



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 18, 2018 – 11:20 PM EST

PDB ID : 2VCP
Title : Crystal structure of N-Wasp VC domain in complex with skeletal actin
Authors : Gaucher, J.F.; Didry, D.; Carlier, M.F.
Deposited on : 2007-09-26
Resolution : 3.20 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20030736
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) : rb-20030736

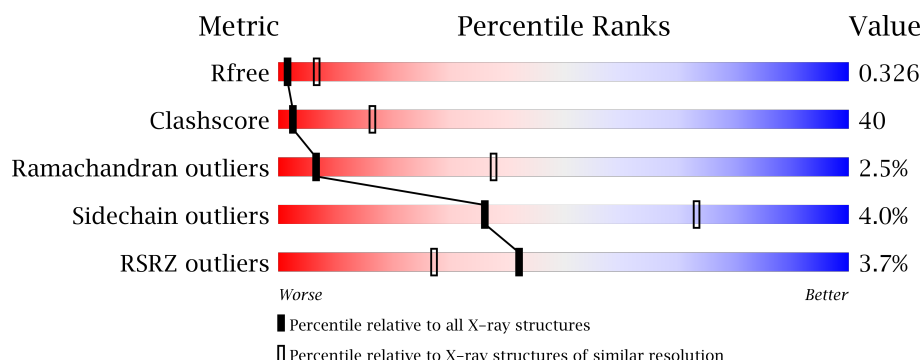
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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	1015 (3.22-3.18)
Clashscore	112137	1009 (3.20-3.20)
Ramachandran outliers	110173	1118 (3.22-3.18)
Sidechain outliers	110143	1117 (3.22-3.18)
RSRZ outliers	101464	1020 (3.22-3.18)

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	375	<div> <div>3%</div> <div>38% 58%</div> <div>..</div> </div>
1	B	375	<div> <div>3%</div> <div>39% 55% 5%</div> <div>.</div> </div>
2	D	93	<div> <div>2%</div> <div>11% 11% 78%</div> </div>
2	E	93	<div> <div>2%</div> <div>13% 9% 78%</div> </div>

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 6156 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.

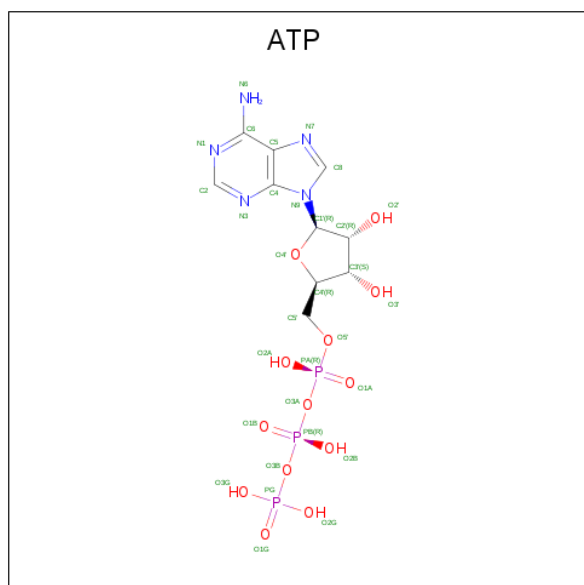
- Molecule 1 is a protein called ACTIN, ALPHA SKELETAL MUSCLE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	371	Total	C	N	O	S	0	0	0
			2900	1837	489	553	21			
1	B	371	Total	C	N	O	S	0	0	0
			2900	1837	489	553	21			

- Molecule 2 is a protein called NEURAL WISKOTT-ALDRICH SYNDROME PROTEIN.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	D	20	Total	C	N	O	0	0	1
			146	89	30	27			
2	E	20	Total	C	N	O	0	0	1
			146	89	30	27			

- Molecule 3 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
3	B	1	Total	C	N	O	P	0	0
			31	10	5	13	3		

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Ca	0	0
			1	1		
4	A	1	Total	Ca	0	0
			1	1		

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.

