



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 07:25 AM GMT

PDB ID : 3AQL  
Title : Structure of bacterial protein (apo form II)  
Authors : Toh, Y.; Takeshita, D.; Tomita , K.  
Deposited on : 2010-11-09  
Resolution : 3.00 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto: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.

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

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

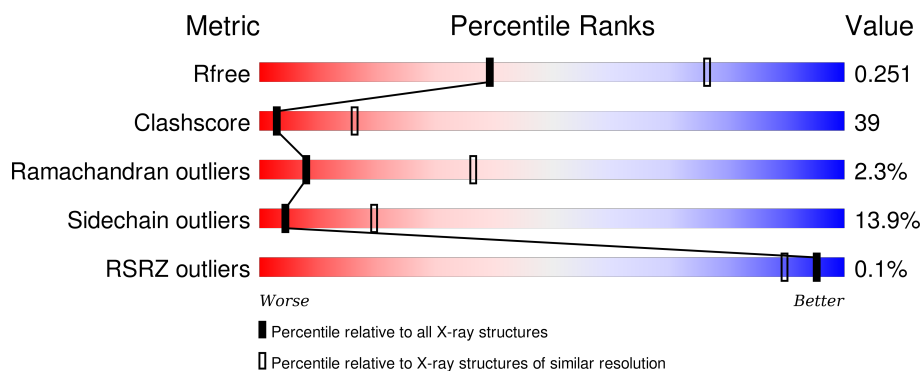
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.00 Å.

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



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

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	415	<div> <div style="width: 37%; background-color: red;"></div> <div style="width: 48%; background-color: yellow;"></div> <div style="width: 8%; background-color: orange;"></div> <div style="width: 7%; background-color: grey;"></div> </div> <div> <div style="width: 37%; background-color: green;"></div> <div style="width: 48%; background-color: yellow;"></div> <div style="width: 8%; background-color: orange;"></div> <div style="width: 7%; background-color: grey;"></div> </div>
1	B	415	<div> <div style="width: 38%; background-color: red;"></div> <div style="width: 46%; background-color: yellow;"></div> <div style="width: 10%; background-color: orange;"></div> <div style="width: 7%; background-color: grey;"></div> </div> <div> <div style="width: 38%; background-color: green;"></div> <div style="width: 46%; background-color: yellow;"></div> <div style="width: 10%; background-color: orange;"></div> <div style="width: 7%; background-color: grey;"></div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6342 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 Poly(A) polymerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	388	Total	C	N	O	S	0	0	0
			3164	2022	568	560	14			
1	B	388	Total	C	N	O	S	0	0	0
			3164	2022	568	560	14			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	234	HIS	ARG	ENGINEERED MUTATION	UNP C9QS13
B	234	HIS	ARG	ENGINEERED MUTATION	UNP C9QS13

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Mg	0	0
			1	1		
2	A	1	Total	Mg	0	0
			1	1		

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).

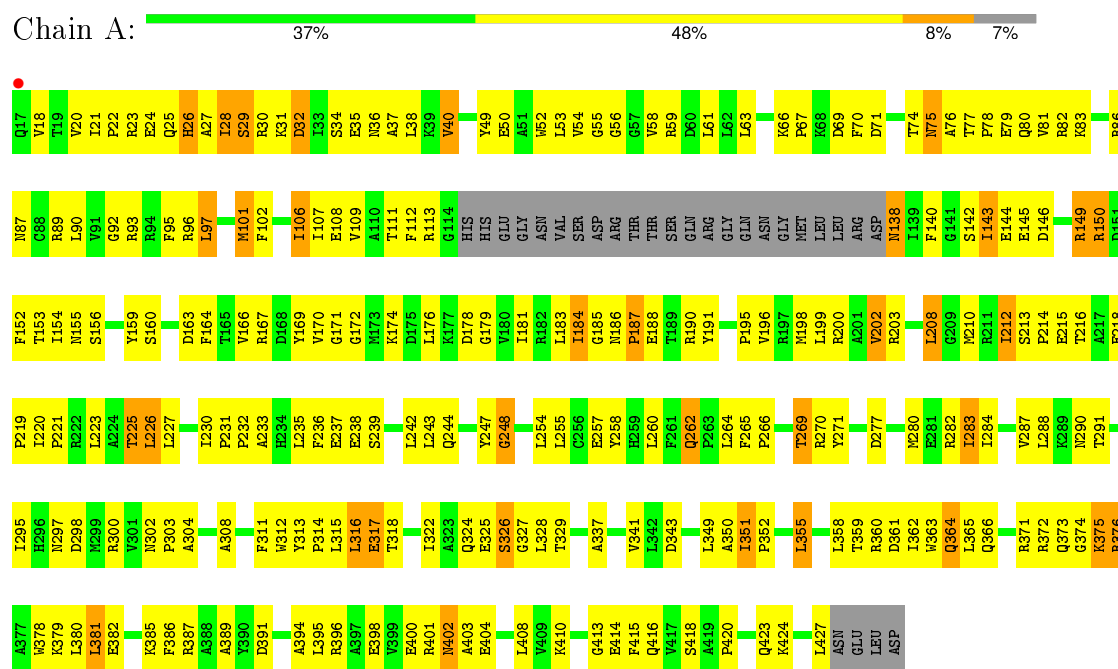


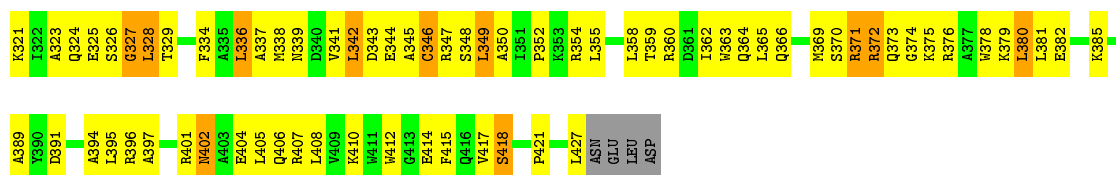
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		

### 3 Residue-property plots

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

#### • Molecule 1: Poly(A) polymerase





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 4 <sub>2</sub> 2 <sub>1</sub> 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	133.01Å 133.01Å 176.84Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.55 – 3.00 49.36 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.1 (29.55-3.00) 98.6 (49.36-2.80)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.08	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.73 (at 2.81Å)	Xtriage
Refinement program	CNS 1.3	Depositor
R, $R_{free}$	0.237 , 0.251 0.237 , 0.251	Depositor DCC
$R_{free}$ test set	1590 reflections (4.95%)	DCC
Wilson B-factor (Å <sup>2</sup> )	69.7	Xtriage
Anisotropy	0.435	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 43.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.45$ , $\langle L^2 \rangle = 0.27$	Xtriage
Outliers	0 of 39381 reflections	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	6342	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	94.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.94% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: GOL, MG

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	0.47	0/3234	0.67	1/4371 (0.0%)
1	B	0.46	0/3234	0.65	1/4371 (0.0%)
All	All	0.46	0/6468	0.66	2/8742 (0.0%)

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
1	B	0	2
All	All	0	3

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	29	SER	N-CA-C	-8.07	89.22	111.00
1	B	93	ARG	N-CA-C	5.53	125.92	111.00

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	36	ASN	Peptide
1	B	36	ASN	Peptide
1	B	92	GLY	Peptide



## 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	3164	0	3197	259	0
1	B	3164	0	3197	248	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	6	0	8	1	0
3	B	6	0	8	0	0
All	All	6342	0	6410	500	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 39.

