE	2.64	0.65
1:A:1009:ASP:N	1:A:1009:ASP:OD1	2.30	0.65
1:B:780:ILE:HG22	1:B:788:LEU:HD23	1.79	0.65
1:B:900:TYR:CE2	1:B:964:LEU:HD23	2.31	0.65
1:A:766:MET:CG	1:A:777:LEU:HB2	2.17	0.65
1:A:863:GLY:N	1:A:866:GLU:OE2	2.30	0.65
1:A:765:VAL:CG2	1:A:766:MET:N	2.60	0.65
1:B:931:GLU:C	1:B:932:ARG:HD3	2.17	0.65
1:A:926:ILE:O	1:A:930:GLY:N	2.30	0.65
1:B:708:LYS:HE3	1:B:711:GLU:HG3	1.77	0.65
1:B:923:ILE:N	1:B:923:ILE:CD1	2.58	0.65
1:A:721:GLY:N	1:A:724:GLY:O	2.30	0.65
1:A:825:MET:HA	1:A:825:MET:CE	2.26	0.65
1:B:885:SER:O	1:B:889:ARG:N	2.30	0.65
1:A:966:ILE:CG1	1:A:967:GLU:N	2.59	0.65
1:A:738:VAL:HG23	1:A:740:ILE:HD11	1.77	0.64
1:B:1012:ASP:OD1	1:B:1014:ASP:N	2.30	0.64
1:B:916:ASP:OD1	1:B:917:GLY:N	2.30	0.64
1:B:716:LYS:CG	1:B:717:VAL:N	2.57	0.64

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:793:MET:O	2:A:1101:3LH:NAW	2.30	0.64
1:A:926:ILE:CG1	1:A:927:LEU:HD12	2.22	0.64
1:A:777:LEU:HD12	1:A:779:GLY:N	2.11	0.64
1:A:801:TYR:CE1	1:A:805:HIS:CG	2.85	0.64
1:A:938:ILE:HG21	1:A:979:LEU:HD22	1.80	0.64
1:A:926:ILE:CA	1:A:929:LYS:HB2	2.27	0.64
1:B:967:GLU:HG2	1:B:971:MET:CE	2.28	0.64
1:A:935:GLN:HA	1:A:944:TYR:HD2	1.55	0.63
1:B:995:SER:OG	1:B:998:TYR:N	2.30	0.63
1:B:998:TYR:HD2	1:B:998:TYR:C	2.02	0.63
1:A:707:LEU:O	1:A:781:CYS:CB	2.35	0.63
1:A:982:GLN:N	1:A:982:GLN:OE1	2.30	0.63
1:A:898:TRP:CH2	1:A:927:LEU:HD23	2.33	0.63
1:A:725:THR:HG21	1:A:727:TYR:CE2	2.30	0.63
1:A:845:VAL:CG1	1:A:851:VAL:CG1	2.76	0.63
1:B:799:LEU:CB	1:B:840:ALA:CB	2.77	0.63
1:B:959:PRO:CB	1:B:964:LEU:HD11	2.28	0.63
1:A:788:LEU:C	1:A:789:ILE:HD12	2.19	0.63
1:B:984:ASP:OD1	1:B:984:ASP:C	2.36	0.63
1:A:845:VAL:HG12	1:A:851:VAL:CG1	2.29	0.63
1:A:706:ILE:O	1:A:707:LEU:CD2	2.43	0.62
1:A:777:LEU:HD13	1:A:789:ILE:O	1.99	0.62
1:A:863:GLY:H	1:A:866:GLU:CD	2.01	0.62
1:A:860:LYS:CD	1:A:869:TYR:OH	2.44	0.62
1:A:943:VAL:CG2	1:A:971:MET:HE3	2.28	0.62
1:B:743:ALA:HB3	1:B:856:PHE:HE2	1.62	0.62
1:B:888:HIS:HB2	1:B:890:ILE:CG2	2.29	0.62
1:A:760:LEU:HD22	1:B:945:MET:CE	2.29	0.62
1:A:752:SER:HB2	1:A:753:PRO:HD2	1.80	0.62
1:B:782:LEU:H	1:B:782:LEU:CD1	2.10	0.62
1:B:825:MET:HE2	1:B:961:PHE:CZ	2.33	0.62
1:A:761:ASP:N	1:A:761:ASP:OD1	2.31	0.62
1:A:847:THR:CB	1:A:848:PRO:CD	2.77	0.62
1:A:727:TYR:N	1:A:727:TYR:HD2	1.98	0.62
1:A:783:THR:CG2	1:A:787:GLN:HG3	2.30	0.62
1:A:777:LEU:HD22	1:A:788:LEU:HD22	1.82	0.62
1:A:869:TYR:C	1:A:869:TYR:CD1	2.73	0.62
1:A:985:GLU:CA	1:A:985:GLU:OE1	2.44	0.62
1:A:900:TYR:HD1	1:A:901:GLY:N	1.97	0.62
1:B:793:MET:HB3	1:B:794:PRO:HD2	1.81	0.61
1:B:795:PHE:CE1	1:B:998:TYR:CE1	2.88	0.61

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:773:HIS:O	1:A:852:LYS:CA	2.48	0.61
1:A:900:TYR:HD2	1:A:961:PHE:HE1	1.49	0.61
1:A:785:THR:O	1:A:785:THR:HG23	1.99	0.61
1:A:815:LEU:CD2	1:A:979:LEU:HD12	2.29	0.61
1:A:935:GLN:CA	1:A:944:TYR:CD2	2.76	0.61
1:B:799:LEU:HB2	1:B:840:ALA:HB3	1.80	0.61
1:B:898:TRP:HE3	1:B:958:ARG:NH1	1.99	0.61
1:B:931:GLU:C	1:B:932:ARG:CD	2.69	0.61
1:A:926:ILE:HG13	1:A:927:LEU:CD1	2.24	0.61
1:A:926:ILE:O	1:A:929:LYS:CA	2.48	0.61
1:B:932:ARG:HH12	1:B:951:TRP:CB	2.11	0.61
1:B:983:GLY:CA	1:B:986:ARG:HD2	2.31	0.61
1:A:836:ARG:NH1	1:A:891:TYR:CZ	2.67	0.61
1:A:898:TRP:CZ2	1:A:927:LEU:HD23	2.36	0.61
1:A:760:LEU:HD13	1:B:949:LYS:HG3	1.83	0.61
1:B:716:LYS:HG3	1:B:717:VAL:H	1.60	0.61
1:B:892:THR:H	1:B:895:SER:HB3	1.65	0.60
1:B:918:ILE:CG2	1:B:919:PRO:CD	2.79	0.60
1:A:771:ASN:OD1	1:A:772:PRO:N	2.34	0.60
1:A:727:TYR:N	1:A:727:TYR:CD2	2.69	0.60
1:A:874:GLY:O	1:A:876:VAL:HG13	2.01	0.60
1:A:747:LEU:CD1	1:A:747:LEU:H	2.10	0.60
1:A:836:ARG:HB2	1:A:858:LEU:HB3	1.83	0.60
1:A:898:TRP:O	1:A:902:VAL:HG23	2.01	0.60
1:B:945:MET:CA	1:B:948:VAL:HG23	2.31	0.60
1:B:967:GLU:HG2	1:B:971:MET:HE3	1.84	0.60
1:A:746:GLU:CD	1:A:785:THR:HG21	2.22	0.60
1:B:834:VAL:HG12	1:B:834:VAL:O	2.02	0.60
1:B:887:LEU:HB3	1:B:888:HIS:CE1	2.37	0.60
1:A:806:LYS:O	1:A:809:ILE:CB	2.45	0.60
1:B:723:PHE:HD1	1:B:836:ARG:HE	1.43	0.60
1:A:770:ASP:O	1:A:770:ASP:CG	2.40	0.59
1:A:788:LEU:C	1:A:789:ILE:CD1	2.71	0.59
1:B:1014:ASP:OD2	1:B:1014:ASP:N	2.34	0.59
1:B:847:THR:HG23	1:B:850:HIS:CB	2.19	0.59
1:B:888:HIS:HB2	1:B:890:ILE:HG23	1.84	0.59
1:A:769:VAL:O	1:A:776:ARG:CG	2.46	0.59
1:B:715:ILE:HG22	1:B:716:LYS:HB3	1.83	0.59
1:A:747:LEU:CD1	1:A:786:VAL:O	2.49	0.59
1:A:847:THR:OG1	1:A:849:GLN:CG	2.49	0.59
1:B:793:MET:HG3	1:B:846:LYS:CA	2.31	0.59