Chain A:

3%

38%

58%

ASP
GLU
ASP
GLU
GLU
T5
L8
D11
N12
N11
G13
G15
S14
V17
K18
A29
V30
F31
P32
S33
I34
V35
G36
R37
P38
R39
H40
Q41
G42
V43
M44
V45
G46
M47
G48
Q49
K50
D51
S52
Y53
Q59
S60
K61
R62
R63
I64
L65
T66
L67
P70
I71
E72
I76
T77
V78

Chain B:

3% 39% 55% 1%

ASP GLU ASP GLU T5 L8

N12 G13 S14 G15 L16 V17 K18 F21

A29 V30 F31 P32 S33 I34 V35 G36 R37 P38 R39 H40 Q41 G42 V43 M44 V45 G46 M47 G48 Q49 K50 D51 S52 Y53 V54 G55

Q59 S60 K61 R62 G63 I64 L65 T66 L67 P70 I71 T76

T77 N78 W79 D80 D81 M82

T85 W86 H87 H88 T89 F90 Y91 N92 E93 L94 A95

V96 A97 P98 E99

P102 T103 L104 L105 T106 E107

L110 K113 V114 A114 M115 A116 E117 K118 M119 Q120 G121 I122 M123 F124

F127 M128 V129 P130 A131 M132

A135 I136 Q137 A138 V139 L140 S141 I142

ASP GLU ASP GLU T5 L8

N12 G13 S14 G15 L16 V17 K18 F21

A29 V30 F31 P32 S33 I34 V35 G36 R37 P38 R39 H40 Q41 G42 V43 M44 V45 G46 M47 G48 Q49 K50 D51 S52 Y53 V54 G55

Q59 S60 K61 R62 G63 I64 L65 T66 L67 P70 I71 T76

T77 N78 W79 D80 D81 M82

T85 W86 H87 H88 T89 F90 Y91 N92 E93 L94 A95

V96 A97 P98 E99

P102 T103 L104 L105 T106 E107

L110 K113 V114 A114 M115 A116 E117 K118 M119 Q120 G121 I122 M123 F124

F127 M128 V129 P130 A131 M132

A135 I136 Q137 A138 V139 L140 S141 I142

4 Data and refinement statistics

Property	Value	Source
Space group	P 61	Depositor
Cell constants a, b, c, α , β , γ	136.24Å 136.24Å 205.41Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 3.20 48.29 – 3.20	Depositor EDS
% Data completeness (in resolution range)	91.4 (20.00-3.20) 98.5 (48.29-3.20)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.00 (at 3.19Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.275 , 0.331 0.281 , 0.326	Depositor DCC
R_{free} test set	1567 reflections (4.69%)	DCC
Wilson B-factor (Å ²)	57.0	Xtriage
Anisotropy	0.043	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 75.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.448 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.63	EDS
Total number of atoms	6156	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.01% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CA, HIC, ATP

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	0.51	0/2950	0.74	0/3994
1	B	0.57	0/2950	0.76	0/3994
2	D	0.61	0/145	0.73	0/193
2	E	0.63	0/145	0.88	0/193
All	All	0.55	0/6190	0.75	0/8374

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2900	0	2872	218	0
1	B	2900	0	2872	264	0
2	D	146	0	155	16	0
2	E	146	0	155	11	0
3	A	31	0	12	1	0
3	B	31	0	12	3	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
All	All	6156	0	6078	493	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 40.