All (500) 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:93:ARG:CG	1:B:94:ARG:H	1.22	1.42
1:A:183:LEU:HD23	1:A:184:ILE:N	1.48	1.28
1:A:372:ARG:HA	1:A:372:ARG:NH1	1.52	1.22
1:B:93:ARG:CG	1:B:94:ARG:N	1.93	1.16
1:B:93:ARG:HG2	1:B:94:ARG:N	1.54	1.13
1:A:97:LEU:HD21	1:A:108:GLU:HG2	1.14	1.11
1:A:97:LEU:CD2	1:A:108:GLU:HG2	1.81	1.10
1:B:84:LEU:O	1:B:84:LEU:HD12	1.52	1.09
1:A:184:ILE:HG22	1:A:190:ARG:HH12	1.08	1.09
1:B:184:ILE:HG22	1:B:190:ARG:HH12	0.99	1.08
1:B:374:GLY:HA2	1:B:427:LEU:HD22	1.28	1.08
1:B:28:ILE:HG13	1:B:29:SER:H	0.93	1.08
1:A:381:LEU:HD23	1:A:415:PHE:CE2	1.90	1.06
1:B:93:ARG:HG3	1:B:94:ARG:H	0.90	1.05
1:B:28:ILE:CG1	1:B:29:SER:H	1.68	1.04
1:A:372:ARG:HH11	1:A:372:ARG:HA	0.92	1.04
1:B:183:LEU:HD23	1:B:184:ILE:H	1.13	1.04
1:B:28:ILE:HG13	1:B:29:SER:N	1.63	1.03
1:A:191:TYR:CD1	1:A:198:MET:HG3	1.94	1.02
1:B:184:ILE:HG22	1:B:190:ARG:NH1	1.72	1.02
1:B:184:ILE:CG2	1:B:190:ARG:HH12	1.75	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:402:ASN:HD22	1:A:403:ALA:N	1.61	0.99
1:A:183:LEU:HD23	1:A:184:ILE:H	0.82	0.97
1:B:28:ILE:HB	1:B:30:ARG:HG3	1.46	0.96
1:A:191:TYR:HD1	1:A:198:MET:HG3	1.30	0.96
1:A:212:ILE:HD12	1:A:212:ILE:H	1.27	0.95
1:B:95:PHE:O	1:B:96:ARG:HG2	1.66	0.94
1:A:183:LEU:CD2	1:A:184:ILE:H	1.79	0.92
1:B:192:ARG:HH11	1:B:192:ARG:HG2	1.35	0.91
1:A:77:THR:H	1:A:80:GLN:HE21	1.11	0.91
1:B:372:ARG:HE	1:B:407:ARG:HH21	1.16	0.90
1:A:183:LEU:CD2	1:A:184:ILE:N	2.35	0.90
1:A:150:ARG:HG3	1:A:150:ARG:HH21	1.36	0.90
1:A:21:ILE:HG23	1:A:166:VAL:HG13	1.55	0.86
1:B:302:ASN:HD22	1:B:303:PRO:HD2	1.41	0.86
1:A:280:MET:HE2	1:A:314:PRO:HD3	1.57	0.86
1:A:34:SER:HB3	1:A:38:LEU:HD21	1.58	0.86
1:B:280:MET:HE2	1:B:314:PRO:HD3	1.58	0.85
1:B:28:ILE:HB	1:B:30:ARG:CG	2.07	0.85
1:A:184:ILE:HG22	1:A:190:ARG:NH1	1.91	0.84
1:B:352:PRO:HG2	1:B:355:LEU:HD23	1.60	0.83
1:A:219:PRO:O	1:A:223:LEU:HD12	1.78	0.83
1:B:28:ILE:HD12	1:B:30:ARG:CD	2.10	0.82
1:B:170:VAL:HG12	1:B:171:GLY:H	1.44	0.82
1:B:304:ALA:HB2	1:B:355:LEU:HD12	1.58	0.82
1:A:244:GLN:HE22	1:A:303:PRO:HA	1.45	0.82
1:A:34:SER:CB	1:A:38:LEU:HD21	2.10	0.81
1:B:93:ARG:HG3	1:B:94:ARG:N	1.75	0.81
1:A:381:LEU:HD23	1:A:415:PHE:HE2	1.45	0.81
1:A:160:SER:HB3	1:A:163:ASP:OD1	1.82	0.79
1:B:183:LEU:HD23	1:B:184:ILE:N	1.94	0.79
1:A:372:ARG:CA	1:A:372:ARG:NH1	2.40	0.79
1:B:244:GLN:HE22	1:B:303:PRO:HA	1.48	0.79
1:B:170:VAL:HG12	1:B:171:GLY:N	1.98	0.78
1:A:77:THR:H	1:A:80:GLN:NE2	1.82	0.77
1:B:50:GLU:HG2	1:B:52:TRP:HE1	1.50	0.77
1:A:402:ASN:HD22	1:A:402:ASN:C	1.87	0.77
1:B:184:ILE:CG2	1:B:185:GLY:N	2.48	0.77
1:A:308:ALA:HB2	1:A:359:THR:HG23	1.67	0.76
1:B:35:GLU:O	1:B:36:ASN:OD1	2.02	0.75
1:B:244:GLN:NE2	1:B:303:PRO:HA	2.02	0.75
1:B:184:ILE:HG22	1:B:185:GLY:N	2.00	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:35:GLU:HA	1:B:35:GLU:OE1	1.86	0.75
1:A:150:ARG:HA	3:A:602:GOL:H31	1.68	0.75
1:B:232:PRO:HB2	1:B:350:ALA:HB2	1.68	0.74
1:A:170:VAL:HG12	1:A:171:GLY:H	1.52	0.74
1:A:86:ARG:HG3	1:A:87:ASN:HD22	1.53	0.74
1:B:371:ARG:O	1:B:371:ARG:HG2	1.87	0.73
1:A:97:LEU:HD21	1:A:108:GLU:CG	2.07	0.73
1:A:96:ARG:O	1:A:97:LEU:O	2.06	0.73
1:A:77:THR:O	1:A:81:VAL:HG23	1.89	0.73
1:A:181:ILE:CD1	1:A:210:MET:HG3	2.19	0.72
1:A:381:LEU:HD23	1:A:415:PHE:CD2	2.24	0.72
1:A:235:LEU:HD13	1:A:264:LEU:HD23	1.71	0.72
1:B:218:GLU:HB3	1:B:219:PRO:HD3	1.71	0.72
1:B:28:ILE:HB	1:B:30:ARG:CD	2.20	0.72
1:A:212:ILE:H	1:A:212:ILE:CD1	2.02	0.71
1:A:26:HIS:O	1:A:28:ILE:N	2.24	0.71
1:A:77:THR:N	1:A:80:GLN:HE21	1.87	0.71
1:B:183:LEU:HB2	1:B:216:THR:HG23	1.72	0.70
1:B:186:ASN:ND2	1:B:188:GLU:HB3	2.07	0.70
1:B:21:ILE:HB	1:B:166:VAL:HG13	1.74	0.70
1:A:96:ARG:O	1:A:97:LEU:C	2.28	0.70
1:B:144:GLU:HA	1:B:169:TYR:CD1	2.26	0.70
1:A:232:PRO:HB2	1:A:350:ALA:HB2	1.74	0.70
1:B:28:ILE:HD12	1:B:30:ARG:HD2	1.72	0.70
1:A:230:ILE:HG23	1:A:231:PRO:HD2	1.73	0.69
1:A:223:LEU:O	1:A:226:LEU:HB2	1.91	0.69
1:A:138:ASN:HD22	1:A:138:ASN:N	1.90	0.69
1:B:372:ARG:NE	1:B:407:ARG:HH21	1.89	0.69
1:B:151:ASP:OD2	1:B:200:ARG:NH1	2.26	0.69
1:A:28:ILE:HD13	1:A:30:ARG:HG2	1.74	0.69
1:B:374:GLY:CA	1:B:427:LEU:HD22	2.17	0.69
1:B:28:ILE:HD12	1:B:30:ARG:HD3	1.73	0.68
1:A:244:GLN:NE2	1:A:303:PRO:HA	2.07	0.68
1:A:89:ARG:HD2	1:A:101:MET:CE	2.22	0.68
1:B:184:ILE:HG22	1:B:185:GLY:H	1.57	0.68
1:A:184:ILE:CG2	1:A:185:GLY:N	2.57	0.68
1:B:186:ASN:HD21	1:B:188:GLU:HB3	1.57	0.68
1:B:202:VAL:HG13	1:B:254:LEU:HB3	1.74	0.68
