



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 11:47 pm GMT

PDB ID : 2DWQ
Title : Thermus thermophilus YchF GTP-binding protein
Authors : Kukimoto-Niino, M.; Murayama, K.; Shorouzu, M.; Kuramitsu, S.; Yokoyama, S.; RIKEN Structural Genomics/Proteomics Initiative (RSGI)
Deposited on : 2006-08-16
Resolution : 2.95 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : recalc28949

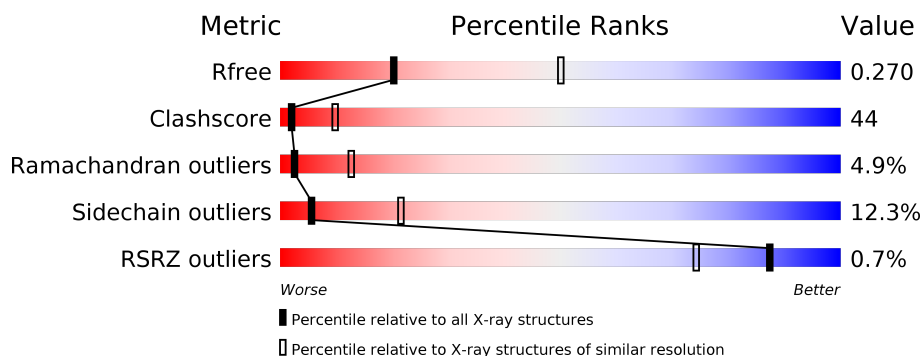
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.95 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}	100719	2395 (3.00-2.92)
Clashscore	112137	2773 (3.00-2.92)
Ramachandran outliers	110173	2680 (3.00-2.92)
Sidechain outliers	110143	2683 (3.00-2.92)
RSRZ outliers	101464	2421 (3.00-2.92)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	368	
1	B	368	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5410 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 GTP-binding protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	354	Total	C	N	O	S	0	0	0
			2748	1739	496	510	3			
1	B	337	Total	C	N	O	S	0	0	0
			2631	1668	475	486	2			

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	22	Total	O	0	0
			22	22		
2	B	9	Total	O	0	0
			9	9		

L266	L267	E268	E269	G270	L271	L272	E273	L274	A275	G278	Y279	E280	E281	L282	L285	L286	F287	F288	F289	A290	G291	E292	G293	E294	R295	R296	A297	L298	F299	V300	R301	R302	G303	T304	K305	A306	P307	A310	G311	E312	L313	L314	L315	D316	M317	F321	L322	R323	A324	E325	V326	L327	R328	L329	R330
K331	L332	A335	R340	K342	E343	R344	G345	W346	E350	G351	K352	D353	V356	I362	Y363	V364	L365	F366	A367	G368																																			

4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	52.94Å 54.36Å 92.58Å 80.11° 76.46° 73.12°	Depositor
Resolution (Å)	37.04 – 2.95 37.03 – 2.95	Depositor EDS
% Data completeness (in resolution range)	94.2 (37.04-2.95) 91.3 (37.03-2.95)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.12	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.36 (at 2.95Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.208 , 0.281 0.200 , 0.270	Depositor DCC
R_{free} test set	1872 reflections (9.87%)	DCC
Wilson B-factor (Å ²)	62.8	Xtriage
Anisotropy	0.507	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 64.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5410	wwPDB-VP
Average B, all atoms (Å ²)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.69% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

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	0.95	1/2795 (0.0%)	1.09	4/3787 (0.1%)
1	B	0.76	0/2675	0.99	1/3625 (0.0%)
All	All	0.86	1/5470 (0.0%)	1.04	5/7412 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	144	GLU	CG-CD	5.05	1.59	1.51

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	84	HIS	N-CA-C	6.34	128.13	111.00
1	B	280	ARG	NE-CZ-NH1	-6.22	117.19	120.30
1	A	86	GLY	N-CA-C	-5.79	98.61	113.10
1	A	100	VAL	CG1-CB-CG2	-5.36	102.32	110.90
1	A	62	ARG	N-CA-C	-5.00	97.50	111.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	51	TYR	Sidechain

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	2748	0	2784	220	0
1	B	2631	0	2666	274	0
2	A	22	0	0	6	0
2	B	9	0	0	2	0
All	All	5410	0	5450	481	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 44.

All (481) 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:23:ARG:HE	1:B:251:GLU:HG2	0.95	1.08
1:A:16:THR:HB	1:A:243:ALA:HB1	1.37	1.05
1:A:302:ARG:HB2	1:A:302:ARG:HH11	1.18	1.04
1:A:244:ARG:HG3	1:A:244:ARG:HH11	1.24	1.02
1:B:258:ARG:HE	1:B:258:ARG:HA	1.24	1.02
1:A:302:ARG:HB2	1:A:302:ARG:NH1	1.75	1.01
1:B:23:ARG:NE	1:B:251:GLU:HG2	1.76	0.99
1:A:340:ARG:HD3	1:B:267:GLN:CB	1.91	0.99
1:B:340:ARG:HG2	1:B:340:ARG:HH11	1.30	0.95
1:B:293:LYS:HD2	1:B:294:GLU:H	1.32	0.94
1:A:85:LYS:HB3	1:A:92:GLN:HE22	1.34	0.90
1:A:302:ARG:CB	1:A:302:ARG:HH11	1.84	0.90
1:B:147:LEU:O	1:B:151:ARG:HB2	1.70	0.90
1:B:14:LYS:HZ3	1:B:77:ALA:HB2	1.36	0.89
1:A:98:ARG:HG3	1:A:199:LEU:HD21	1.52	0.89
1:A:260:LEU:HD11	1:A:264:TYR:HE1	1.36	0.88
1:A:340:ARG:HD3	1:B:267:GLN:HB3	1.55	0.88
1:A:63:VAL:HG22	1:A:64:PRO:HD2	1.54	0.88
1:A:340:ARG:HD3	1:B:267:GLN:HB2	1.56	0.86
1:B:23:ARG:HE	1:B:251:GLU:CG	1.86	0.86
1:A:244:ARG:HG3	1:A:244:ARG:NH1	1.88	0.86
1:A:340:ARG:HG3	2:A:371:HOH:O	1.77	0.85
1:B:5:GLY:HA3	1:B:100:VAL:HG11	1.61	0.82