All (493) 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:298:VAL:HG22	1:B:330:ILE:HB	1.40	1.03
1:B:210:ARG:O	1:B:214:GLU:HG3	1.60	1.01
1:B:8:LEU:HD22	1:B:94:LEU:HD13	1.42	1.00
1:A:205:GLU:HA	1:A:208:ILE:HD12	1.47	0.97
1:B:135:ALA:HB1	1:B:140:LEU:HD21	1.46	0.97
1:B:148:THR:HG21	2:E:438:LEU:HB3	1.48	0.94
1:A:180:LEU:HD21	1:A:260:THR:HG22	1.50	0.94
1:B:317:ILE:HG22	1:B:327:ILE:HD12	1.50	0.93
1:B:205:GLU:HA	1:B:208:ILE:HD12	1.51	0.92
1:B:44:MET:HA	1:B:47:MET:HG2	1.54	0.89
1:A:201:VAL:HG23	1:A:202:THR:H	1.38	0.89
1:A:142:LEU:HD22	1:A:165:ILE:HD12	1.56	0.87
1:B:201:VAL:HG23	1:B:202:THR:H	1.37	0.87
1:A:298:VAL:HG22	1:A:330:ILE:HB	1.55	0.86
1:A:44:MET:HA	1:A:47:MET:HG2	1.56	0.86
1:B:297:ASN:HD22	1:B:329:ILE:HD12	1.41	0.86
1:B:104:LEU:HD21	1:B:346:LEU:HD23	1.59	0.85
1:B:76:ILE:HD13	1:B:82:MET:HG2	1.58	0.85
1:A:210:ARG:O	1:A:214:GLU:HG3	1.77	0.85
1:B:99:GLU:HA	1:B:128:ASN:O	1.78	0.83
1:B:250:ILE:HG12	1:B:254:ARG:HG3	1.60	0.82
1:B:298:VAL:HG22	1:B:330:ILE:CB	2.11	0.80
1:A:99:GLU:HA	1:A:128:ASN:O	1.82	0.79
1:B:218:TYR:HE1	1:B:254:ARG:HB3	1.48	0.79
1:A:59:GLN:O	1:A:62:ARG:HG3	1.83	0.78
1:B:180:LEU:HD21	1:B:260:THR:HG22	1.65	0.78
1:B:277:THR:HA	1:B:280:ASN:HD22	1.48	0.78
1:B:90:PHE:CG	1:B:98:PRO:HG3	2.18	0.78
1:A:193:LEU:O	1:A:196:ARG:HB3	1.84	0.77
1:A:8:LEU:HD22	1:A:94:LEU:HD13	1.64	0.77
1:A:44:MET:HA	1:A:47:MET:CG	2.14	0.77
1:A:35:VAL:HG11	1:A:81:ASP:OD1	1.84	0.77
1:B:118:LYS:O	1:B:122:ILE:HG13	1.86	0.76
1:A:36:GLY:HA3	1:A:65:LEU:HD13	1.67	0.76
1:B:44:MET:HA	1:B:47:MET:CG	2.16	0.75
1:B:149:THR:HG23	1:B:165:ILE:O	1.86	0.75
1:A:76:ILE:HD13	1:A:82:MET:HG2	1.68	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:185:LEU:HD11	1:B:261:LEU:HD11	1.69	0.75
1:B:332:PRO:O	1:B:335:ARG:HB3	1.87	0.75
1:A:261:LEU:HB3	1:A:274:ILE:HD13	1.69	0.75
1:B:36:GLY:HA3	1:B:65:LEU:HD13	1.69	0.75
1:A:201:VAL:HG23	1:A:202:THR:N	2.01	0.74
1:B:38:PRO:HB3	1:B:43:VAL:HB	1.69	0.74
2:D:450:VAL:HG12	2:D:451:ALA:N	2.02	0.74
1:B:201:VAL:HG23	1:B:202:THR:N	2.01	0.74
1:A:349:LEU:O	1:A:353:GLN:NE2	2.20	0.74
1:A:140:LEU:HD13	1:A:343:GLY:N	2.03	0.74