1:B:103:GLY:O	1:B:105:GLU:N	2.26	0.68
1:A:378:TRP:HB3	1:B:299:MET:SD	2.33	0.68
1:A:391:ASP:O	1:A:394:ALA:HB3	1.94	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:92:GLY:C	1:A:93:ARG:HG3	2.15	0.67
1:A:150:ARG:CG	1:A:150:ARG:HH21	2.07	0.67
1:A:78:PRO:O	1:A:82:ARG:HG3	1.95	0.66
1:A:75:ASN:C	1:A:75:ASN:HD22	1.98	0.66
1:A:280:MET:HE2	1:A:314:PRO:CD	2.26	0.66
1:A:89:ARG:HD2	1:A:101:MET:HE2	1.78	0.66
1:A:106:ILE:H	1:A:106:ILE:HD12	1.59	0.66
1:A:27:ALA:O	1:A:28:ILE:C	2.32	0.66
1:A:218:GLU:HB3	1:A:219:PRO:HD3	1.76	0.66
1:B:342:LEU:O	1:B:346:CYS:HB2	1.96	0.66
1:A:300:ARG:HG2	1:B:382:GLU:OE2	1.96	0.66
1:A:402:ASN:HD21	1:A:404:GLU:HB3	1.61	0.65
1:A:358:LEU:O	1:A:362:ILE:HG13	1.96	0.65
1:B:312:TRP:CE2	1:B:396:ARG:HD2	2.31	0.65
1:B:374:GLY:O	1:B:376:ARG:N	2.28	0.65
1:B:349:LEU:H	1:B:349:LEU:HD22	1.60	0.65
1:A:79:GLU:HG3	1:A:82:ARG:HH21	1.61	0.65
1:A:59:ARG:HH11	1:A:155:ASN:ND2	1.95	0.65
1:B:232:PRO:HB3	1:B:348:SER:O	1.96	0.65
1:A:271:TYR:HE1	1:A:317:GLU:HG2	1.62	0.65
1:B:203:ARG:HB2	1:B:242:LEU:HD23	1.79	0.65
1:B:281:GLU:O	1:B:285:GLU:HG3	1.97	0.64
1:B:315:LEU:HA	1:B:341:VAL:HG21	1.79	0.64
1:A:52:TRP:CZ3	1:A:160:SER:HB2	2.32	0.64
1:B:414:GLU:O	1:B:418:SER:HB3	1.98	0.64
1:B:192:ARG:HH11	1:B:192:ARG:CG	2.11	0.63
1:A:106:ILE:O	1:A:107:ILE:HD13	1.98	0.63
1:B:153:THR:HG21	1:B:175:ASP:OD2	1.98	0.63
1:A:149:ARG:HH11	1:A:149:ARG:HB3	1.62	0.63
1:B:270:ARG:HD2	1:B:271:TYR:CE2	2.34	0.63
1:B:34:SER:CB	1:B:38:LEU:HD21	2.29	0.63
1:A:86:ARG:HG3	1:A:87:ASN:ND2	2.12	0.63
1:A:21:ILE:HG13	1:A:25:GLN:HG3	1.81	0.63
1:A:174:LYS:HE2	1:A:178:ASP:OD2	1.98	0.63
1:B:23:ARG:HA	1:B:26:HIS:CE1	2.34	0.62
1:B:371:ARG:HG3	1:B:373:GLN:NE2	2.15	0.62
1:B:204:PHE:O	1:B:208:LEU:HD12	1.99	0.62
1:B:374:GLY:HA2	1:B:427:LEU:CD2	2.19	0.62
1:B:170:VAL:CG1	1:B:171:GLY:H	2.12	0.62
1:A:101:MET:O	1:A:102:PHE:HD1	1.82	0.62
1:B:72:VAL:CG2	1:B:109:VAL:HG22	2.30	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:391:ASP:O	1:B:394:ALA:HB3	1.99	0.62
1:A:212:ILE:HD13	1:A:258:TYR:OH	1.99	0.62
1:A:179:GLY:O	1:A:210:MET:HB2	2.00	0.62
1:A:18:VAL:HG22	1:A:18:VAL:O	1.99	0.62
1:B:244:GLN:HE21	1:B:303:PRO:HB3	1.65	0.61
1:B:402:ASN:ND2	1:B:402:ASN:C	2.54	0.61
1:B:302:ASN:OD1	1:B:385:LYS:NZ	2.28	0.61
1:A:203:ARG:HB2	1:A:242:LEU:CD2	2.29	0.61
1:B:370:SER:HA	1:B:408:LEU:HD11	1.82	0.61
1:A:113:ARG:HG2	1:A:146:ASP:OD1	1.99	0.61
1:A:26:HIS:CD2	1:A:28:ILE:HA	2.36	0.61
1:A:101:MET:C	1:A:102:PHE:HD1	2.04	0.61
1:B:103:GLY:C	1:B:105:GLU:H	2.02	0.60
1:A:28:ILE:CD1	1:A:30:ARG:HG2	2.31	0.60
1:A:312:TRP:NE1	1:A:396:ARG:HD2	2.16	0.60
1:B:308:ALA:HB2	1:B:359:THR:HG23	1.82	0.60
1:A:106:ILE:N	1:A:106:ILE:HD12	2.17	0.60
1:A:202:VAL:CG2	1:A:254:LEU:HB3	2.32	0.60
1:A:184:ILE:HG22	1:A:185:GLY:N	2.17	0.59
1:A:184:ILE:HG22	1:A:185:GLY:H	1.67	0.59
1:A:187:PRO:HB3	1:A:191:TYR:HE2	1.67	0.59
1:B:372:ARG:HB2	1:B:372:ARG:HH11	1.66	0.59
1:B:33:ILE:HG22	1:B:33:ILE:O	2.02	0.59
1:A:381:LEU:CD2	1:A:415:PHE:CD2	2.85	0.59
1:B:34:SER:HB2	1:B:38:LEU:HD21	1.85	0.59
1:B:397:ALA:HB2	1:B:405:LEU:HB3	1.85	0.59
1:B:27:ALA:O	1:B:28:ILE:C	2.41	0.59
1:A:262:GLN:HB2	1:A:269:THR:HG21	1.85	0.58
1:B:323:ALA:O	1:B:327:GLY:HA2	2.02	0.58
1:A:184:ILE:CG2	1:A:190:ARG:HH12	1.98	0.58
1:A:77:THR:HB	1:A:80:GLN:H	1.67	0.58
1:B:179:GLY:CA	1:B:210:MET:HG2	2.34	0.58
1:B:326:SER:O	1:B:328:LEU:HD22	2.04	0.58
1:A:29:SER:OG	1:A:159:TYR:CE1	2.57	0.58
1:B:306:LEU:O	1:B:310:MET:HG3	2.04	0.58
1:A:223:LEU:HB3	1:A:226:LEU:HD12	1.85	0.58
1:B:95:PHE:O	1:B:96:ARG:CG	2.47	0.58
1:A:235:LEU:O	1:A:239:SER:HB3	2.03	0.58
1:A:418:SER:O	1:A:423:GLN:NE2	2.35	0.58
1:B:73:THR:HA	1:B:110:ALA:O	2.03	0.58
1:B:183:LEU:CD2	1:B:184:ILE:H	2.03	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:223:LEU:O	1:B:226:LEU:HB2	2.03	0.57
1:B:30:ARG:NE	1:B:33:ILE:HD11	2.20	0.57
1:A:28:ILE:HG23	1:A:28:ILE:O	2.05	0.57
1:B:280:MET:CE	1:B:314:PRO:HD3	2.32	0.57
1:B:202:VAL:O	1:B:205:ALA:HB3	2.04	0.57
1:A:326:SER:O	1:A:328:LEU:HD12	2.05	0.57
1:A:208:LEU:HD13	1:A:210:MET:CE	2.35	0.57
1:B:202:VAL:CG1	1:B:254:LEU:HB3	2.34	0.57
1:A:202:VAL:HG22	1:A:254:LEU:HB3	1.87	0.57
1:A:420:PRO:O	1:A:424:LYS:HB2	2.05	0.57
1:B:402:ASN:C	1:B:402:ASN:HD22	2.07	0.56
1:A:402:ASN:ND2	1:A:404:GLU:N	2.54	0.56
1:B:352:PRO:CG	1:B:355:LEU:HD23	2.33	0.56
1:A:235:LEU:HD13	1:A:264:LEU:CD2	2.35	0.56
1:B:219:PRO:O	1:B:223:LEU:HD12	2.04	0.56