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:833:LEU:CD1	1:B:833:LEU:H	2.12	0.59
1:B:936:PRO:CB	1:B:939:CYS:HB2	2.28	0.59
1:A:799:LEU:HB2	1:A:840:ALA:CB	2.32	0.59
1:B:771:ASN:CG	1:B:774:VAL:HG23	2.22	0.59
1:B:998:TYR:CD2	1:B:998:TYR:C	2.74	0.59
1:A:1017:LEU:C	1:A:1017:LEU:CD2	2.69	0.59
1:A:740:ILE:CD1	1:A:740:ILE:H	2.14	0.59
1:B:762:GLU:O	1:B:766:MET:HG3	2.02	0.59
1:A:820:GLN:NE2	1:A:849:GLN:O	2.28	0.59
1:B:747:LEU:H	1:B:747:LEU:CD1	1.95	0.59
1:B:887:LEU:C	1:B:888:HIS:ND1	2.56	0.59
1:B:892:THR:O	1:B:895:SER:CB	2.51	0.59
1:A:699:PRO:HB3	1:B:977:ARG:O	2.03	0.59
1:B:926:ILE:O	1:B:929:LYS:CB	2.50	0.59
1:A:796:GLY:O	1:A:845:VAL:HG23	2.02	0.58
1:A:717:VAL:HG23	1:A:717:VAL:O	2.03	0.58
1:A:796:GLY:O	1:A:845:VAL:CG2	2.51	0.58
1:B:700:ASN:OD1	1:B:702:ALA:HB2	2.03	0.58
1:B:918:ILE:HG23	1:B:919:PRO:CD	2.30	0.58
1:A:703:LEU:HD11	1:A:705:ARG:HD3	1.86	0.58
1:A:975:PRO:CD	1:A:976:GLN:H	2.15	0.58
1:A:731:TRP:HE1	1:A:733:PRO:HA	1.68	0.58
1:B:964:LEU:HD12	1:B:964:LEU:N	2.16	0.58
1:A:892:THR:O	1:A:895:SER:N	2.36	0.58
1:B:954:ASP:OD1	1:B:956:ASP:N	2.36	0.58
1:B:983:GLY:HA2	1:B:986:ARG:HD2	1.84	0.58
1:B:780:ILE:CG2	1:B:788:LEU:HD23	2.32	0.58
1:B:836:ARG:NH2	1:B:859:ALA:HB2	2.18	0.58
1:B:715:ILE:HD11	1:B:730:LEU:HG	1.86	0.58
1:B:831:ARG:CB	1:B:833:LEU:HD11	2.34	0.58
1:B:926:ILE:O	1:B:929:LYS:N	2.37	0.58
1:A:975:PRO:HD2	1:A:976:GLN:H	1.69	0.58
1:B:876:VAL:HG23	1:B:878:ILE:CD1	2.34	0.58
1:A:738:VAL:HG23	1:A:740:ILE:CD1	2.33	0.58
1:A:799:LEU:HB2	1:A:840:ALA:HB3	1.85	0.58
1:A:888:HIS:O	1:A:890:ILE:HG13	2.03	0.58
1:B:708:LYS:CG	1:B:711:GLU:OE1	2.51	0.58
1:B:898:TRP:C	1:B:898:TRP:CD1	2.75	0.58
1:B:945:MET:HA	1:B:948:VAL:HG21	1.84	0.58
1:B:700:ASN:OD1	1:B:702:ALA:N	2.30	0.57
1:B:793:MET:CE	1:B:852:LYS:HD3	2.33	0.57

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:877:PRO:O	1:B:881:MET:HG3	2.03	0.57
1:B:887:LEU:CB	1:B:888:HIS:CE1	2.87	0.57
1:A:746:GLU:HG3	1:A:785:THR:HG23	1.85	0.57
1:A:847:THR:OG1	1:A:849:GLN:HG3	2.04	0.57
1:B:923:ILE:H	1:B:923:ILE:HD13	1.69	0.57
1:B:981:ILE:O	1:B:984:ASP:N	2.37	0.57
1:A:755:ALA:O	1:A:759:ILE:HG12	2.04	0.57
1:B:952:MET:HG3	1:B:957:SER:HG	1.70	0.57
1:A:785:THR:O	1:A:785:THR:HG22	2.03	0.57
1:A:892:THR:H	1:A:895:SER:HB3	1.69	0.57
1:B:747:LEU:O	1:B:747:LEU:HD13	2.05	0.57
1:B:797:CYS:HB2	1:B:841:ARG:O	2.04	0.57
1:B:918:ILE:HG22	1:B:919:PRO:HD2	1.82	0.57
1:B:815:LEU:HD12	1:B:975:PRO:HB3	1.86	0.57
1:A:769:VAL:HG21	1:A:774:VAL:CG1	2.34	0.57
1:A:836:ARG:CD	1:A:858:LEU:O	2.53	0.57
1:B:811:SER:HB3	1:B:981:ILE:HD11	1.87	0.57
1:A:791:GLN:HG3	1:A:792:LEU:N	2.20	0.56
1:A:804:GLU:CD	1:A:805:HIS:HE1	2.09	0.56
1:B:877:PRO:O	1:B:881:MET:CG	2.52	0.56
1:B:820:GLN:O	1:B:823:LYS:HB2	2.05	0.56
1:A:984:ASP:OD1	1:A:984:ASP:C	2.43	0.56
1:B:932:ARG:HG2	1:B:932:ARG:NH1	2.17	0.56
1:A:766:MET:HG2	1:A:777:LEU:HB3	1.79	0.56
1:B:723:PHE:CE1	1:B:836:ARG:NE	2.74	0.56
1:A:905:TRP:O	1:A:909:THR:HG22	2.05	0.56
1:B:706:ILE:CA	1:B:707:LEU:HD23	2.32	0.56
1:B:886:ILE:HG22	1:B:887:LEU:HD23	1.86	0.56
1:A:738:VAL:CG2	1:A:738:VAL:O	2.52	0.56
1:A:815:LEU:HD12	1:A:972:ALA:HA	1.87	0.56
1:B:770:ASP:O	1:B:827:TYR:OH	2.22	0.56
1:A:981:ILE:HG21	1:A:987:MET:HE3	1.88	0.56
1:A:721:GLY:CA	1:A:724:GLY:O	2.54	0.56
1:A:777:LEU:CD2	1:A:788:LEU:HD22	2.36	0.56
1:A:757:LYS:O	1:A:761:ASP:OD1	2.25	0.55
1:A:858:LEU:N	1:A:858:LEU:CD2	2.66	0.55
1:A:923:ILE:O	1:A:927:LEU:HD13	2.07	0.55
1:A:931:GLU:O	1:A:932:ARG:HD3	2.06	0.55
1:A:941:ILE:O	1:A:945:MET:HB2	2.06	0.55
1:B:887:LEU:CB	1:B:888:HIS:ND1	2.68	0.55
1:B:897:VAL:CG1	1:B:950:CYS:SG	2.95	0.55