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:260:LEU:O	1:A:263:ALA:HB3	1.80	0.81
1:A:319:ARG:HH11	1:A:319:ARG:HG2	1.44	0.81
1:B:61:GLU:HB2	1:B:62:ARG:HH11	1.45	0.81
1:A:322:ILE:O	1:A:323:ARG:HG2	1.81	0.80
1:A:245:LEU:HG	1:A:249:LEU:HD11	1.66	0.78
1:B:158:ARG:HD2	1:B:159:GLU:N	1.98	0.77
1:B:40:VAL:HG22	1:B:74:VAL:HG22	1.66	0.77
1:B:229:ARG:HD3	2:B:376:HOH:O	1.83	0.77
1:A:171:TYR:CE2	1:A:175:GLN:NE2	2.52	0.76
1:A:54:GLN:HG2	1:A:63:VAL:CG2	2.15	0.76
1:A:215:LEU:CD1	1:A:245:LEU:HD23	2.16	0.76
1:A:260:LEU:HD12	1:A:260:LEU:O	1.85	0.75
1:A:260:LEU:HD11	1:A:264:TYR:CE1	2.21	0.75
1:A:88:GLY:O	1:A:92:GLN:HG3	1.86	0.75
1:B:14:LYS:HA	1:B:106:VAL:HG21	1.68	0.74
1:A:98:ARG:HG3	1:A:199:LEU:CD2	2.16	0.74
1:B:291:GLY:HA3	1:B:293:LYS:HE3	1.69	0.74
1:B:340:ARG:NH1	1:B:340:ARG:HG2	2.02	0.74
1:B:285:LEU:O	1:B:285:LEU:HD12	1.86	0.74
1:B:78:GLY:O	1:B:80:VAL:N	2.21	0.73
1:A:258:ARG:HA	1:A:258:ARG:HE	1.53	0.73
1:B:244:ARG:HB3	1:B:244:ARG:HH11	1.54	0.72
1:B:322:ILE:O	1:B:323:ARG:HD3	1.90	0.72
1:B:246:GLU:OE2	1:B:271:LEU:HD12	1.90	0.72
1:A:25:ASN:O	1:A:28:ALA:HB3	1.89	0.72
1:A:314:HIS:ND1	1:A:315:SER:N	2.38	0.71
1:B:322:ILE:HD12	1:B:366:PHE:HA	1.70	0.71
1:A:367:ASN:HD22	1:A:367:ASN:C	1.94	0.70
1:B:244:ARG:NH1	1:B:244:ARG:HB2	2.05	0.70
1:A:12:VAL:HG12	1:A:108:ARG:HB3	1.72	0.70
1:B:244:ARG:NH1	1:B:244:ARG:CB	2.54	0.70
1:B:322:ILE:HG22	1:B:323:ARG:HG2	1.72	0.70
1:A:170:LEU:O	1:A:174:LEU:HD12	1.90	0.70
1:A:215:LEU:HD11	1:A:245:LEU:HD23	1.74	0.70
1:A:59:LYS:HD3	1:A:292:GLU:OE1	1.92	0.70
1:B:206:TYR:HB2	1:B:238:VAL:HG22	1.74	0.70
1:A:224:VAL:HG12	1:A:224:VAL:O	1.90	0.70
1:A:240:VAL:O	1:A:241:VAL:HG13	1.91	0.70
1:B:188:ALA:C	1:B:190:ALA:H	1.96	0.69
1:B:139:ASP:OD2	1:B:198:LEU:HB3	1.91	0.69
1:B:25:ASN:C	1:B:25:ASN:HD22	1.93	0.69