1:B:20:VAL:HG23	1:B:167:ARG:HD3	1.87	0.56
1:A:40:VAL:HG11	1:A:107:ILE:HG21	1.86	0.56
1:B:249:TYR:CZ	1:B:253:LYS:HE3	2.40	0.56
1:B:167:ARG:NH1	1:B:169:TYR:OH	2.39	0.56
1:A:290:ASN:HD21	1:B:421:PRO:HG3	1.71	0.56
1:A:312:TRP:CE2	1:A:396:ARG:HD2	2.40	0.56
1:B:35:GLU:CA	1:B:35:GLU:OE1	2.53	0.56
1:B:170:VAL:CG1	1:B:171:GLY:N	2.67	0.56
1:A:37:ALA:O	1:A:40:VAL:HG13	2.06	0.56
1:A:238:GLU:O	1:A:242:LEU:HG	2.05	0.56
1:B:179:GLY:C	1:B:210:MET:HG2	2.26	0.56
1:B:365:LEU:O	1:B:369:MET:HG3	2.07	0.55
1:A:150:ARG:NH2	1:A:150:ARG:CG	2.67	0.55
1:B:402:ASN:ND2	1:B:404:GLU:H	2.05	0.55
1:A:203:ARG:HB2	1:A:242:LEU:HD23	1.87	0.55
1:A:410:LYS:O	1:A:414:GLU:HG3	2.07	0.55
1:B:153:THR:HG22	1:B:170:VAL:HG12	1.89	0.55
1:A:181:ILE:HD11	1:A:210:MET:HG3	1.89	0.55
1:B:243:LEU:HA	1:B:248:GLY:HA2	1.88	0.55
1:B:302:ASN:HD22	1:B:303:PRO:CD	2.14	0.55
1:B:153:THR:HG22	1:B:170:VAL:CG1	2.37	0.55
1:B:260:LEU:O	1:B:263:PRO:HD2	2.08	0.54
1:A:95:PHE:CD1	1:A:96:ARG:HG3	2.42	0.54
1:A:413:GLY:O	1:B:417:VAL:HG11	2.07	0.54
1:B:302:ASN:ND2	1:B:303:PRO:HD2	2.17	0.54
1:A:297:ASN:ND2	1:B:378:TRP:CE2	2.73	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:195:PRO:O	1:A:198:MET:HB2	2.07	0.54
1:B:185:GLY:H	1:B:190:ARG:NH1	2.05	0.54
1:A:304:ALA:HB2	1:A:355:LEU:HD12	1.88	0.54
1:A:402:ASN:C	1:A:402:ASN:ND2	2.61	0.54
1:B:152:PHE:CD2	1:B:152:PHE:N	2.75	0.54
1:B:52:TRP:CZ3	1:B:160:SER:HB2	2.43	0.53
1:B:278:SER:HB2	1:B:279:PRO:CD	2.38	0.53
1:B:339:ASN:O	1:B:343:ASP:HB2	2.08	0.53
1:A:34:SER:HB2	1:A:38:LEU:HD21	1.88	0.53
1:B:337:ALA:O	1:B:341:VAL:HG23	2.08	0.53
1:B:192:ARG:HG2	1:B:192:ARG:NH1	2.12	0.53
1:A:164:PHE:N	1:A:164:PHE:CD1	2.77	0.53
1:A:375:LYS:HD2	1:A:375:LYS:H	1.74	0.53
1:A:408:LEU:N	1:A:408:LEU:HD23	2.24	0.53
1:B:164:PHE:CD1	1:B:164:PHE:N	2.77	0.53
1:A:337:ALA:O	1:A:341:VAL:HG23	2.09	0.53
1:A:365:LEU:HD12	1:A:389:ALA:HB2	1.90	0.52
1:B:158:TYR:O	1:B:166:VAL:HA	2.09	0.52
1:B:372:ARG:HE	1:B:407:ARG:NH2	1.95	0.52
1:B:325:GLU:O	1:B:326:SER:C	2.48	0.52
1:B:26:HIS:NE2	1:B:29:SER:HB3	2.24	0.52
1:B:144:GLU:HA	1:B:169:TYR:CE1	2.44	0.52
1:B:37:ALA:HA	1:B:40:VAL:HG23	1.92	0.52
1:B:94:ARG:O	1:B:96:ARG:O	2.28	0.52
1:B:53:LEU:O	1:B:58:VAL:HG11	2.09	0.52
1:A:318:THR:O	1:A:322:ILE:HG13	2.09	0.52
1:A:400:GLU:O	1:A:401:ARG:C	2.45	0.52
1:A:183:LEU:HB2	1:A:216:THR:HG23	1.91	0.52
1:B:280:MET:HE2	1:B:314:PRO:CD	2.34	0.52
1:A:101:MET:HG2	1:A:102:PHE:N	2.23	0.52
1:A:280:MET:CE	1:A:314:PRO:HG3	2.39	0.51
1:A:87:ASN:HD22	1:A:87:ASN:N	2.07	0.51
1:B:21:ILE:HB	1:B:166:VAL:CG1	2.40	0.51
1:B:34:SER:HB3	1:B:38:LEU:HD21	1.92	0.51
1:A:183:LEU:HD13	1:A:187:PRO:HA	1.92	0.51
1:A:191:TYR:CD1	1:A:198:MET:CG	2.82	0.51
1:A:59:ARG:O	1:A:63:LEU:HD12	2.11	0.51
1:B:37:ALA:HB2	1:B:107:ILE:HG12	1.93	0.51
1:B:345:ALA:C	1:B:347:ARG:H	2.14	0.51
1:A:83:LYS:HG2	1:A:86:ARG:HH21	1.75	0.51
1:B:154:ILE:HG12	1:B:155:ASN:N	2.24	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:26:HIS:O	1:B:26:HIS:CD2	2.63	0.51
1:A:223:LEU:HD23	1:A:226:LEU:CD1	2.40	0.51
1:B:225:THR:O	1:B:228:ASN:ND2	2.44	0.50
1:B:28:ILE:HB	1:B:30:ARG:HD2	1.93	0.50
1:A:49:TYR:HB3	1:A:75:ASN:HD21	1.76	0.50
1:B:401:ARG:HG3	1:B:401:ARG:HH21	1.75	0.50
1:B:36:ASN:O	1:B:102:PHE:CZ	2.65	0.50
1:B:278:SER:O	1:B:282:ARG:CD	2.59	0.50
1:A:291:THR:O	1:A:295:ILE:HG12	2.12	0.50
1:A:220:ILE:HB	1:A:221:PRO:HD3	1.94	0.50
1:A:26:HIS:C	1:A:26:HIS:CD2	2.85	0.50
1:B:278:SER:O	1:B:282:ARG:HD2	2.12	0.50
1:A:22:PRO:HD2	1:A:25:GLN:CD	2.32	0.50
1:B:96:ARG:HG3	1:B:97:LEU:N	2.27	0.49
1:B:164:PHE:N	1:B:164:PHE:HD1	2.10	0.49
1:A:302:ASN:ND2	1:A:385:LYS:NZ	2.60	0.49
1:B:328:LEU:N	1:B:328:LEU:HD23	2.27	0.49
1:B:224:ALA:O	1:B:226:LEU:N	2.45	0.49
1:A:283:ILE:CG2	1:A:284:ILE:N	2.75	0.49
1:A:170:VAL:HG12	1:A:171:GLY:N	2.24	0.49
1:A:202:VAL:HG11	1:A:255:LEU:CD2	2.42	0.49
1:A:402:ASN:ND2	1:A:403:ALA:N	2.44	0.49
1:A:223:LEU:HD23	1:A:226:LEU:HD12	1.93	0.49
1:A:35:GLU:O	1:A:37:ALA:N	2.41	0.49
1:B:23:ARG:HB3	1:B:164:PHE:HB3	1.95	0.49
1:B:30:ARG:HE	1:B:33:ILE:HG13	1.78	0.49
1:A:199:LEU:O	1:A:200:ARG:C	2.49	0.49
1:B:41:MET:CE	1:B:53:LEU:HD13	2.43	0.49
1:A:381:LEU:CD2	1:A:415:PHE:CE2	2.81	0.49
1:A:150:ARG:NH2	1:A:150:ARG:HG3	2.14	0.49
1:B:139:ILE:HD13	1:B:139:ILE:N	2.28	0.49
1:A:373:GLN:HG2	1:A:376:ARG:HG3	1.95	0.49
1:B:93:ARG:HG2	1:B:94:ARG:CA	2.38	0.49
1:B:30:ARG:HE	1:B:33:ILE:CG1	2.25	0.49
1:A:372:ARG:CZ	1:A:372:ARG:HA	2.36	0.49