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:967:GLU:CG	1:B:971:MET:HE3	2.36	0.55
1:A:848:PRO:HG2	1:A:849:GLN:HG2	1.89	0.55
1:A:926:ILE:CG1	1:A:927:LEU:CD1	2.84	0.55
1:B:794:PRO:CD	1:B:795:PHE:H	2.19	0.55
1:B:897:VAL:HG12	1:B:950:CYS:SG	2.47	0.55
1:B:831:ARG:O	1:B:833:LEU:HD12	2.05	0.55
1:B:879:LYS:HB2	1:B:880:TRP:CE3	2.42	0.55
1:A:806:LYS:O	1:A:809:ILE:N	2.37	0.55
1:A:905:TRP:CD1	1:A:947:MET:HE1	2.41	0.55
1:B:831:ARG:C	1:B:833:LEU:HD11	2.21	0.55
1:B:890:ILE:HG13	1:B:890:ILE:O	2.04	0.55
1:A:981:ILE:HG21	1:A:987:MET:CE	2.37	0.55
1:B:706:ILE:O	1:B:707:LEU:CD2	2.51	0.55
1:B:809:ILE:O	1:B:987:MET:HE3	2.05	0.54
1:A:955:ALA:O	1:A:958:ARG:HG3	2.07	0.54
1:B:737:LYS:O	1:B:1009:ASP:OD2	2.25	0.54
1:A:760:LEU:CD1	1:B:949:LYS:HG3	2.37	0.54
1:B:843:VAL:HG22	1:B:853:ILE:HG22	1.89	0.54
1:B:891:TYR:N	1:B:891:TYR:CD1	2.73	0.54
1:A:789:ILE:N	1:A:789:ILE:HD12	2.20	0.54
1:A:835:HIS:ND1	1:A:837:ASP:O	2.41	0.54
1:A:853:ILE:HG22	1:A:854:THR:N	2.23	0.54
1:B:713:LYS:NZ	1:B:715:ILE:HG13	2.22	0.54
1:B:716:LYS:O	1:B:728:LYS:N	2.41	0.54
1:B:831:ARG:HB3	1:B:833:LEU:HD11	1.89	0.54
1:A:781:CYS:HG	1:A:783:THR:CG2	2.20	0.54
1:A:922:GLU:O	1:A:925:SER:N	2.40	0.54
1:A:926:ILE:O	1:A:929:LYS:N	2.40	0.54
1:B:939:CYS:SG	1:B:943:VAL:CG1	2.96	0.54
1:A:792:LEU:HD11	2:A:1101:3LH:NAW	2.23	0.54
1:A:731:TRP:HD1	1:A:732:ILE:N	2.02	0.54
1:A:879:LYS:HD3	1:A:915:TYR:HB2	1.90	0.54
1:A:760:LEU:HD22	1:B:945:MET:HE3	1.89	0.53
1:A:783:THR:HG23	1:A:787:GLN:HG3	1.89	0.53
1:A:825:MET:SD	1:A:838:LEU:CD2	2.96	0.53
1:B:998:TYR:HE2	1:B:1002:MET:SD	2.30	0.53
1:A:746:GLU:OE1	1:A:785:THR:HG21	2.08	0.53
1:A:976:GLN:OE1	1:A:984:ASP:CG	2.46	0.53
1:A:860:LYS:CD	1:A:869:TYR:CE2	2.92	0.53
1:A:708:LYS:HG3	1:A:711:GLU:HB2	1.90	0.53
1:A:914:PRO:HB2	1:A:915:TYR:CD2	2.43	0.53

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:893:HIS:O	1:B:896:ASP:HB2	2.09	0.53
1:A:845:VAL:HG13	1:A:851:VAL:CG1	2.38	0.53
1:B:841:ARG:HH12	1:B:877:PRO:HB3	1.74	0.53
1:B:790:MET:HB3	1:B:856:PHE:CE2	2.43	0.53
1:B:967:GLU:CG	1:B:971:MET:CE	2.86	0.53
1:A:978:TYR:N	1:A:978:TYR:CD1	2.76	0.53
1:A:898:TRP:C	1:A:898:TRP:CD1	2.82	0.53
1:B:876:VAL:HG23	1:B:878:ILE:HD13	1.90	0.53
1:A:914:PRO:HB2	1:A:915:TYR:HD2	1.74	0.52
1:B:793:MET:CE	1:B:852:LYS:CD	2.87	0.52
1:A:860:LYS:HD3	1:A:869:TYR:CE2	2.44	0.52
1:A:825:MET:SD	1:A:838:LEU:HD23	2.49	0.52
1:B:958:ARG:HB2	1:B:959:PRO:HD2	1.90	0.52
1:A:927:LEU:N	1:A:927:LEU:HD12	2.23	0.52
1:B:773:HIS:O	1:B:852:LYS:HA	2.09	0.52
1:A:898:TRP:CZ2	1:A:927:LEU:CD2	2.92	0.52
1:A:877:PRO:O	1:A:877:PRO:HG2	2.10	0.52
1:B:847:THR:OG1	1:B:849:GLN:N	2.42	0.52
1:B:879:LYS:HB2	1:B:880:TRP:CZ3	2.44	0.52
1:A:777:LEU:HD12	1:A:778:LEU:CA	2.36	0.52
1:B:721:GLY:O	1:B:748:ARG:HD2	2.09	0.52
1:B:742:VAL:HG21	1:B:789:ILE:HG23	1.91	0.52
1:B:876:VAL:HB	1:B:877:PRO:CD	2.37	0.52
1:B:954:ASP:OD1	1:B:955:ALA:N	2.43	0.52
1:A:835:HIS:O	1:A:896:ASP:OD1	2.28	0.51
1:A:726:VAL:C	1:A:727:TYR:HD2	2.14	0.51
1:B:809:ILE:HG21	1:B:910:PHE:HE1	1.74	0.51
1:B:922:GLU:O	1:B:926:ILE:HG23	2.11	0.51
1:A:853:ILE:HG22	1:A:854:THR:H	1.74	0.51
1:A:770:ASP:OD1	1:A:770:ASP:C	2.48	0.51
1:A:927:LEU:O	1:A:930:GLY:N	2.44	0.51
1:B:740:ILE:CG2	1:B:741:PRO:CD	2.89	0.51
1:A:714:LYS:HB3	1:A:727:TYR:HD1	1.75	0.51
1:A:967:GLU:O	1:A:971:MET:HG2	2.11	0.51
1:A:738:VAL:HG22	1:A:738:VAL:O	2.11	0.50
1:B:733:PRO:HB2	1:B:736:GLU:CB	2.41	0.50
1:B:900:TYR:O	1:B:904:VAL:HG23	2.11	0.50
1:B:923:ILE:N	1:B:923:ILE:HD12	2.25	0.50
1:B:742:VAL:HB	1:B:790:MET:O	2.10	0.50
1:B:847:THR:OG1	1:B:850:HIS:N	2.44	0.50
1:B:747:LEU:HD11	1:B:785:THR:HB	1.91	0.50