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:326:VAL:HG22	1:A:362:ILE:HG12	1.74	0.69
1:A:267:GLN:HG3	1:B:340:ARG:CZ	2.23	0.69
1:B:244:ARG:CB	1:B:244:ARG:HH11	2.05	0.69
1:B:152:LYS:O	1:B:152:LYS:HD3	1.94	0.68
1:B:158:ARG:O	1:B:161:LEU:HD13	1.93	0.68
1:A:63:VAL:HG22	1:A:64:PRO:CD	2.22	0.68
1:B:189:VAL:O	1:B:189:VAL:HG12	1.94	0.68
1:B:278:GLY:O	1:B:282:LEU:HG	1.94	0.68
1:B:285:LEU:HD21	1:B:302:ARG:HA	1.76	0.67
1:B:92:GLN:OE1	1:B:92:GLN:HA	1.92	0.67
1:A:80:VAL:HG21	1:A:93:PHE:CD1	2.30	0.67
1:B:5:GLY:CA	1:B:100:VAL:HG11	2.25	0.67
1:B:8:GLY:O	1:B:10:PRO:HD3	1.95	0.66
1:B:49:ARG:O	1:B:53:LEU:HB2	1.96	0.66
1:B:212:GLU:O	1:B:215:LEU:HB2	1.95	0.65
1:B:285:LEU:CD2	1:B:302:ARG:HA	2.27	0.65
1:B:61:GLU:HB2	1:B:62:ARG:NH1	2.10	0.65
1:B:226:ALA:O	1:B:229:ARG:HB3	1.97	0.65
1:A:259:GLU:O	1:A:262:ALA:HB3	1.96	0.65
1:A:15:SER:O	1:A:19:ASN:HB2	1.98	0.64
1:A:246:GLU:OE1	1:A:270:GLY:N	2.30	0.64
1:B:74:VAL:O	1:B:74:VAL:HG12	1.97	0.64
1:A:2:LEU:HB3	1:A:282:LEU:HD13	1.80	0.64
1:B:127:ASP:O	1:B:131:VAL:HG23	1.98	0.64
1:A:149:ARG:O	1:A:152:LYS:HG3	1.97	0.64
1:B:143:LEU:O	1:B:147:LEU:HB2	1.97	0.64
1:A:276:ARG:HB2	1:A:280:ARG:HH12	1.62	0.64
1:B:216:PRO:HG2	1:B:217:ASP:OD2	1.97	0.63
1:B:16:THR:O	1:B:19:ASN:HB3	1.99	0.63
1:B:335:ALA:HB2	1:B:346:TRP:CZ3	2.32	0.63
1:A:23:ARG:O	1:A:26:ALA:HB3	1.99	0.63
1:B:229:ARG:HG2	1:B:229:ARG:HH11	1.64	0.63
1:B:293:LYS:HD2	1:B:294:GLU:N	2.10	0.63
1:A:124:PRO:HA	2:A:382:HOH:O	1.97	0.63
1:A:36:ILE:HD13	1:A:38:LYS:HE2	1.78	0.63
1:B:253:SER:O	1:B:256:GLU:HB3	1.99	0.63
1:B:135:LEU:HD23	1:B:199:LEU:HD12	1.81	0.63
1:B:78:GLY:C	1:B:80:VAL:H	2.01	0.63
1:A:240:VAL:O	1:A:241:VAL:CG1	2.47	0.62
1:B:67:VAL:HG12	1:B:296:ARG:HG3	1.82	0.62
1:A:188:ALA:O	1:A:189:VAL:C	2.38	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:186:SER:HB3	1:B:189:VAL:CG2	2.29	0.62
1:B:340:ARG:O	1:B:343:GLU:HB2	2.00	0.62
1:B:181:ARG:NH2	1:B:204:VAL:HG21	2.15	0.61
1:A:330:ASP:OD2	1:A:330:ASP:N	2.33	0.61
1:B:158:ARG:NH1	1:B:159:GLU:HB2	2.16	0.61
1:B:161:LEU:O	1:B:165:GLU:HG3	2.00	0.61
1:B:317:MET:HG3	1:B:366:PHE:CE2	2.35	0.61
1:B:50:LEU:HD23	1:B:288:PHE:CE2	2.35	0.61
1:A:54:GLN:HG2	1:A:63:VAL:HG22	1.82	0.61
1:A:54:GLN:HG2	1:A:63:VAL:HG21	1.81	0.61
1:A:150:LEU:HD23	1:A:153:GLU:OE2	1.99	0.61
1:B:154:ALA:HA	1:B:160:ARG:HB2	1.82	0.61
1:B:228:ARG:O	1:B:232:LEU:HD23	2.01	0.61
1:A:340:ARG:CD	1:B:267:GLN:HB3	2.29	0.61
1:A:47:ASP:O	1:A:50:LEU:HB2	2.01	0.61
1:A:256:GLU:HA	1:A:259:GLU:HG2	1.83	0.60
1:B:9:LEU:HG	1:B:127:ASP:HB3	1.83	0.60
1:B:258:ARG:NE	1:B:258:ARG:HA	2.08	0.60
1:B:222:PRO:HA	1:B:225:GLU:HG3	1.83	0.60
1:A:36:ILE:HG12	1:A:38:LYS:HG2	1.84	0.60
1:A:262:ALA:O	1:A:265:GLY:N	2.32	0.60
1:B:77:ALA:O	1:B:80:VAL:HG23	2.01	0.60
1:A:151:ARG:HA	1:A:164:LEU:HD11	1.84	0.60
1:B:314:HIS:CE1	1:B:316:ASP:OD1	2.55	0.60
1:A:259:GLU:O	1:A:263:ALA:N	2.28	0.59
1:B:335:ALA:HB2	1:B:346:TRP:CE3	2.38	0.59
1:A:152:LYS:HD2	1:A:152:LYS:C	2.23	0.59
1:B:186:SER:HB3	1:B:189:VAL:HG23	1.84	0.59
1:A:255:GLU:O	1:A:258:ARG:HB3	2.03	0.59
1:B:231:ALA:HB1	1:B:236:ALA:O	2.03	0.59
1:B:317:MET:HG3	1:B:366:PHE:CD2	2.39	0.58
1:B:73:PHE:CZ	1:B:274:LEU:HG	2.37	0.58
1:A:172:VAL:O	1:A:176:GLU:HG3	2.01	0.58
1:B:214:ASP:O	1:B:218:GLY:HA2	2.04	0.58
1:B:256:GLU:O	1:B:257:ALA:C	2.40	0.58
1:A:7:VAL:HG12	1:A:76:ILE:HB	1.86	0.58
1:B:146:ARG:HH21	1:B:150:LEU:HG	1.68	0.58
1:B:24:ALA:HB2	1:B:250:ALA:O	2.04	0.58
1:A:298:TRP:CH2	1:A:313:ILE:HA	2.39	0.57
1:B:154:ALA:HB1	1:B:164:LEU:HD22	1.85	0.57
1:A:7:VAL:HG11	1:A:97:ILE:HD11	1.85	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:254:GLY:C	1:B:256:GLU:H	2.06	0.57