1:A:24:GLU:HG2	1:A:25:GLN:N	2.28	0.48
1:B:186:ASN:O	1:B:187:PRO:C	2.51	0.48
1:A:53:LEU:HD12	1:A:53:LEU:HA	1.62	0.48
1:A:21:ILE:HG12	1:A:26:HIS:HB3	1.96	0.48
1:A:391:ASP:O	1:A:395:LEU:HD13	2.12	0.48
1:B:244:GLN:NE2	1:B:303:PRO:CA	2.74	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:371:ARG:O	1:A:373:GLN:N	2.44	0.48
1:B:154:ILE:HD12	1:B:210:MET:CE	2.42	0.48
1:B:76:ALA:O	1:B:111:THR:HG23	2.14	0.48
1:B:84:LEU:O	1:B:84:LEU:CD1	2.43	0.48
1:B:257:GLU:O	1:B:257:GLU:HG2	2.14	0.48
1:A:31:LYS:O	1:A:31:LYS:HG2	2.11	0.48
1:B:261:PHE:CE2	1:B:265:PHE:HB2	2.49	0.48
1:A:152:PHE:CD2	1:A:152:PHE:N	2.82	0.48
1:B:405:LEU:C	1:B:407:ARG:N	2.66	0.48
1:A:208:LEU:HD13	1:A:210:MET:HE1	1.95	0.48
1:B:280:MET:HA	1:B:313:TYR:HD2	1.79	0.48
1:B:28:ILE:CD1	1:B:30:ARG:HD2	2.43	0.48
1:B:215:GLU:H	1:B:215:GLU:CD	2.17	0.48
1:B:163:ASP:O	1:B:165:THR:HG23	2.13	0.47
1:B:326:SER:O	1:B:328:LEU:CD2	2.61	0.47
1:A:77:THR:HG22	1:A:79:GLU:H	1.79	0.47
1:A:265:PHE:O	1:A:266:PRO:C	2.51	0.47
1:A:52:TRP:CE3	1:A:160:SER:HB2	2.50	0.47
1:A:230:ILE:CG2	1:A:231:PRO:HD2	2.44	0.47
1:A:109:VAL:HG12	1:A:109:VAL:O	2.14	0.47
1:B:376:ARG:O	1:B:379:LYS:HB3	2.14	0.47
1:B:28:ILE:CG1	1:B:29:SER:N	2.35	0.47
1:B:410:LYS:O	1:B:414:GLU:HG3	2.14	0.47
1:A:243:LEU:HA	1:A:248:GLY:HA2	1.97	0.47
1:A:280:MET:HE2	1:A:314:PRO:CG	2.44	0.47
1:B:154:ILE:HD12	1:B:210:MET:HE1	1.97	0.47
1:B:96:ARG:O	1:B:97:LEU:O	2.33	0.46
1:A:280:MET:CE	1:A:314:PRO:HD3	2.36	0.46
1:B:230:ILE:HG23	1:B:231:PRO:HD2	1.97	0.46
1:A:374:GLY:HA2	1:A:427:LEU:HD22	1.97	0.46
1:B:365:LEU:HD12	1:B:389:ALA:HB2	1.98	0.46
1:B:36:ASN:HD22	1:B:39:LYS:HG3	1.80	0.46
1:A:187:PRO:O	1:A:188:GLU:C	2.53	0.46
1:A:67:PRO:HG2	1:A:70:PHE:CZ	2.51	0.46
1:A:95:PHE:O	1:A:96:ARG:HB2	2.15	0.46
1:A:21:ILE:HA	1:A:22:PRO:HD3	1.46	0.46
1:A:280:MET:O	1:A:283:ILE:HG22	2.15	0.46
1:B:59:ARG:HH11	1:B:155:ASN:ND2	2.13	0.46
1:B:280:MET:HE1	1:B:314:PRO:HG3	1.98	0.46
1:A:181:ILE:N	1:A:181:ILE:HD12	2.30	0.46
1:A:190:ARG:NH1	1:A:190:ARG:HG3	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:402:ASN:HD21	1:A:404:GLU:N	2.13	0.46
1:A:302:ASN:HD21	1:A:385:LYS:NZ	2.14	0.46
1:A:20:VAL:O	1:A:20:VAL:HG13	2.14	0.46
1:A:360:ARG:O	1:A:364:GLN:HG2	2.16	0.46
1:A:195:PRO:HB2	1:A:230:ILE:HD11	1.98	0.45
1:B:352:PRO:HG2	1:B:355:LEU:CD2	2.40	0.45
1:B:305:PHE:O	1:B:306:LEU:C	2.54	0.45
1:A:280:MET:HA	1:A:313:TYR:CD2	2.51	0.45
1:B:360:ARG:O	1:B:364:GLN:HG2	2.17	0.45
1:B:291:THR:O	1:B:295:ILE:HG12	2.17	0.45
1:A:152:PHE:CD1	1:A:181:ILE:HG23	2.52	0.45
1:A:379:LYS:O	1:A:382:GLU:HB3	2.17	0.45
1:B:53:LEU:HD12	1:B:71:ASP:O	2.16	0.45
1:A:28:ILE:CG1	1:A:30:ARG:HG2	2.47	0.45
1:A:163:ASP:C	1:A:164:PHE:HD1	2.19	0.45
1:B:227:LEU:HD11	1:B:260:LEU:HD22	1.97	0.45
1:B:106:ILE:O	1:B:107:ILE:HD12	2.17	0.45
1:A:351:ILE:HA	1:A:352:PRO:HD3	1.76	0.45
1:B:192:ARG:NH1	1:B:192:ARG:CG	2.72	0.45
1:A:138:ASN:N	1:A:138:ASN:ND2	2.62	0.45
1:B:278:SER:CB	1:B:279:PRO:CD	2.94	0.45
1:B:283:ILE:CG2	1:B:284:ILE:N	2.78	0.45
1:B:27:ALA:O	1:B:29:SER:N	2.50	0.45
1:B:315:LEU:HD21	1:B:334:PHE:CZ	2.52	0.45
1:B:152:PHE:CD1	1:B:181:ILE:HG22	2.51	0.45
1:B:385:LYS:HD3	1:B:385:LYS:HA	1.51	0.45
1:A:380:LEU:C	1:A:382:GLU:N	2.69	0.45
1:B:191:TYR:CD1	1:B:198:MET:HG3	2.52	0.45
1:A:61:LEU:HD23	1:A:61:LEU:HA	1.62	0.45
1:B:349:LEU:HD22	1:B:349:LEU:N	2.31	0.45
1:A:144:GLU:HG3	1:A:169:TYR:CD2	2.52	0.45
1:B:380:LEU:HD22	1:B:412:TRP:CH2	2.52	0.45
1:A:23:ARG:HB2	1:A:164:PHE:HB3	1.98	0.44
1:B:338:MET:O	1:B:342:LEU:HB2	2.17	0.44
1:A:202:VAL:HG11	1:A:255:LEU:HD23	2.00	0.44
1:B:113:ARG:HD2	1:B:146:ASP:OD1	2.17	0.44
1:A:385:LYS:O	1:A:386:PHE:C	2.55	0.44
1:A:154:ILE:HG13	1:A:155:ASN:ND2	2.33	0.44
1:A:59:ARG:NH1	1:A:155:ASN:ND2	2.64	0.44
1:B:91:VAL:O	1:B:91:VAL:HG12	2.16	0.44
1:B:354:ARG:O	1:B:358:LEU:HD13	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:186:ASN:O	1:A:187:PRO:C	2.56	0.44
1:A:302:ASN:ND2	1:A:385:LYS:HZ2	2.15	0.44
1:B:312:TRP:CZ2	1:B:396:ARG:HD2	2.52	0.44
1:B:401:ARG:CG	1:B:401:ARG:HH21	2.30	0.44
1:A:142:SER:O	1:A:145:GLU:N	2.50	0.44
1:A:378:TRP:CZ3	1:A:423:GLN:OE1	2.71	0.44
1:A:257:GLU:O	1:A:257:GLU:HG2	2.18	0.44
1:A:225:THR:O	1:A:227:LEU:N	2.51	0.44
1:A:37:ALA:HB2	1:A:107:ILE:HG13	1.99	0.44
1:A:363:TRP:O	1:A:366:GLN:HB2	2.17	0.44
1:A:233:ALA:HA	1:A:350:ALA:HB3	2.00	0.43
1:A:358:LEU:HD23	1:A:385:LYS:CE	2.48	0.43
1:B:280:MET:CE	1:B:314:PRO:HG3	2.47	0.43