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:717:VAL:O	1:A:717:VAL:HG22	2.12	0.50
1:B:945:MET:HA	1:B:948:VAL:HG23	1.92	0.50
1:B:790:MET:HB3	1:B:856:PHE:CZ	2.46	0.50
1:B:817:TRP:O	1:B:821:ILE:HG13	2.11	0.50
1:A:935:GLN:HG2	1:A:936:PRO:O	2.12	0.50
1:A:770:ASP:OD1	1:A:770:ASP:O	2.30	0.50
1:A:798:LEU:HD13	1:A:907:LEU:HD21	1.93	0.50
1:A:833:LEU:HD23	1:A:861:LEU:HD13	1.92	0.50
1:B:1012:ASP:OD1	1:B:1014:ASP:OD2	2.30	0.50
1:A:700:ASN:OD1	1:A:700:ASN:O	2.30	0.50
1:A:726:VAL:HA	1:A:744:ILE:O	2.11	0.50
1:A:769:VAL:CG2	1:A:769:VAL:O	2.60	0.50
1:B:1015:GLU:O	1:B:1016:TYR:O	2.30	0.50
1:B:945:MET:CA	1:B:948:VAL:CG2	2.89	0.50
1:A:781:CYS:SG	1:A:783:THR:HG23	2.48	0.49
1:A:837:ASP:CG	1:A:842:ASN:HD21	2.15	0.49
1:A:908:MET:HG3	1:A:939:CYS:SG	2.52	0.49
1:A:985:GLU:O	1:A:985:GLU:OE1	2.30	0.49
1:B:811:SER:HA	1:B:814:LEU:HD12	1.92	0.49
1:B:893:HIS:O	1:B:896:ASP:N	2.45	0.49
1:B:984:ASP:O	1:B:984:ASP:OD1	2.30	0.49
1:A:714:LYS:HB3	1:A:727:TYR:CD1	2.48	0.49
1:A:777:LEU:HD11	1:A:779:GLY:CA	2.42	0.49
1:B:939:CYS:SG	1:B:943:VAL:HG12	2.52	0.49
1:A:721:GLY:O	1:A:724:GLY:O	2.30	0.49
1:B:725:THR:CB	1:B:746:GLU:O	2.52	0.49
1:B:812:GLN:OE1	1:B:975:PRO:HG3	2.11	0.49
1:B:892:THR:O	1:B:895:SER:N	2.46	0.49
1:A:753:PRO:O	1:A:756:ASN:HB2	2.12	0.49
1:B:845:VAL:HG13	1:B:847:THR:O	2.12	0.49
1:B:879:LYS:HD3	1:B:914:PRO:O	2.13	0.49
1:B:897:VAL:HG21	1:B:959:PRO:O	2.12	0.49
1:A:746:GLU:HG3	1:A:785:THR:CG2	2.42	0.49
1:A:879:LYS:HB2	1:A:880:TRP:CE3	2.47	0.49
1:A:974:ASP:OD1	1:A:974:ASP:O	2.30	0.49
1:B:898:TRP:CE3	1:B:958:ARG:NH1	2.80	0.49
1:B:837:ASP:O	1:B:837:ASP:OD1	2.30	0.49
1:B:935:GLN:HA	1:B:944:TYR:HD2	1.73	0.49
1:A:761:ASP:O	1:A:765:VAL:HG13	2.12	0.49
1:A:806:LYS:HA	1:A:809:ILE:HG12	1.93	0.49
1:A:946:ILE:HA	1:A:949:LYS:HE3	1.95	0.49

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:887:LEU:HB2	1:B:888:HIS:ND1	2.27	0.49
1:A:805:HIS:C	1:A:809:ILE:HG12	2.33	0.49
1:A:769:VAL:HG23	1:A:769:VAL:O	2.13	0.49
1:A:812:GLN:O	1:A:816:ASN:OD1	2.30	0.49
1:A:981:ILE:O	1:A:984:ASP:HB2	2.13	0.49
1:B:897:VAL:O	1:B:900:TYR:N	2.46	0.49
1:A:699:PRO:CB	1:B:977:ARG:O	2.61	0.49
1:A:805:HIS:O	1:A:809:ILE:HG12	2.13	0.48
1:A:940:THR:O	1:A:941:ILE:C	2.50	0.48
1:A:984:ASP:OD1	1:A:984:ASP:O	2.30	0.48
1:B:986:ARG:O	1:B:987:MET:O	2.32	0.48
1:A:1014:ASP:O	1:A:1017:LEU:N	2.46	0.48
1:A:837:ASP:OD1	1:A:837:ASP:O	2.30	0.48
1:A:862:LEU:HD22	1:A:866:GLU:OE2	2.13	0.48
1:B:935:GLN:N	1:B:944:TYR:CE2	2.73	0.48
1:A:714:LYS:HD3	1:A:727:TYR:CD1	2.48	0.48
1:A:944:TYR:CD1	1:A:944:TYR:C	2.86	0.48
1:A:892:THR:HG23	1:A:895:SER:H	1.77	0.48
1:B:944:TYR:O	1:B:944:TYR:CD1	2.67	0.48
1:A:809:ILE:HD13	1:A:809:ILE:HA	1.65	0.48
1:B:941:ILE:HG22	1:B:942:ASP:N	2.27	0.48
1:A:966:ILE:HG12	1:A:967:GLU:H	1.74	0.48
1:B:887:LEU:HB2	1:B:888:HIS:CE1	2.49	0.48
1:B:947:MET:O	1:B:950:CYS:HB2	2.14	0.48
1:B:905:TRP:HD1	1:B:947:MET:CE	2.27	0.48
1:A:781:CYS:HG	1:A:783:THR:HG23	1.79	0.48
1:B:926:ILE:O	1:B:930:GLY:N	2.46	0.48
1:A:975:PRO:CD	1:A:976:GLN:N	2.77	0.47
1:B:765:VAL:O	1:B:769:VAL:HG23	2.14	0.47
1:B:939:CYS:SG	1:B:943:VAL:HG11	2.54	0.47
1:A:765:VAL:O	1:A:769:VAL:HG13	2.14	0.47
1:B:738:VAL:CG2	1:B:739:LYS:N	2.76	0.47
1:B:706:ILE:HA	1:B:780:ILE:O	2.14	0.47
1:B:914:PRO:O	1:B:915:TYR:C	2.51	0.47
1:A:889:ARG:HG3	1:A:889:ARG:NH1	2.29	0.47
1:B:831:ARG:O	1:B:832:ARG:CB	2.51	0.47
1:B:941:ILE:CG2	1:B:942:ASP:N	2.75	0.47
1:B:964:LEU:N	1:B:964:LEU:CD1	2.77	0.47
1:A:948:VAL:HG12	1:A:949:LYS:N	2.28	0.47
1:A:806:LYS:C	1:A:809:ILE:H	2.15	0.47
1:B:718:LEU:HD11	1:B:728:LYS:HB2	1.93	0.47

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:943:VAL:HG12	1:B:944:TYR:N	2.30	0.47
1:B:965:ILE:O	1:B:969:SER:CB	2.46	0.47
1:A:783:THR:HG21	1:A:787:GLN:HG3	1.96	0.47
1:A:832:ARG:O	1:A:861:LEU:CD1	2.63	0.47
1:A:798:LEU:HD23	1:A:798:LEU:O	2.13	0.47
1:A:940:THR:HG21	1:A:978:TYR:HA	1.97	0.47
1:B:919:PRO:O	1:B:923:ILE:HD13	2.15	0.47
1:A:792:LEU:HD11	2:A:1101:3LH:CAN	2.44	0.47
1:A:730:LEU:CD2	1:A:739:LYS:CB	2.93	0.47
1:A:861:LEU:HD12	1:A:862:LEU:H	0.63	0.47
1:A:961:PHE:O	1:A:962:ARG:C	2.52	0.47
1:B:973:ARG:HA	1:B:973:ARG:HD2	1.33	0.47
1:A:706:ILE:CA	1:A:707:LEU:HD23	2.35	0.47
1:A:836:ARG:HB2	1:A:858:LEU:CB	2.44	0.47
1:A:746:GLU:OE1	1:A:785:THR:CG2	2.63	0.47
1:A:760:LEU:HD22	1:B:945:MET:HE2	1.96	0.47
1:B:837:ASP:CG	1:B:842:ASN:ND2	2.66	0.47
1:A:802:VAL:HG23	1:A:803:ARG:N	2.30	0.46
1:A:900:TYR:CD2	1:A:961:PHE:CE1	3.00	0.46
1:A:977:ARG:HG2	1:A:978:TYR:CE1	2.50	0.46
1:B:770:ASP:O	1:B:827:TYR:CZ	2.69	0.46
1:A:747:LEU:HD13	1:A:786:VAL:HB	1.96	0.46
1:A:932:ARG:HG3	1:A:951:TRP:CE3	2.50	0.46
1:B:717:VAL:HA	1:B:727:TYR:HA	1.98	0.46
1:B:879:LYS:CD	1:B:914:PRO:O	2.63	0.46
1:B:892:THR:H	1:B:895:SER:CB	2.29	0.46
1:B:944:TYR:C	1:B:944:TYR:CD1	2.87	0.46
1:A:777:LEU:HD11	1:A:779:GLY:O	2.15	0.46
1:B:725:THR:O	1:B:745:LYS:HA	2.16	0.46
1:B:892:THR:O	1:B:895:SER:OG	2.30	0.46
1:B:923:ILE:CD1	1:B:923:ILE:H	2.23	0.46
1:A:841:ARG:HG2	1:A:842:ASN:N	2.30	0.46
1:B:995:SER:OG	1:B:998:TYR:HB3	2.15	0.46
1:A:740:ILE:H	1:A:740:ILE:HD13	1.81	0.46
1:B:892:THR:HG23	1:B:895:SER:H	1.80	0.46
1:B:732:ILE:HD12	1:B:732:ILE:N	2.31	0.46
1:A:773:HIS:O	1:A:852:LYS:HB3	2.15	0.46
1:B:893:HIS:HA	1:B:896:ASP:HB2	1.97	0.46
1:A:815:LEU:CD2	1:A:979:LEU:CD1	2.94	0.46
1:B:794:PRO:HD2	1:B:795:PHE:H	1.80	0.46
1:B:895:SER:OG	1:B:896:ASP:N	2.49	0.46