1:B:135:LEU:CD2	1:B:199:LEU:HD12	2.34	0.57
1:B:245:LEU:O	1:B:249:LEU:HG	2.05	0.57
1:A:108:ARG:O	1:A:124:PRO:HB3	2.03	0.57
1:B:46:GLU:HB2	1:B:272:GLN:OE1	2.03	0.57
1:B:132:GLU:O	1:B:136:LEU:HG	2.03	0.57
1:B:152:LYS:HD3	1:B:152:LYS:C	2.24	0.57
1:B:106:VAL:HA	1:B:207:VAL:HB	1.87	0.57
1:B:273:ARG:HG2	1:B:273:ARG:HH11	1.70	0.57
1:A:276:ARG:HH12	1:B:344:ARG:CZ	2.17	0.57
1:A:42:VAL:O	1:A:44:PRO:HD3	2.05	0.57
1:A:244:ARG:O	1:A:247:ALA:HB3	2.05	0.56
1:A:357:GLN:O	1:A:360:ASP:HB2	2.05	0.56
1:A:58:ALA:HB2	1:A:63:VAL:HG23	1.86	0.56
1:A:150:LEU:CD1	1:A:164:LEU:HD12	2.35	0.56
1:A:85:LYS:HB3	1:A:92:GLN:NE2	2.14	0.56
1:B:154:ALA:CB	1:B:164:LEU:HD22	2.35	0.56
1:B:62:ARG:CD	1:B:62:ARG:N	2.68	0.56
1:A:256:GLU:O	1:A:259:GLU:HG3	2.05	0.56
1:A:319:ARG:NH1	1:A:319:ARG:HG2	2.16	0.56
1:B:15:SER:O	1:B:16:THR:C	2.44	0.56
1:A:97:ILE:O	1:A:202:LYS:HE3	2.06	0.56
1:B:213:GLU:CD	1:B:213:GLU:H	2.09	0.56
1:B:71:VAL:CG2	1:B:275:ALA:HB1	2.35	0.56
1:B:54:GLN:NE2	1:B:66:VAL:HG13	2.21	0.56
1:A:215:LEU:HD13	1:A:266:LEU:HD11	1.88	0.56
1:A:351:GLY:O	1:A:353:ASP:N	2.39	0.56
1:B:305:LYS:HD3	1:B:353:ASP:HA	1.86	0.56
1:A:10:PRO:HA	2:A:389:HOH:O	2.05	0.56
1:A:367:ASN:ND2	1:A:367:ASN:C	2.60	0.56
1:A:288:PHE:HB3	1:A:296:ARG:O	2.05	0.55
1:B:364:VAL:HG12	1:B:365:LEU:N	2.21	0.55
1:A:252:LEU:HD11	1:A:260:LEU:HD23	1.88	0.55
1:A:254:GLY:O	1:A:258:ARG:HB2	2.06	0.55
1:B:7:VAL:HG23	1:B:8:GLY:N	2.21	0.55
1:B:135:LEU:HD22	1:B:199:LEU:HB3	1.89	0.55
1:B:132:GLU:OE1	1:B:200:THR:HG22	2.07	0.55
1:A:181:ARG:HD2	1:A:234:GLU:O	2.06	0.55
1:A:157:ASP:C	1:A:157:ASP:OD2	2.45	0.54
1:A:260:LEU:HD12	1:A:263:ALA:HB3	1.89	0.54
1:B:147:LEU:O	1:B:151:ARG:CB	2.50	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:225:GLU:O	1:B:229:ARG:HB2	2.07	0.54
1:B:321:PHE:HE1	1:B:324:ALA:HB2	1.72	0.54
1:B:188:ALA:O	1:B:190:ALA:N	2.41	0.54
1:B:301:ARG:O	1:B:302:ARG:C	2.46	0.54
1:B:155:ARG:C	1:B:157:ASP:H	2.11	0.54
1:B:290:ALA:CB	1:B:295:VAL:HG23	2.38	0.54
1:B:328:PRO:HG2	1:B:331:LYS:HG2	1.89	0.54
1:B:109:CYS:SG	1:B:224:VAL:HG22	2.48	0.54
1:A:276:ARG:HH12	1:B:344:ARG:NH2	2.05	0.54
1:A:282:LEU:N	1:A:282:LEU:HD23	2.22	0.54
1:B:65:PRO:CD	1:B:293:LYS:O	2.56	0.54
1:B:14:LYS:HE2	1:B:75:ASP:OD1	2.07	0.54
1:A:328:PRO:HB2	1:A:330:ASP:OD2	2.09	0.53
1:B:244:ARG:HB2	1:B:244:ARG:CZ	2.38	0.53
1:B:6:ILE:HD11	1:B:73:PHE:HD2	1.73	0.53
1:A:210:VAL:HG11	1:A:224:VAL:HG21	1.89	0.53
1:A:189:VAL:O	1:A:192:PHE:N	2.41	0.53
1:B:230:LYS:HE2	1:B:234:GLU:HG3	1.91	0.53
1:A:319:ARG:C	1:A:319:ARG:HD2	2.28	0.53
1:B:151:ARG:HA	1:B:164:LEU:HD13	1.90	0.53
1:A:280:ARG:HG3	1:A:280:ARG:HH11	1.73	0.53
1:A:87:GLU:H	1:A:87:GLU:CD	2.11	0.53
1:A:150:LEU:HD13	1:A:164:LEU:CD1	2.39	0.53
1:A:225:GLU:O	1:A:229:ARG:HG3	2.08	0.53
1:B:101:ALA:O	1:B:203:PRO:HD2	2.09	0.53
1:B:13:GLY:O	1:B:15:SER:N	2.42	0.53
1:B:73:PHE:CE2	1:B:274:LEU:HD21	2.44	0.52
1:A:212:GLU:OE1	1:A:244:ARG:HG2	2.09	0.52
1:A:77:ALA:O	1:A:78:GLY:C	2.48	0.52
1:B:127:ASP:N	1:B:127:ASP:OD2	2.42	0.52
1:A:309:ALA:HB2	1:A:356:VAL:HG21	1.91	0.52
1:B:65:PRO:HD2	1:B:293:LYS:O	2.08	0.52
1:A:170:LEU:O	1:A:173:HIS:HB3	2.10	0.52
1:B:252:LEU:HD12	1:B:260:LEU:CD2	2.40	0.52
1:A:267:GLN:HG2	1:B:340:ARG:CG	2.39	0.52
1:B:188:ALA:C	1:B:190:ALA:N	2.61	0.52
1:B:340:ARG:HH11	1:B:340:ARG:CG	2.12	0.52
1:A:256:GLU:O	1:A:259:GLU:CG	2.57	0.52
1:B:285:LEU:HD12	1:B:285:LEU:C	2.30	0.52
1:B:14:LYS:NZ	1:B:77:ALA:HB2	2.18	0.52
1:A:276:ARG:O	1:A:280:ARG:NH1	2.43	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:150:LEU:HD23	1:B:153:GLU:OE2	2.10	0.51
1:B:71:VAL:HG21	1:B:275:ALA:HB1	1.92	0.51
1:A:211:ALA:O	1:A:214:ASP:HB2	2.10	0.51