1:A:199:LEU:O	1:A:202:VAL:HG12	2.17	0.43
1:A:311:PHE:C	1:A:314:PRO:HD2	2.39	0.43
1:A:358:LEU:HD23	1:A:385:LYS:HE3	2.00	0.43
1:B:247:TYR:O	1:B:249:TYR:N	2.51	0.43
1:A:315:LEU:HA	1:A:341:VAL:HG21	2.00	0.43
1:B:362:ILE:O	1:B:366:GLN:HG2	2.18	0.43
1:B:66:LYS:HA	1:B:67:PRO:HD2	1.70	0.43
1:A:59:ARG:HG2	1:A:63:LEU:HD12	2.01	0.43
1:B:405:LEU:HA	1:B:405:LEU:HD23	1.74	0.43
1:B:142:SER:HB3	1:B:145:GLU:HG3	2.01	0.43
1:A:190:ARG:HH11	1:A:190:ARG:HG3	1.84	0.43
1:A:195:PRO:HA	1:A:198:MET:HE2	2.00	0.43
1:A:26:HIS:ND1	1:A:166:VAL:HG12	2.34	0.43
1:B:278:SER:HB2	1:B:279:PRO:HD2	1.99	0.43
1:A:74:THR:HG23	1:A:76:ALA:H	1.83	0.43
1:A:38:LEU:N	1:A:38:LEU:HD23	2.34	0.43
1:B:312:TRP:CE2	1:B:316:LEU:HD22	2.54	0.43
1:B:179:GLY:HA2	1:B:210:MET:HG2	2.01	0.42
1:A:20:VAL:HG23	1:A:167:ARG:HD3	2.00	0.42
1:B:50:GLU:HG2	1:B:52:TRP:NE1	2.27	0.42
1:B:295:ILE:HD11	1:B:301:VAL:HG11	2.01	0.42
1:A:89:ARG:HD2	1:A:101:MET:HE1	1.98	0.42
1:A:29:SER:O	1:A:29:SER:OG	2.37	0.42
1:A:381:LEU:HD21	1:A:416:GLN:HA	2.00	0.42
1:A:247:TYR:O	1:A:248:GLY:C	2.57	0.42
1:A:143:ILE:HG23	1:A:144:GLU:N	2.34	0.42
1:A:236:PHE:O	1:A:237:GLU:C	2.57	0.42
1:B:381:LEU:HD22	1:B:415:PHE:CE2	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:312:TRP:CE2	1:A:316:LEU:HD22	2.54	0.42
1:A:66:LYS:HA	1:A:67:PRO:HD2	1.90	0.42
1:B:395:LEU:O	1:B:396:ARG:C	2.58	0.42
1:B:38:LEU:H	1:B:38:LEU:HD23	1.83	0.42
1:B:336:LEU:HA	1:B:336:LEU:HD12	1.79	0.42
1:A:208:LEU:HD13	1:A:210:MET:HE2	2.01	0.42
1:B:199:LEU:HD23	1:B:199:LEU:HA	1.78	0.42
1:A:395:LEU:O	1:A:398:GLU:N	2.52	0.42
1:B:203:ARG:HB2	1:B:242:LEU:CD2	2.46	0.42
1:B:224:ALA:O	1:B:225:THR:C	2.56	0.42
1:A:74:THR:O	1:A:111:THR:HA	2.20	0.42
1:B:342:LEU:HA	1:B:342:LEU:HD12	1.77	0.42
1:B:26:HIS:O	1:B:27:ALA:C	2.58	0.41
1:B:144:GLU:HG3	1:B:169:TYR:CG	2.55	0.41
1:A:55:GLY:O	1:A:56:GLY:C	2.57	0.41
1:B:97:LEU:HD11	1:B:108:GLU:HG2	2.01	0.41
1:A:95:PHE:O	1:A:96:ARG:CB	2.68	0.41
1:A:163:ASP:OD1	1:A:163:ASP:N	2.53	0.41
1:B:202:VAL:CG1	1:B:254:LEU:CB	2.97	0.41
1:A:382:GLU:OE1	1:B:299:MET:HE3	2.19	0.41
1:A:385:LYS:HA	1:A:385:LYS:HD3	1.53	0.41
1:B:182:ARG:HG2	1:B:183:LEU:O	2.19	0.41
1:A:219:PRO:O	1:A:223:LEU:CD1	2.61	0.41
1:B:154:ILE:HG12	1:B:155:ASN:H	1.83	0.41
1:B:160:SER:HB3	1:B:163:ASP:OD1	2.20	0.41
1:B:255:LEU:HD23	1:B:255:LEU:HA	1.92	0.41
1:B:275:ASN:ND2	1:B:277:ASP:H	2.18	0.41
1:A:242:LEU:HD13	1:A:255:LEU:HD11	2.01	0.41
1:B:84:LEU:HG	1:B:85:PHE:CE2	2.56	0.41
1:A:30:ARG:O	1:A:32:ASP:N	2.54	0.41
1:A:283:ILE:HG22	1:A:284:ILE:N	2.36	0.41
1:A:106:ILE:C	1:A:107:ILE:HD13	2.41	0.41
1:A:361:ASP:O	1:A:365:LEU:HG	2.21	0.41
1:A:28:ILE:O	1:A:30:ARG:HG3	2.20	0.41
1:B:54:VAL:HG13	1:B:158:TYR:CD2	2.55	0.41
1:B:144:GLU:CA	1:B:169:TYR:CE1	3.03	0.41
1:B:227:LEU:O	1:B:230:ILE:HB	2.21	0.41
1:A:49:TYR:HB3	1:A:75:ASN:ND2	2.34	0.41
1:A:287:VAL:HG13	1:A:288:LEU:N	2.36	0.41
1:B:202:VAL:HG21	1:B:260:LEU:HD12	2.02	0.41
1:B:59:ARG:NE	1:B:208:LEU:HD21	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:195:PRO:O	1:B:198:MET:HB2	2.21	0.41
1:A:260:LEU:HA	1:A:260:LEU:HD23	1.85	0.41
1:A:184:ILE:HG23	1:A:185:GLY:N	2.36	0.41
1:A:196:VAL:C	1:A:198:MET:N	2.74	0.41
1:B:26:HIS:HE1	1:B:164:PHE:O	2.04	0.41
1:A:79:GLU:HA	1:A:82:ARG:HE	1.84	0.41
1:A:218:GLU:O	1:A:221:PRO:HD2	2.21	0.41
1:A:50:GLU:HG2	1:A:75:ASN:OD1	2.21	0.41
1:A:59:ARG:HD3	1:A:155:ASN:ND2	2.35	0.41
1:B:154:ILE:C	1:B:156:SER:H	2.23	0.41
1:A:324:GLN:HG2	1:A:325:GLU:N	2.36	0.41
1:B:183:LEU:CD2	1:B:184:ILE:N	2.75	0.41
1:A:37:ALA:CB	1:A:107:ILE:HG13	2.51	0.41
1:B:359:THR:O	1:B:360:ARG:C	2.59	0.41
1:A:77:THR:HG22	1:A:78:PRO:HD2	2.03	0.40
1:B:242:LEU:HD13	1:B:255:LEU:HD11	2.03	0.40
1:B:41:MET:HE2	1:B:53:LEU:HD13	2.02	0.40
1:A:400:GLU:O	1:A:402:ASN:N	2.54	0.40
1:A:30:ARG:HB3	1:A:32:ASP:OD1	2.22	0.40
1:B:342:LEU:HD22	1:B:363:TRP:HZ3	1.84	0.40
1:A:53:LEU:O	1:A:58:VAL:HG11	2.21	0.40
1:A:153:THR:HG22	1:A:170:VAL:CG1	2.51	0.40
1:B:144:GLU:HG3	1:B:169:TYR:CD1	2.56	0.40
1:A:75:ASN:HB3	1:A:112:PHE:CE1	2.56	0.40
1:A:270:ARG:HD2	1:A:271:TYR:CE2	2.56	0.40
1:B:321:LYS:O	1:B:325:GLU:HB3	2.21	0.40
1:A:297:ASN:ND2	1:B:378:TRP:NE1	2.69	0.40
1:B:235:LEU:HA	1:B:235:LEU:HD23	1.91	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	384/415 (92%)	329 (86%)	47 (12%)	8 (2%)	9	40
1	B	384/415 (92%)	335 (87%)	39 (10%)	10 (3%)	7	33
All	All	768/830 (92%)	664 (86%)	86 (11%)	18 (2%)	8	36