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:714:LYS:CB	1:A:727:TYR:HD1	2.29	0.45
1:A:753:PRO:O	1:A:756:ASN:N	2.49	0.45
1:A:862:LEU:HA	1:A:866:GLU:OE2	2.16	0.45
1:B:747:LEU:O	1:B:747:LEU:CD1	2.63	0.45
1:B:821:ILE:HG23	1:B:853:ILE:CG2	2.46	0.45
1:B:916:ASP:C	1:B:916:ASP:OD1	2.55	0.45
1:A:741:PRO:C	1:A:742:VAL:CG1	2.84	0.45
1:B:908:MET:HB3	1:B:936:PRO:HG2	1.99	0.45
1:A:823:LYS:HG3	1:A:965:ILE:HG21	1.99	0.45
1:A:898:TRP:HZ2	1:A:927:LEU:HD21	1.81	0.45
1:A:897:VAL:HG22	1:A:961:PHE:CE2	2.51	0.45
1:A:798:LEU:HD23	1:A:798:LEU:HA	1.69	0.45
1:A:831:ARG:HA	1:A:831:ARG:HD2	1.38	0.45
1:A:898:TRP:HZ2	1:A:927:LEU:CD2	2.28	0.45
1:B:780:ILE:HA	1:B:789:ILE:CD1	2.46	0.45
1:B:981:ILE:O	1:B:984:ASP:CB	2.65	0.45
1:A:936:PRO:HD2	1:A:944:TYR:CD2	2.35	0.45
1:A:825:MET:O	1:A:828:LEU:HB2	2.17	0.45
1:A:941:ILE:HG12	1:A:945:MET:CE	2.46	0.45
1:B:740:ILE:HG22	1:B:741:PRO:N	2.32	0.45
1:B:793:MET:HE1	1:B:852:LYS:HD3	1.98	0.44
1:A:927:LEU:CD1	1:A:927:LEU:N	2.80	0.44
1:A:944:TYR:CD1	1:A:944:TYR:O	2.70	0.44
1:B:742:VAL:CG1	1:B:778:LEU:HD12	2.47	0.44
1:B:877:PRO:O	1:B:881:MET:HG2	2.17	0.44
1:A:801:TYR:CD1	1:A:805:HIS:HB2	2.46	0.44
1:A:933:LEU:HB2	1:A:951:TRP:CH2	2.53	0.44
1:B:724:GLY:HA3	1:B:745:LYS:HE3	1.99	0.44
1:B:832:ARG:N	1:B:833:LEU:HD12	2.33	0.44
1:B:900:TYR:CD2	1:B:964:LEU:HD23	2.53	0.44
1:B:1015:GLU:C	1:B:1016:TYR:O	2.52	0.44
1:B:712:PHE:CD1	1:B:712:PHE:O	2.70	0.44
1:B:860:LYS:HG3	1:B:861:LEU:H	1.82	0.44
1:B:958:ARG:HB2	1:B:959:PRO:CD	2.48	0.44
1:B:960:LYS:O	1:B:964:LEU:CD1	2.62	0.44
1:B:897:VAL:HG11	1:B:959:PRO:HD2	1.99	0.44
1:B:898:TRP:HD1	1:B:898:TRP:C	2.20	0.44
1:B:981:ILE:O	1:B:984:ASP:HB2	2.17	0.44
1:A:730:LEU:HD23	1:A:739:LYS:CB	2.42	0.44
1:A:838:LEU:O	1:A:880:TRP:CD1	2.70	0.44
1:B:1015:GLU:O	1:B:1016:TYR:C	2.54	0.44

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:885:SER:O	1:B:889:ARG:HA	2.17	0.44
1:A:815:LEU:O	1:A:819:VAL:HG23	2.18	0.44
1:B:771:ASN:CB	1:B:774:VAL:HG21	2.42	0.44
1:B:838:LEU:HD13	1:B:839:ALA:H	1.75	0.44
1:B:880:TRP:HE3	1:B:880:TRP:H	1.64	0.44
1:B:914:PRO:HB2	1:B:915:TYR:HD1	1.83	0.44
1:A:756:ASN:HA	1:A:756:ASN:HD22	1.55	0.44
1:A:941:ILE:O	1:A:945:MET:CB	2.66	0.44
1:A:975:PRO:CG	1:A:976:GLN:N	2.81	0.44
1:A:974:ASP:O	1:A:978:TYR:HD1	2.00	0.44
1:A:732:ILE:HG22	1:A:733:PRO:HD2	2.00	0.43
1:A:760:LEU:HD13	1:B:949:LYS:CG	2.47	0.43
1:B:805:HIS:ND1	1:B:805:HIS:N	2.66	0.43
1:B:815:LEU:HD12	1:B:975:PRO:CB	2.47	0.43
1:B:832:ARG:O	1:B:861:LEU:HB2	2.18	0.43
1:A:742:VAL:HG21	1:A:789:ILE:HG23	2.00	0.43
1:B:885:SER:HA	1:B:890:ILE:H	1.83	0.43
1:A:757:LYS:HE3	1:A:761:ASP:OD2	2.18	0.43
1:A:848:PRO:CD	1:A:849:GLN:H	2.32	0.43
1:B:883:LEU:HA	1:B:883:LEU:HD12	1.75	0.43
1:B:726:VAL:C	1:B:727:TYR:CD1	2.91	0.43
1:B:976:GLN:HB2	1:B:976:GLN:HE21	1.68	0.43
1:B:771:ASN:ND2	1:B:827:TYR:CD1	2.73	0.43
1:B:958:ARG:CB	1:B:959:PRO:CD	2.96	0.43
1:A:847:THR:OG1	1:A:849:GLN:HG2	2.18	0.43
1:A:893:HIS:O	1:A:896:ASP:HB2	2.19	0.43
1:A:941:ILE:HG12	1:A:945:MET:HE2	2.01	0.43
1:B:708:LYS:CE	1:B:711:GLU:HG3	2.47	0.43
1:B:751:THR:OG1	1:B:784:SER:O	2.34	0.43
1:B:981:ILE:HG13	1:B:984:ASP:HB2	2.01	0.43
1:A:1014:ASP:O	1:A:1017:LEU:CB	2.64	0.43
1:A:726:VAL:HG11	2:A:1101:3LH:CAG	2.48	0.43
1:A:898:TRP:CZ3	1:A:958:ARG:NH2	2.87	0.43
1:A:812:GLN:OE1	1:A:816:ASN:OD1	2.37	0.43
1:B:982:GLN:CG	1:B:982:GLN:O	2.66	0.43
1:B:763:ALA:HB2	1:B:788:LEU:HD21	2.00	0.43
2:A:1101:3LH:CAP	2:A:1101:3LH:OAE	2.61	0.43
1:B:885:SER:O	1:B:889:ARG:CA	2.66	0.43
1:B:955:ALA:O	1:B:958:ARG:HG3	2.19	0.43
1:B:815:LEU:CD1	1:B:975:PRO:HA	2.49	0.43
1:B:744:ILE:HA	1:B:788:LEU:O	2.19	0.42