1:B:13:GLY:O	1:B:14:LYS:C	2.49	0.51
1:B:161:LEU:HB2	1:B:162:PRO:HD3	1.92	0.51
1:A:214:ASP:O	1:A:215:LEU:C	2.48	0.51
1:B:296:ARG:HD3	1:B:298:TRP:CZ2	2.46	0.51
1:A:125:LEU:O	1:A:128:ALA:HB3	2.10	0.51
1:B:189:VAL:O	1:B:189:VAL:CG1	2.58	0.51
1:A:304:THR:HG23	1:A:308:ARG:HB3	1.91	0.51
1:B:70:HIS:N	1:B:70:HIS:ND1	2.59	0.51
1:B:256:GLU:O	1:B:259:GLU:N	2.43	0.51
1:B:329:TRP:CG	1:B:330:ASP:N	2.78	0.51
1:A:259:GLU:O	1:A:262:ALA:N	2.44	0.51
1:A:10:PRO:CA	2:A:389:HOH:O	2.58	0.50
1:A:85:LYS:CB	1:A:92:GLN:HE22	2.16	0.50
1:B:260:LEU:O	1:B:261:LEU:C	2.50	0.50
1:B:262:ALA:O	1:B:265:GLY:N	2.43	0.50
1:A:319:ARG:CG	1:A:319:ARG:NH1	2.74	0.50
1:B:242:SER:O	1:B:246:GLU:HG2	2.11	0.50
1:B:307:PRO:HG2	1:B:352:LYS:HB2	1.93	0.50
1:B:62:ARG:N	1:B:62:ARG:HD3	2.26	0.50
1:A:217:ASP:OD1	1:A:273:ARG:NH2	2.45	0.50
1:A:85:LYS:HG2	1:A:87:GLU:O	2.12	0.50
1:A:259:GLU:HG3	1:A:260:LEU:H	1.76	0.50
1:B:18:PHE:CD2	1:B:18:PHE:O	2.65	0.50
1:B:256:GLU:C	1:B:258:ARG:N	2.60	0.50
1:B:110:PHE:O	1:B:110:PHE:CD2	2.65	0.50
1:B:159:GLU:O	1:B:162:PRO:HD2	2.11	0.50
1:B:261:LEU:HB3	1:B:266:LEU:CB	2.42	0.50
1:B:273:ARG:NH1	1:B:273:ARG:HG2	2.25	0.50
1:B:2:LEU:HD11	1:B:301:ARG:HH21	1.75	0.50
1:B:210:VAL:HG23	1:B:211:ALA:O	2.12	0.49
1:B:249:LEU:O	1:B:251:GLU:N	2.45	0.49
1:A:150:LEU:HD12	1:A:164:LEU:HD12	1.93	0.49
1:B:256:GLU:HG3	1:B:259:GLU:HG2	1.95	0.49
1:B:310:ALA:HB1	1:B:317:MET:HB3	1.92	0.49
1:A:322:ILE:O	1:A:323:ARG:CG	2.58	0.49
1:B:255:GLU:OE1	1:B:255:GLU:HA	2.13	0.49
1:B:299:THR:O	1:B:300:VAL:HG13	2.13	0.49
1:A:244:ARG:CG	1:A:244:ARG:HH11	2.07	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:150:LEU:CD2	1:A:153:GLU:OE2	2.60	0.48
1:A:160:ARG:NH1	1:A:163:LEU:HD22	2.28	0.48
1:A:306:ALA:N	1:A:354:TYR:O	2.39	0.48
1:A:9:LEU:O	1:A:12:VAL:HG22	2.12	0.48
1:B:221:ASN:OD1	1:B:224:VAL:HG23	2.13	0.48
1:A:183:PHE:CD1	1:A:184:PRO:HD2	2.48	0.48
1:B:254:GLY:C	1:B:256:GLU:N	2.67	0.48
1:B:322:ILE:HD12	1:B:365:LEU:O	2.13	0.48
1:B:92:GLN:O	1:B:93:PHE:C	2.51	0.48
1:A:240:VAL:C	1:A:241:VAL:HG13	2.32	0.48
1:A:6:ILE:HD11	1:A:73:PHE:CD2	2.48	0.48
1:A:144:GLU:HG3	1:A:171:TYR:CE1	2.48	0.48
1:A:216:PRO:HB3	1:A:266:LEU:HD22	1.95	0.48
1:A:223:GLN:C	1:A:225:GLU:H	2.16	0.48
1:B:307:PRO:O	1:B:310:ALA:HB3	2.14	0.48
1:B:12:VAL:HG12	1:B:108:ARG:CB	2.44	0.48
1:B:50:LEU:CD2	1:B:288:PHE:CE2	2.96	0.48
1:B:221:ASN:CG	1:B:224:VAL:HG23	2.34	0.48
1:B:254:GLY:O	1:B:256:GLU:N	2.47	0.48
1:B:184:PRO:HA	1:B:185:PRO:HD3	1.66	0.48
1:B:186:SER:C	1:B:188:ALA:H	2.17	0.48
1:B:322:ILE:HD12	1:B:366:PHE:CA	2.40	0.48
1:A:267:GLN:HG2	1:B:340:ARG:HG3	1.95	0.48
1:B:166:ALA:O	1:B:170:LEU:N	2.42	0.48
1:B:65:PRO:HG2	1:B:294:GLU:HA	1.94	0.48
1:A:224:VAL:CG1	1:A:224:VAL:O	2.62	0.47
1:A:230:LYS:HA	1:A:230:LYS:HE2	1.95	0.47
1:B:317:MET:O	1:B:321:PHE:HB2	2.13	0.47
1:A:259:GLU:HG3	1:A:260:LEU:N	2.30	0.47
1:A:135:LEU:HD22	1:A:199:LEU:HD13	1.96	0.47
1:A:214:ASP:C	1:A:215:LEU:O	2.50	0.47
1:A:230:LYS:O	1:A:233:GLU:N	2.43	0.47
1:B:172:VAL:O	1:B:176:GLU:HG3	2.14	0.47
1:A:302:ARG:NH1	1:A:302:ARG:CB	2.56	0.47
1:A:36:ILE:O	1:A:36:ILE:HG23	2.15	0.47
1:B:220:GLY:O	1:B:222:PRO:HD3	2.14	0.47
1:A:150:LEU:HD13	1:A:164:LEU:HD13	1.96	0.47
1:A:96:HIS:O	1:A:98:ARG:N	2.48	0.47
1:B:174:LEU:HD11	1:B:180:ALA:HB2	1.97	0.47
1:B:261:LEU:HB3	1:B:266:LEU:HB2	1.97	0.47
1:A:106:VAL:O	1:A:107:LEU:HD23	2.14	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:227:VAL:HG12	1:A:228:ARG:N	2.30	0.47
1:B:148:GLU:O	1:B:149:ARG:C	2.52	0.47
1:B:229:ARG:HG2	1:B:229:ARG:NH1	2.29	0.47
1:B:364:VAL:HG12	1:B:365:LEU:H	1.78	0.47
1:A:110:PHE:O	1:A:110:PHE:CG	2.68	0.46
1:A:171:TYR:CD2	1:A:175:GLN:NE2	2.79	0.46