All (18) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	248	GLY
1	A	327	GLY
1	B	28	ILE
1	B	97	LEU
1	B	104	PRO
1	B	248	GLY
1	B	375	LYS
1	A	28	ILE
1	A	97	LEU
1	A	172	GLY
1	B	327	GLY
1	B	92	GLY
1	B	94	ARG
1	A	226	LEU
1	A	187	PRO
1	B	172	GLY
1	B	278	SER
1	A	214	PRO

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	334/358 (93%)	290 (87%)	44 (13%)	5	22
1	B	334/358 (93%)	285 (85%)	49 (15%)	4	18
All	All	668/716 (93%)	575 (86%)	93 (14%)	4	19

All (93) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	26	HIS
1	A	32	ASP
1	A	40	VAL
1	A	54	VAL
1	A	69	ASP
1	A	71	ASP
1	A	75	ASN
1	A	90	LEU
1	A	101	MET
1	A	106	ILE
1	A	138	ASN
1	A	140	PHE
1	A	143	ILE
1	A	149	ARG
1	A	150	ARG
1	A	156	SER
1	A	176	LEU
1	A	184	ILE
1	A	202	VAL
1	A	208	LEU
1	A	212	ILE
1	A	213	SER
1	A	215	GLU
1	A	225	THR
1	A	262	GLN
1	A	269	THR
1	A	277	ASP
1	A	282	ARG
1	A	283	ILE
1	A	298	ASP
1	A	316	LEU
1	A	317	GLU
1	A	326	SER
1	A	329	THR
1	A	343	ASP
1	A	349	LEU
1	A	351	ILE
1	A	355	LEU
1	A	364	GLN
1	A	375	LYS
1	A	376	ARG
1	A	381	LEU
1	A	387	ARG