1:A:153:LEU:HD23	1:A:299:MET:HG2	1.69	0.73
1:B:267:ILE:HG13	1:B:267:ILE:O	1.88	0.73
1:B:337:TYR:O	1:B:341:ILE:HG13	1.87	0.73
1:A:124:PHE:O	1:A:128:ASN:HA	1.88	0.73
1:A:189:LEU:CD2	1:A:213:LYS:HB2	2.18	0.73
1:B:317:ILE:HG22	1:B:327:ILE:CD1	2.18	0.72
1:A:116:ARG:HG2	1:A:370:VAL:HG21	1.71	0.72
1:B:147:ARG:NH2	1:B:330:ILE:HG12	2.04	0.72
1:B:159:VAL:HG22	1:B:160:THR:N	2.05	0.72
1:A:294:TYR:HB3	1:A:327:ILE:HD13	1.72	0.71
1:B:177:ARG:HG3	1:B:178:LEU:N	2.04	0.71
1:B:318:THR:HG22	1:B:319:ALA:N	2.05	0.71
1:B:349:LEU:O	1:B:353:GLN:NE2	2.24	0.70
1:B:188:TYR:CE2	1:B:192:ILE:HG21	2.27	0.70
1:B:250:ILE:HG13	1:B:253:GLU:HB2	1.73	0.70
2:E:434:ARG:O	2:E:437:LEU:HB3	1.91	0.70
1:B:62:ARG:NH1	1:B:203:THR:HB	2.06	0.70
1:B:151:ILE:HA	1:B:163:VAL:O	1.91	0.70
1:B:193:LEU:O	1:B:196:ARG:HB3	1.91	0.70
1:B:208:ILE:O	1:B:212:ILE:HG13	1.90	0.70
1:A:200:PHE:HD1	1:A:205:GLU:HB3	1.57	0.69
1:B:12:ASN:O	1:B:137:GLN:NE2	2.26	0.69
1:A:335:ARG:HH11	1:A:335:ARG:HB3	1.57	0.69
1:B:159:VAL:CG2	1:B:160:THR:N	2.56	0.68
1:A:250:ILE:HG13	1:A:253:GLU:HB2	1.73	0.68
1:B:116:ARG:HG2	1:B:370:VAL:HG21	1.75	0.68
1:B:113:LYS:HG3	1:B:114:ALA:N	2.08	0.68
1:B:347:ALA:HA	1:B:352:PHE:CD2	2.29	0.68
1:B:250:ILE:HD11	1:B:254:ARG:HA	1.74	0.68
1:A:151:ILE:HA	1:A:163:VAL:O	1.94	0.67
1:A:180:LEU:HD21	1:A:260:THR:CG2	2.22	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:147:ARG:CZ	1:B:330:ILE:HG12	2.24	0.67
1:B:59:GLN:O	1:B:62:ARG:HG3	1.95	0.67
2:D:450:VAL:HG12	2:D:451:ALA:H	1.57	0.67
1:A:148:THR:HG21	2:D:438:LEU:HB3	1.75	0.66
1:A:332:PRO:O	1:A:335:ARG:NH1	2.28	0.66
1:B:124:PHE:O	1:B:128:ASN:HA	1.96	0.66
1:B:189:LEU:CD2	1:B:213:LYS:HB2	2.24	0.66
1:B:218:TYR:CE1	1:B:254:ARG:HB3	2.31	0.66
1:A:215:LYS:O	1:A:216:LEU:HD23	1.96	0.65
1:B:317:ILE:CG2	1:B:327:ILE:HD12	2.24	0.65
1:B:282:ILE:HG21	1:B:294:TYR:CE2	2.31	0.65
1:A:38:PRO:HB3	1:A:43:VAL:HB	1.78	0.65
1:A:162:ASN:HB2	1:A:176:MET:HB2	1.78	0.65
2:E:436:ALA:HA	2:E:439:ASP:HB2	1.78	0.65
1:B:257:CYS:HB3	1:B:258:PRO:HD3	1.77	0.65
1:A:159:VAL:HG22	1:A:160:THR:N	2.12	0.64
1:A:212:ILE:HG12	1:A:240:TYR:CD2	2.33	0.64
1:A:321:ALA:HB1	1:A:322:PRO:HD2	1.80	0.64