1:B:210:VAL:O	1:B:242:SER:HB2	2.14	0.46
1:B:311:GLY:O	1:B:313:ILE:N	2.48	0.46
1:A:253:SER:O	1:A:257:ALA:N	2.39	0.46
1:A:326:VAL:HA	1:A:361:VAL:O	2.14	0.46
1:B:23:ARG:CZ	1:B:251:GLU:HG2	2.43	0.46
1:B:17:LEU:C	1:B:19:ASN:H	2.19	0.46
1:B:25:ASN:C	1:B:25:ASN:ND2	2.65	0.46
1:A:272:GLN:O	1:A:273:ARG:C	2.52	0.46
1:B:163:LEU:CD1	1:B:192:PHE:HB2	2.45	0.46
1:B:300:VAL:CG1	1:B:304:THR:HG21	2.46	0.46
1:A:136:LEU:HD11	1:A:177:GLY:O	2.15	0.46
1:A:198:LEU:O	1:A:201:ALA:HB3	2.15	0.46
1:A:223:GLN:O	1:A:226:ALA:N	2.49	0.46
1:B:66:VAL:O	1:B:66:VAL:HG23	2.16	0.46
1:A:13:GLY:O	1:A:14:LYS:C	2.53	0.46
1:B:107:LEU:HB3	1:B:124:PRO:HB2	1.98	0.46
1:B:241:VAL:HG23	1:B:242:SER:N	2.30	0.46
1:B:249:LEU:C	1:B:251:GLU:N	2.68	0.46
1:B:332:LEU:HG	1:B:332:LEU:O	2.16	0.46
1:B:50:LEU:CD2	1:B:288:PHE:HE2	2.28	0.46
1:B:6:ILE:HD11	1:B:73:PHE:CD2	2.51	0.46
1:A:96:HIS:O	1:A:99:GLU:N	2.48	0.46
1:B:73:PHE:CE2	1:B:274:LEU:HG	2.50	0.46
1:B:311:GLY:C	1:B:313:ILE:N	2.69	0.46
1:B:17:LEU:C	1:B:19:ASN:N	2.70	0.45
1:A:301:ARG:O	1:A:302:ARG:C	2.55	0.45
1:A:339:ALA:O	1:A:343:GLU:HG3	2.16	0.45
1:A:80:VAL:HG21	1:A:93:PHE:CE1	2.51	0.45
1:A:96:HIS:C	1:A:98:ARG:N	2.69	0.45
1:B:188:ALA:O	1:B:191:ARG:N	2.48	0.45
1:B:47:ASP:OD1	1:B:49:ARG:NH2	2.49	0.45
1:A:254:GLY:O	1:A:258:ARG:N	2.44	0.45
1:B:314:HIS:NE2	1:B:316:ASP:OD1	2.49	0.45
1:B:50:LEU:HD23	1:B:288:PHE:CD2	2.52	0.45
1:A:267:GLN:HG2	1:B:340:ARG:CD	2.47	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:80:VAL:HG11	1:A:93:PHE:CD1	2.51	0.45
1:B:246:GLU:HB3	1:B:271:LEU:HD11	1.99	0.45
1:B:73:PHE:CE2	1:B:274:LEU:CD2	3.00	0.45
1:A:271:LEU:HD23	1:A:271:LEU:HA	1.76	0.45
1:B:259:GLU:O	1:B:262:ALA:HB3	2.17	0.45
1:A:223:GLN:C	1:A:225:GLU:N	2.70	0.45
1:A:327:ILE:HD11	1:A:331:LYS:HB2	1.98	0.45
1:A:317:MET:CE	1:A:364:VAL:HB	2.46	0.45
1:B:15:SER:O	1:B:17:LEU:N	2.50	0.45
1:A:80:VAL:O	1:A:81:LYS:O	2.35	0.45
1:B:221:ASN:HB3	1:B:224:VAL:HB	1.98	0.45
1:A:170:LEU:HD23	1:A:170:LEU:HA	1.71	0.45
1:A:249:LEU:O	1:A:250:ALA:C	2.55	0.45
1:B:136:LEU:HA	1:B:136:LEU:HD23	1.85	0.45
1:A:307:PRO:HG3	1:A:321:PHE:CD2	2.52	0.44
1:A:326:VAL:HG22	1:A:362:ILE:CG1	2.46	0.44
1:B:136:LEU:HD23	1:B:174:LEU:HD23	1.99	0.44
1:B:194:LYS:HA	2:B:371:HOH:O	2.17	0.44
1:B:327:ILE:O	1:B:327:ILE:HG23	2.16	0.44
1:A:123:ASP:C	1:A:123:ASP:OD2	2.55	0.44
1:B:280:ARG:CG	1:B:280:ARG:HH11	2.30	0.44
1:B:21:LEU:HD11	1:B:42:VAL:N	2.32	0.44
1:B:71:VAL:HG23	1:B:275:ALA:HB1	2.00	0.44
1:B:9:LEU:O	1:B:12:VAL:HG22	2.17	0.44
1:A:241:VAL:HG12	1:A:270:GLY:CA	2.47	0.44
1:A:50:LEU:HD22	1:A:295:VAL:HG12	2.00	0.44
1:A:56:THR:HG22	1:A:57:PHE:CE1	2.53	0.44
1:B:124:PRO:C	1:B:126:GLU:N	2.70	0.44
1:B:78:GLY:C	1:B:80:VAL:N	2.66	0.44
1:A:106:VAL:C	1:A:107:LEU:HD23	2.38	0.44
1:A:2:LEU:HD12	1:A:284:LEU:HD21	1.99	0.44
1:B:238:VAL:O	1:B:238:VAL:HG12	2.17	0.44
1:A:53:LEU:HD11	1:A:329:TRP:HB2	2.00	0.44
1:A:214:ASP:O	1:A:215:LEU:O	2.36	0.44
1:B:158:ARG:CZ	1:B:159:GLU:HB2	2.48	0.44
1:B:22:THR:O	1:B:23:ARG:C	2.56	0.44
1:B:306:ALA:HB3	1:B:307:PRO:HD3	1.99	0.44
1:B:221:ASN:HA	1:B:222:PRO:HD2	1.86	0.44
1:A:11:ASN:N	2:A:389:HOH:O	2.26	0.44
1:A:68:PRO:HB2	2:A:387:HOH:O	2.18	0.44
1:B:178:LYS:HA	1:B:179:PRO:HD3	1.86	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:244:ARG:HG3	1:B:245:LEU:N	2.33	0.43
1:B:321:PHE:CE1	1:B:324:ALA:HB2	2.53	0.43
1:A:7:VAL:O	1:A:105:HIS:HA	2.17	0.43
1:B:12:VAL:HG12	1:B:108:ARG:H	1.83	0.43
1:B:270:GLY:HA2	1:B:273:ARG:CD	2.49	0.43
1:B:316:ASP:N	1:B:316:ASP:OD1	2.45	0.43
1:B:326:VAL:HG21	1:B:350:GLU:HG3	2.01	0.43
1:A:245:LEU:HG	1:A:249:LEU:CD1	2.43	0.43
1:B:12:VAL:HG12	1:B:108:ARG:HB2	1.99	0.43