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Mol	Chain	Res	Type
1	A	402	ASN
1	B	20	VAL
1	B	24	GLU
1	B	30	ARG
1	B	38	LEU
1	B	50	GLU
1	B	54	VAL
1	B	58	VAL
1	B	77	THR
1	B	84	LEU
1	B	100	VAL
1	B	104	PRO
1	B	113	ARG
1	B	138	ASN
1	B	139	ILE
1	B	148	GLN
1	B	149	ARG
1	B	154	ILE
1	B	156	SER
1	B	164	PHE
1	B	165	THR
1	B	184	ILE
1	B	189	THR
1	B	192	ARG
1	B	208	LEU
1	B	213	SER
1	B	215	GLU
1	B	225	THR
1	B	256	CYS
1	B	269	THR
1	B	275	ASN
1	B	277	ASP
1	B	298	ASP
1	B	300	ARG
1	B	302	ASN
1	B	316	LEU
1	B	324	GLN
1	B	328	LEU
1	B	329	THR
1	B	336	LEU
1	B	342	LEU
1	B	344	GLU

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Mol	Chain	Res	Type
1	B	346	CYS
1	B	349	LEU
1	B	371	ARG
1	B	372	ARG
1	B	380	LEU
1	B	402	ASN
1	B	406	GLN
1	B	418	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (28) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	26	HIS
1	A	45	ASN
1	A	75	ASN
1	A	80	GLN
1	A	87	ASN
1	A	155	ASN
1	A	244	GLN
1	A	275	ASN
1	A	286	GLN
1	A	290	ASN
1	A	302	ASN
1	A	364	GLN
1	A	402	ASN
1	A	406	GLN
1	B	17	GLN
1	B	26	HIS
1	B	45	ASN
1	B	87	ASN
1	B	148	GLN
1	B	155	ASN
1	B	186	ASN
1	B	244	GLN
1	B	275	ASN
1	B	290	ASN
1	B	364	GLN
1	B	402	ASN
1	B	406	GLN
1	B	416	GLN

### 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 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 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	$\# Z  > 2$
3	GOL	A	602	-	5,5,5	0.36	0	5,5,5	0.28	0
3	GOL	B	601	-	5,5,5	0.34	0	5,5,5	0.52	0

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
3	GOL	A	602	-	-	0/4/4/4	0/0/0/0
3	GOL	B	601	-	-	0/4/4/4	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	602	GOL	1	0

## 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	388/415 (93%)	-0.27	1 (0%) 94 84	60, 92, 126, 145	0
1	B	388/415 (93%)	-0.34	0 100 100	64, 94, 126, 154	0
All	All	776/830 (93%)	-0.30	1 (0%) 95 90	60, 92, 126, 154	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	17	GLN	2.1

### 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
3	GOL	B	601	6/6	0.93	0.22	1.05	96,103,106,108	0
3	GOL	A	602	6/6	0.85	0.20	-0.73	68,85,94,95	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	MG	A	500	1/1	0.94	0.27	-	80,80,80,80	0
2	MG	B	501	1/1	0.87	0.12	-	83,83,83,83	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.