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:705:ARG:H	1:A:705:ARG:HG2	1.42	0.42
1:A:974:ASP:O	1:A:978:TYR:CD1	2.72	0.42
1:A:878:ILE:HA	1:A:878:ILE:HD12	1.73	0.42
1:A:960:LYS:O	1:A:963:GLU:HB2	2.20	0.42
2:A:1101:3LH:CBA	2:A:1101:3LH:CAM	2.98	0.42
1:B:713:LYS:HZ1	1:B:715:ILE:HG13	1.83	0.42
1:A:732:ILE:HG23	1:A:738:VAL:O	2.20	0.42
1:A:804:GLU:OE1	1:A:805:HIS:HE1	1.94	0.42
1:A:927:LEU:C	1:A:930:GLY:H	2.23	0.42
1:A:811:SER:HA	1:A:981:ILE:HD12	2.00	0.42
1:B:742:VAL:CG2	1:B:789:ILE:HG23	2.49	0.42
1:B:794:PRO:CD	1:B:795:PHE:N	2.83	0.42
1:B:909:THR:O	1:B:910:PHE:HB2	2.19	0.42
1:B:977:ARG:HG2	1:B:978:TYR:CE1	2.54	0.42
1:B:977:ARG:HG2	1:B:978:TYR:CD1	2.54	0.42
1:A:881:MET:HE3	1:A:881:MET:HB3	1.85	0.42
1:B:880:TRP:CE3	1:B:880:TRP:N	2.87	0.42
1:B:914:PRO:C	1:B:915:TYR:CD1	2.93	0.42
1:A:926:ILE:CG1	1:A:927:LEU:N	2.82	0.42
1:B:834:VAL:N	1:B:859:ALA:O	2.44	0.42
1:B:890:ILE:C	1:B:891:TYR:CD1	2.93	0.42
1:A:878:ILE:HG12	1:A:920:ALA:HB1	2.02	0.42
1:A:889:ARG:HH11	1:A:889:ARG:HA	1.84	0.42
1:B:794:PRO:CG	1:B:795:PHE:H	2.33	0.42
1:A:801:TYR:CE1	1:A:805:HIS:CD2	3.07	0.42
1:B:828:LEU:HD13	1:B:858:LEU:HD21	2.02	0.42
1:B:841:ARG:HG3	1:B:842:ASN:OD1	2.19	0.42
1:B:860:LYS:HG3	1:B:861:LEU:N	2.35	0.42
1:B:889:ARG:HG2	1:B:889:ARG:NH2	2.35	0.42
1:B:905:TRP:HD1	1:B:947:MET:HE1	1.85	0.42
1:A:825:MET:HB3	1:A:825:MET:HE2	1.78	0.41
1:A:847:THR:O	1:A:850:HIS:O	2.38	0.41
1:A:888:HIS:O	1:A:889:ARG:C	2.57	0.41
1:B:786:VAL:HG13	1:B:787:GLN:N	2.35	0.41
1:B:946:ILE:H	1:B:946:ILE:HG12	1.48	0.41
1:A:731:TRP:HE1	1:A:733:PRO:CA	2.30	0.41
1:A:827:TYR:C	1:A:827:TYR:CD1	2.94	0.41
1:B:711:GLU:HG2	1:B:732:ILE:O	2.20	0.41
1:B:832:ARG:CA	1:B:833:LEU:HD12	2.49	0.41
1:B:926:ILE:O	1:B:929:LYS:CA	2.68	0.41
1:B:946:ILE:HA	1:B:949:LYS:HD3	2.02	0.41

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:962:ARG:HG2	1:B:963:GLU:N	2.35	0.41
1:A:752:SER:CB	1:A:753:PRO:HD2	2.50	0.41
1:B:964:LEU:O	1:B:968:PHE:HD2	2.04	0.41
1:A:753:PRO:HA	1:A:756:ASN:HB2	2.03	0.41
1:A:935:GLN:N	1:A:944:TYR:CE2	2.88	0.41
1:B:877:PRO:HA	3:B:1101:CL:CL	2.58	0.41
1:B:707:LEU:HD13	1:B:731:TRP:CE2	2.54	0.41
1:A:773:HIS:O	1:A:853:ILE:N	2.49	0.41
1:A:878:ILE:HG21	1:A:923:ILE:CG1	2.47	0.41
1:A:908:MET:HB3	1:A:936:PRO:HB3	2.03	0.41
1:B:795:PHE:HD1	1:B:998:TYR:HD1	1.60	0.41
1:A:777:LEU:HD11	1:A:779:GLY:C	2.41	0.41
1:A:877:PRO:O	1:A:877:PRO:CG	2.68	0.41
1:A:940:THR:C	1:A:942:ASP:N	2.73	0.41
1:A:811:SER:HB3	1:A:984:ASP:OD2	2.21	0.41
1:A:881:MET:HE2	1:A:886:ILE:HG12	2.03	0.41
1:B:905:TRP:HB2	1:B:947:MET:HE3	2.03	0.41
1:A:771:ASN:CG	1:A:772:PRO:HD2	2.41	0.41
1:B:792:LEU:HD12	1:B:792:LEU:HA	1.84	0.41
1:B:931:GLU:C	1:B:932:ARG:HD2	2.35	0.41
1:B:981:ILE:CB	1:B:984:ASP:HB2	2.51	0.41
1:A:1014:ASP:CG	1:A:1015:GLU:N	2.74	0.41
1:B:789:ILE:N	1:B:789:ILE:CD1	2.73	0.41
1:B:934:PRO:O	1:B:935:GLN:C	2.56	0.41
1:B:959:PRO:CG	1:B:964:LEU:HD11	2.51	0.41
1:A:825:MET:CE	1:A:825:MET:CA	2.89	0.40
1:A:856:PHE:O	1:A:857:GLY:C	2.57	0.40
1:A:891:TYR:CD1	1:A:891:TYR:N	2.89	0.40
1:B:793:MET:HE2	1:B:852:LYS:CD	2.51	0.40
1:B:861:LEU:HA	1:B:861:LEU:HD23	1.58	0.40
1:A:759:ILE:H	1:A:759:ILE:HG12	1.69	0.40
1:A:914:PRO:O	1:A:915:TYR:C	2.59	0.40
1:A:940:THR:OG1	1:A:978:TYR:O	2.28	0.40
1:A:811:SER:HA	1:A:981:ILE:CD1	2.52	0.40
1:B:905:TRP:CD1	1:B:947:MET:HE1	2.57	0.40
1:B:998:TYR:CD2	1:B:998:TYR:O	2.51	0.40
1:A:706:ILE:HD13	1:B:932:ARG:HB2	2.04	0.40
1:A:733:PRO:HG2	1:A:736:GLU:HG3	2.03	0.40
1:A:838:LEU:HA	1:A:838:LEU:HD13	1.77	0.40
1:A:850:HIS:HE2	1:A:852:LYS:HE2	1.86	0.40
1:B:794:PRO:CG	1:B:795:PHE:N	2.84	0.40