1:A:158:ARG:O	1:A:161:LEU:HB2	2.18	0.43
1:B:167:ALA:O	1:B:168:GLU:C	2.56	0.43
1:A:207:VAL:CG2	1:A:274:LEU:CD1	2.97	0.43
1:A:20:ALA:HA	1:A:23:ARG:HB3	2.00	0.43
1:B:158:ARG:HD2	1:B:159:GLU:HB2	2.01	0.43
1:B:242:SER:O	1:B:242:SER:OG	2.33	0.43
1:B:327:ILE:HD13	1:B:332:LEU:HB2	1.99	0.43
1:B:273:ARG:CG	1:B:273:ARG:HH11	2.32	0.43
1:A:157:ASP:OD2	1:A:159:GLU:N	2.52	0.43
1:A:160:ARG:HH12	1:A:163:LEU:HD22	1.84	0.43
1:A:71:VAL:HG21	1:A:275:ALA:O	2.19	0.43
1:B:212:GLU:CG	1:B:244:ARG:HD3	2.49	0.43
1:B:25:ASN:OD1	1:B:42:VAL:HG22	2.19	0.43
1:A:217:ASP:O	1:A:218:GLY:C	2.56	0.42
1:B:179:PRO:HB2	1:B:181:ARG:HG2	2.01	0.42
1:B:252:LEU:HD12	1:B:260:LEU:HD23	2.00	0.42
1:A:143:LEU:O	1:A:144:GLU:C	2.57	0.42
1:B:216:PRO:O	1:B:273:ARG:NH2	2.52	0.42
1:B:299:THR:CG2	1:B:300:VAL:N	2.82	0.42
1:B:50:LEU:HD21	1:B:297:ALA:HB2	1.99	0.42
1:A:51:TYR:HB2	1:B:55:ARG:NH2	2.33	0.42
1:A:179:PRO:HB2	1:A:181:ARG:HG2	2.01	0.42
1:A:181:ARG:NH2	1:A:204:VAL:CG2	2.82	0.42
1:A:242:SER:O	1:A:246:GLU:HB2	2.19	0.42
1:A:45:LEU:HD23	1:A:45:LEU:HA	1.79	0.42
1:B:124:PRO:C	1:B:126:GLU:H	2.22	0.42
1:B:362:ILE:CG2	1:B:363:TYR:N	2.82	0.42
1:B:175:GLN:OE1	1:B:175:GLN:HA	2.19	0.42
1:A:20:ALA:O	1:A:21:LEU:C	2.58	0.42
1:A:245:LEU:CG	1:A:249:LEU:HD11	2.44	0.42
1:A:55:ARG:CZ	1:B:51:TYR:HB3	2.50	0.42
1:A:54:GLN:CG	1:A:63:VAL:HG22	2.48	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:214:ASP:O	1:B:218:GLY:CA	2.68	0.42
1:B:131:VAL:O	1:B:135:LEU:HD12	2.20	0.42
1:B:146:ARG:HD2	1:B:146:ARG:HA	1.60	0.42
1:B:97:ILE:CG2	1:B:199:LEU:HD13	2.50	0.42
1:B:226:ALA:O	1:B:230:LYS:N	2.47	0.42
1:B:268:GLU:HG3	1:B:272:GLN:HB2	2.02	0.42
1:B:295:VAL:O	1:B:295:VAL:CG1	2.68	0.42
1:A:255:GLU:HA	1:A:258:ARG:HB2	2.02	0.41
1:A:342:LYS:HG3	1:A:347:VAL:HG21	2.02	0.41
1:A:112:ASP:HB2	1:A:113:PRO:HD2	2.01	0.41
1:A:16:THR:HB	1:A:243:ALA:CB	2.27	0.41
1:B:155:ARG:C	1:B:157:ASP:N	2.73	0.41
1:B:53:LEU:HA	1:B:53:LEU:HD23	1.82	0.41
1:A:253:SER:O	1:A:254:GLY:C	2.58	0.41
1:A:325:GLU:OE1	1:A:342:LYS:NZ	2.50	0.41
1:A:340:ARG:HD2	1:A:340:ARG:HH11	1.69	0.41
1:A:77:ALA:O	1:A:80:VAL:N	2.53	0.41
1:A:89:LEU:HD23	1:A:89:LEU:HA	1.87	0.41
1:A:110:PHE:O	1:A:111:PRO:C	2.58	0.41
1:A:139:ASP:O	1:A:142:THR:HB	2.21	0.41
1:B:151:ARG:HA	1:B:164:LEU:CD1	2.51	0.41
1:B:209:ASN:OD1	1:B:209:ASN:C	2.57	0.41
1:B:271:LEU:H	1:B:271:LEU:HD12	1.84	0.41
1:B:186:SER:C	1:B:188:ALA:N	2.74	0.41
1:B:307:PRO:O	1:B:310:ALA:N	2.51	0.41
1:B:71:VAL:HB	1:B:73:PHE:HE1	1.84	0.41
1:B:268:GLU:HG3	1:B:272:GLN:CB	2.51	0.41
1:B:23:ARG:HH21	1:B:251:GLU:CG	2.33	0.41
1:A:20:ALA:O	1:A:23:ARG:N	2.53	0.41
1:A:332:LEU:HA	1:A:332:LEU:HD12	1.89	0.41
1:A:351:GLY:O	1:A:352:LYS:C	2.59	0.41
1:B:63:VAL:HA	1:B:64:PRO:HD3	1.92	0.41
1:A:207:VAL:HG21	1:A:274:LEU:CD1	2.51	0.40
1:B:280:ARG:CG	1:B:280:ARG:NH1	2.83	0.40
1:B:21:LEU:C	1:B:21:LEU:HD12	2.42	0.40
1:B:252:LEU:O	1:B:253:SER:C	2.59	0.40
1:B:328:PRO:HB2	1:B:330:ASP:OD1	2.21	0.40
1:A:163:LEU:HD11	1:A:191:ARG:NH2	2.36	0.40
1:A:282:LEU:HB2	1:A:284:LEU:HG	2.04	0.40
1:A:48:GLU:OE1	1:B:55:ARG:NH2	2.54	0.40
1:A:76:ILE:HD13	1:A:76:ILE:HA	1.81	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:341:ALA:C	1:B:343:GLU:N	2.74	0.40
1:A:23:ARG:C	1:A:26:ALA:HB3	2.41	0.40
1:A:81:LYS:O	1:A:82:GLY:C	2.60	0.40
1:B:206:TYR:O	1:B:208:ALA:N	2.52	0.40
1:B:270:GLY:HA2	1:B:273:ARG:HD3	2.03	0.40
1:A:136:LEU:HA	1:A:136:LEU:HD23	1.72	0.40
1:A:146:ARG:HA	1:A:146:ARG:HD2	1.68	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	348/368 (95%)	286 (82%)	48 (14%)	14 (4%)	3	17
1	B	329/368 (89%)	264 (80%)	46 (14%)	19 (6%)	2	9
All	All	677/736 (92%)	550 (81%)	94 (14%)	33 (5%)	2	13

All (33) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	81	LYS
1	A	82	GLY
1	A	189	VAL
1	A	352	LYS
1	B	10	PRO
1	B	79	LEU
1	B	100	VAL
1	B	189	VAL
1	A	56	THR
1	A	188	ALA
1	B	14	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	253	SER
1	B	315	SER
1	B	356	VAL
1	B	151	ARG
1	B	255	GLU
1	B	16	THR
1	B	207	VAL
1	B	258	ARG
1	A	38	LYS
1	A	83	ALA
1	A	263	ALA
1	B	221	ASN
1	B	248	GLU
1	B	262	ALA
1	B	312	GLU
1	B	156	ALA
1	A	111	PRO
1	A	86	GLY
1	A	130	VAL
1	A	241	VAL
1	A	222	PRO
1	B	130	VAL

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	277/289 (96%)	246 (89%)	31 (11%)	7	25
1	B	266/289 (92%)	230 (86%)	36 (14%)	4	17
All	All	543/578 (94%)	476 (88%)	67 (12%)	5	21

All (67) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	9	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	12	VAL
1	A	42	VAL
1	A	44	PRO
1	A	45	LEU
1	A	46	GLU
1	A	84	HIS
1	A	97	ILE
1	A	108	ARG
1	A	112	ASP
1	A	113	PRO
1	A	146	ARG
1	A	151	ARG
1	A	152	LYS
1	A	212	GLU
1	A	214	ASP
1	A	217	ASP
1	A	230	LYS
1	A	244	ARG
1	A	268	GLU
1	A	273	ARG
1	A	274	LEU
1	A	286	THR
1	A	287	PHE
1	A	288	PHE
1	A	299	THR
1	A	302	ARG
1	A	319	ARG
1	A	340	ARG
1	A	349	LEU
1	A	367	ASN
1	B	10	PRO
1	B	12	VAL
1	B	19	ASN
1	B	21	LEU
1	B	25	ASN
1	B	63	VAL
1	B	80	VAL
1	B	92	GLN
1	B	110	PHE
1	B	125	LEU
1	B	127	ASP
1	B	146	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	150	LEU
1	B	155	ARG
1	B	158	ARG
1	B	163	LEU
1	B	182	THR
1	B	217	ASP
1	B	242	SER
1	B	244	ARG
1	B	249	LEU
1	B	251	GLU
1	B	258	ARG
1	B	259	GLU
1	B	264	TYR
1	B	273	ARG
1	B	279	TYR
1	B	287	PHE
1	B	293	LYS
1	B	294	GLU
1	B	295	VAL
1	B	316	ASP
1	B	317	MET
1	B	340	ARG
1	B	352	LYS
1	B	364	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	92	GLN
1	A	357	GLN
1	A	367	ASN
1	B	11	ASN
1	B	19	ASN
1	B	54	GLN

5.3.3 RNA ⓘ

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 [i](#)

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

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å ²)	Q<0.9
1	A	354/368 (96%)	-0.59	0	100 100	14, 49, 90, 119	1 (0%)
1	B	337/368 (91%)	-0.31	5 (1%)	74 55	16, 65, 108, 145	1 (0%)
All	All	691/736 (93%)	-0.45	5 (0%)	87 74	14, 56, 100, 145	2 (0%)

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	159	GLU	2.9
1	B	158	ARG	2.7
1	B	156	ALA	2.4
1	B	157	ASP	2.2
1	B	110	PHE	2.0

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.