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:799:LEU:HG	1:B:800:ASP:N	2.31	0.40
1:B:802:VAL:HG12	1:B:803:ARG:N	2.35	0.40
1:A:799:LEU:O	1:A:803:ARG:HG3	2.22	0.40
1:A:805:HIS:O	1:A:809:ILE:N	2.54	0.40
1:A:795:PHE:CD2	1:A:847:THR:HA	2.57	0.40
1:B:742:VAL:CG2	1:B:789:ILE:CG2	2.94	0.40
1:B:933:LEU:HD12	1:B:951:TRP:CZ2	2.57	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	303/331 (92%)	298 (98%)	5 (2%)	0	100	100
1	B	294/331 (89%)	289 (98%)	5 (2%)	0	100	100
All	All	597/662 (90%)	587 (98%)	10 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	249/290 (86%)	150 (60%)	99 (40%)	0	0

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	250/290 (86%)	171 (68%)	79 (32%)	0	1
All	All	499/580 (86%)	321 (64%)	178 (36%)	0	0

All (178) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	695	SER
1	A	700	ASN
1	A	703	LEU
1	A	705	ARG
1	A	707	LEU
1	A	717	VAL
1	A	720	SER
1	A	726	VAL
1	A	727	TYR
1	A	730	LEU
1	A	731	TRP
1	A	732	ILE
1	A	734	GLU
1	A	736	GLU
1	A	738	VAL
1	A	739	LYS
1	A	740	ILE
1	A	742	VAL
1	A	747	LEU
1	A	751	THR
1	A	754	LYS
1	A	756	ASN
1	A	757	LYS
1	A	761	ASP
1	A	766	MET
1	A	771	ASN
1	A	775	CYS
1	A	776	ARG
1	A	777	LEU
1	A	778	LEU
1	A	781	CYS
1	A	783	THR
1	A	785	THR
1	A	789	ILE
1	A	790	MET
1	A	791	GLN

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	A	792	LEU
1	A	793	MET
1	A	797	CYS
1	A	798	LEU
1	A	799	LEU
1	A	801	TYR
1	A	804	GLU
1	A	805	HIS
1	A	806	LYS
1	A	807	ASP
1	A	809	ILE
1	A	811	SER
1	A	815	LEU
1	A	825	MET
1	A	830	ASP
1	A	831	ARG
1	A	833	LEU
1	A	837	ASP
1	A	838	LEU
1	A	844	LEU
1	A	845	VAL
1	A	847	THR
1	A	849	GLN
1	A	852	LYS
1	A	853	ILE
1	A	854	THR
1	A	858	LEU
1	A	860	LYS
1	A	861	LEU
1	A	866	GLU
1	A	868	GLU
1	A	869	TYR
1	A	876	VAL
1	A	878	ILE
1	A	881	MET
1	A	889	ARG
1	A	892	THR
1	A	898	TRP
1	A	900	TYR
1	A	908	MET
1	A	909	THR
1	A	912	SER

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	A	913	LYS
1	A	918	ILE
1	A	921	SER
1	A	929	LYS
1	A	932	ARG
1	A	958	ARG
1	A	960	LYS
1	A	965	ILE
1	A	966	ILE
1	A	967	GLU
1	A	968	PHE
1	A	970	LYS
1	A	971	MET
1	A	977	ARG
1	A	982	GLN
1	A	985	GLU
1	A	986	ARG
1	A	987	MET
1	A	1009	ASP
1	A	1010	VAL
1	A	1017	LEU
1	B	707	LEU
1	B	708	LYS
1	B	711	GLU
1	B	713	LYS
1	B	717	VAL
1	B	727	TYR
1	B	730	LEU
1	B	737	LYS
1	B	738	VAL
1	B	747	LEU
1	B	752	SER
1	B	754	LYS
1	B	757	LYS
1	B	759	ILE
1	B	768	SER
1	B	774	VAL
1	B	776	ARG
1	B	780	ILE
1	B	781	CYS
1	B	782	LEU
1	B	783	THR

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	B	786	VAL
1	B	787	GLN
1	B	792	LEU
1	B	793	MET
1	B	798	LEU
1	B	799	LEU
1	B	800	ASP
1	B	802	VAL
1	B	805	HIS
1	B	809	ILE
1	B	816	ASN
1	B	833	LEU
1	B	834	VAL
1	B	835	HIS
1	B	837	ASP
1	B	838	LEU
1	B	847	THR
1	B	854	THR
1	B	856	PHE
1	B	860	LYS
1	B	861	LEU
1	B	884	GLU
1	B	888	HIS
1	B	890	ILE
1	B	891	TYR
1	B	898	TRP
1	B	908	MET
1	B	912	SER
1	B	913	LYS
1	B	923	ILE
1	B	924	SER
1	B	926	ILE
1	B	932	ARG
1	B	935	GLN
1	B	938	ILE
1	B	939	CYS
1	B	940	THR
1	B	941	ILE
1	B	946	ILE
1	B	948	VAL
1	B	949	LYS
1	B	952	MET

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	B	953	ILE
1	B	954	ASP
1	B	957	SER
1	B	958	ARG
1	B	962	ARG
1	B	967	GLU
1	B	969	SER
1	B	973	ARG
1	B	976	GLN
1	B	977	ARG
1	B	981	ILE
1	B	986	ARG
1	B	998	TYR
1	B	1009	ASP
1	B	1012	ASP
1	B	1014	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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 ⓘ

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
2	3LH	A	1101	1	33,36,36	3.35	10 (30%)	43,52,52	1.64	7 (16%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	3LH	A	1101	1	-	4/14/14/14	0/5/5/5

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1101	3LH	NAY-NAV	-9.27	1.19	1.37
2	A	1101	3LH	CBD-NBL	-9.21	1.33	1.45
2	A	1101	3LH	CBC-CBB	-6.99	1.31	1.49
2	A	1101	3LH	CAN-NAW	6.75	1.38	1.30
2	A	1101	3LH	CAA-CBA	-6.07	1.38	1.51
2	A	1101	3LH	CBE-NAX	-5.12	1.32	1.41
2	A	1101	3LH	CBH-NAW	-2.66	1.32	1.37
2	A	1101	3LH	CBJ-NBL	-2.32	1.34	1.38
2	A	1101	3LH	CBF-NBL	-2.24	1.33	1.37
2	A	1101	3LH	CAK-CBH	-2.17	1.38	1.41

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1101	3LH	CBD-NBL-CBJ	3.71	122.96	118.76
2	A	1101	3LH	CBG-CAN-NAW	-3.26	120.62	125.05
2	A	1101	3LH	CBA-CBE-NAX	-3.09	113.99	118.81
2	A	1101	3LH	CAG-CBA-CBE	2.93	120.20	117.44
2	A	1101	3LH	CBF-NBL-CBD	-2.47	116.10	118.69
2	A	1101	3LH	CAH-CAG-CBA	-2.42	118.29	121.97
2	A	1101	3LH	CAL-CBG-CAN	-2.12	118.84	122.63

There are no chirality outliers.

All (4) torsion outliers are listed below:

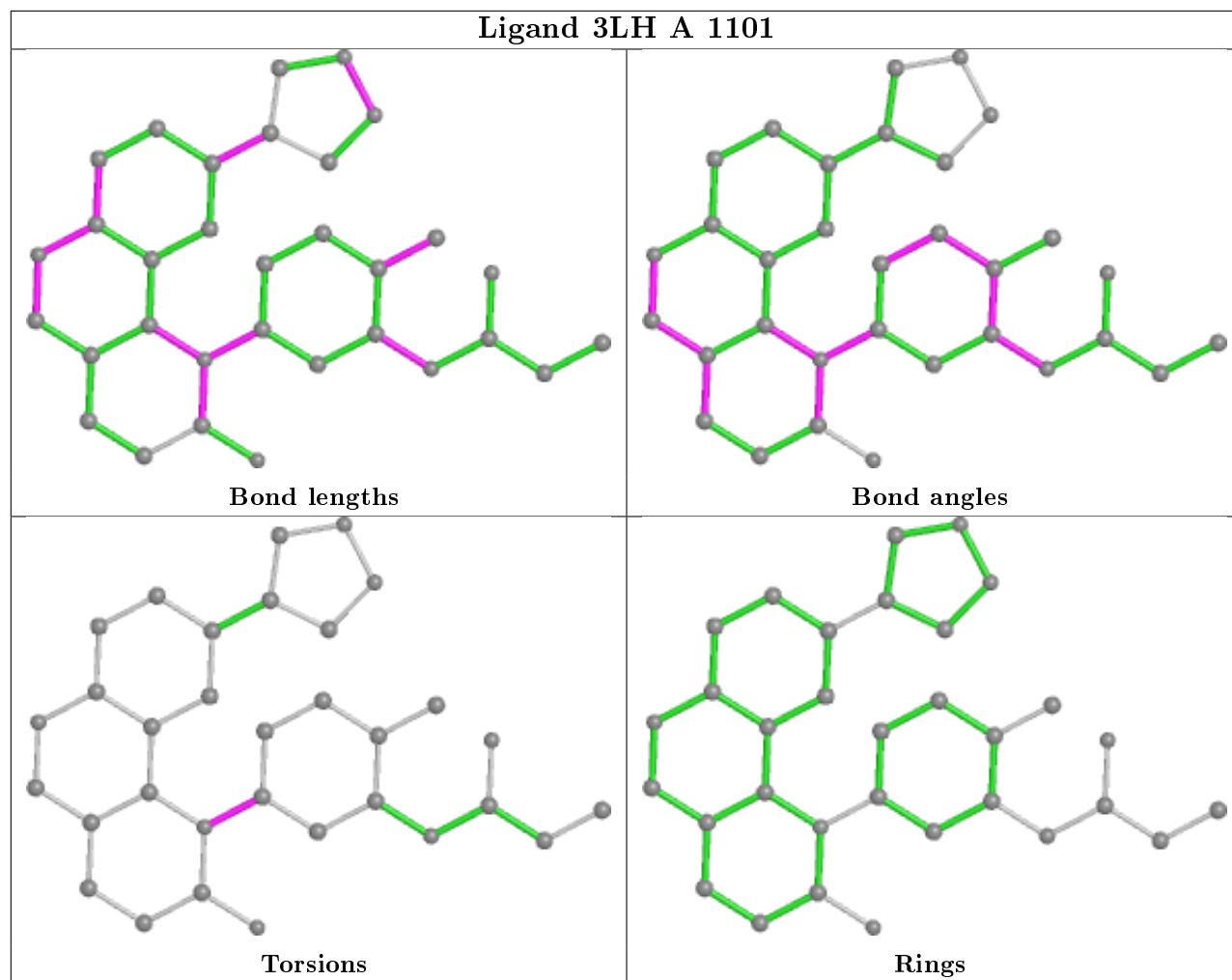
Mol	Chain	Res	Type	Atoms
2	A	1101	3LH	CAP-CBD-NBL-CBJ
2	A	1101	3LH	CAP-CBD-NBL-CBF
2	A	1101	3LH	CAH-CBD-NBL-CBJ
2	A	1101	3LH	CAH-CBD-NBL-CBF

There are no ring outliers.

1 monomer is involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1101	3LH	15	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



## 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 [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, 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	307/331 (92%)	-0.15	2 (0%) 87 88	52, 77, 112, 136	0
1	B	304/331 (91%)	-0.10	2 (0%) 87 88	52, 77, 112, 122	0
All	All	611/662 (92%)	-0.13	4 (0%) 87 88	52, 77, 112, 136	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	987	MET	3.2
1	B	1013	ALA	2.8
1	A	981	ILE	2.3
1	B	998	TYR	2.3

### 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](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

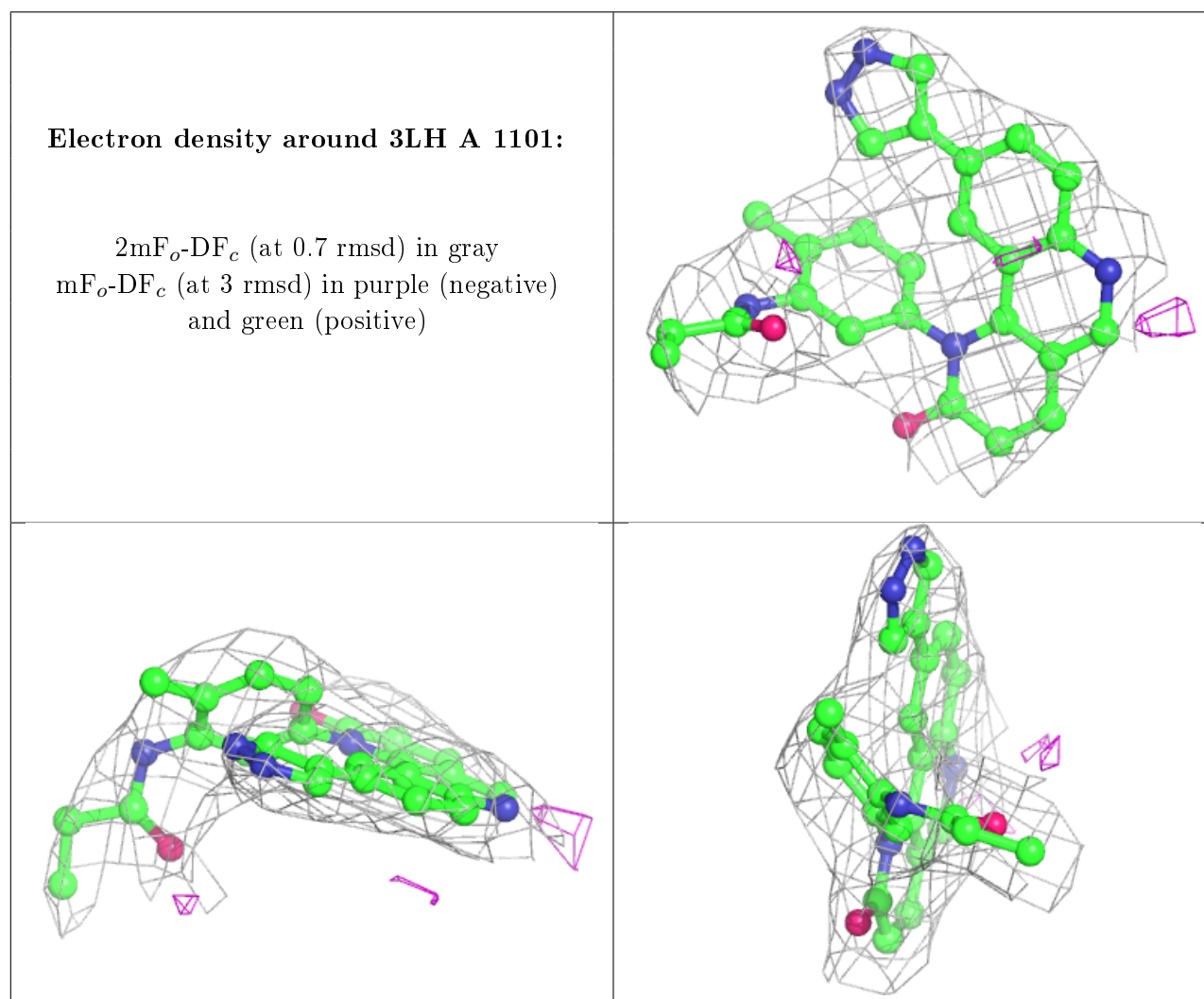
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	3LH	A	1101	32/32	0.91	0.26	64,76,85,87	0

*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	CL	B	1101	1/1	0.95	0.12	93,93,93,93	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



## 6.5 Other polymers ⓘ

There are no such residues in this entry.