1:B:155:SER:HB3	1:B:304:THR:HG23	1.78	0.64
1:A:215:LYS:C	1:A:216:LEU:HD23	2.18	0.64
1:A:321:ALA:HB1	1:A:322:PRO:CD	2.28	0.63
1:B:148:THR:OG1	2:E:442:ARG:NH2	2.30	0.63
1:A:275:HIS:CD2	1:A:276:GLU:HG3	2.33	0.63
1:B:185:LEU:HD22	1:B:257:CYS:O	1.99	0.63
1:B:34:ILE:HD12	1:B:67:LEU:HD13	1.80	0.63
1:A:118:LYS:O	1:A:122:ILE:HG13	1.99	0.63
1:B:216:LEU:HD12	1:B:250:ILE:HG21	1.81	0.63
1:A:135:ALA:HB1	1:A:140:LEU:HD21	1.81	0.62
1:A:332:PRO:O	1:A:335:ARG:HB3	1.99	0.62
1:B:222:ASP:HB3	1:B:225:ASN:HB2	1.81	0.62
1:A:224:GLU:HA	1:A:227:MET:HB2	1.82	0.62
1:A:189:LEU:HD22	1:A:213:LYS:HB2	1.82	0.62
1:B:135:ALA:CB	1:B:140:LEU:HD21	2.27	0.62
1:A:216:LEU:O	1:A:254:ARG:HG2	2.00	0.61
1:B:153:LEU:HD23	1:B:299:MET:HG2	1.81	0.61
1:A:267:ILE:O	1:A:267:ILE:HG13	2.00	0.61
1:B:189:LEU:HB2	1:B:257:CYS:SG	2.41	0.61
1:B:14:SER:HB3	1:B:71:ILE:HG22	1.82	0.61
1:A:45:VAL:HA	1:B:91:TYR:HB3	1.81	0.61
1:B:201:VAL:CG2	1:B:202:THR:H	2.13	0.61
1:A:185:LEU:HD22	1:A:257:CYS:O	2.00	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:282:ILE:HG23	1:B:290:ARG:HB3	1.84	0.60
1:B:151:ILE:O	1:B:151:ILE:HG23	2.01	0.60
1:B:189:LEU:HD13	1:B:257:CYS:HB2	1.83	0.60
1:A:318:THR:HG22	1:A:319:ALA:N	2.16	0.60
1:B:70:PRO:HA	1:B:78:ASN:HB3	1.82	0.60
1:A:113:LYS:HG3	1:A:114:ALA:N	2.16	0.59
1:A:201:VAL:CG2	1:A:202:THR:H	2.14	0.59
1:A:48:GLY:O	1:A:49:GLN:HG2	2.02	0.59
1:A:358:THR:OG1	1:A:361:GLU:HG3	2.01	0.59
1:A:91:TYR:O	1:A:95:ARG:HA	2.02	0.59
1:B:129:VAL:HB	1:B:130:PRO:HD2	1.83	0.59
1:B:209:VAL:HA	1:B:212:ILE:HD12	1.84	0.59
1:A:104:LEU:HD21	1:A:346:LEU:HD23	1.84	0.59
1:A:159:VAL:CG2	1:A:160:THR:N	2.66	0.59
1:B:148:THR:HG21	2:E:438:LEU:CB	2.28	0.59
1:B:250:ILE:CG1	1:B:254:ARG:HG3	2.31	0.59
1:B:106:THR:HA	1:B:135:ALA:O	2.03	0.59
1:B:123:MET:O	1:B:127:PHE:HB2	2.03	0.58
1:B:297:ASN:HD22	1:B:329:ILE:CD1	2.15	0.58
1:A:238:LYS:O	1:A:249:THR:HG23	2.04	0.58
1:A:145:SER:HB2	1:A:147:ARG:HH12	1.68	0.58
1:A:222:ASP:HB3	1:A:225:ASN:HB2	1.84	0.58
1:B:164:PRO:C	1:B:165:ILE:HG13	2.21	0.58
1:B:15:GLY:O	1:B:16:LEU:HD23	2.03	0.58
1:A:250:ILE:HG12	1:A:254:ARG:HG3	1.83	0.58
1:B:277:THR:HA	1:B:280:ASN:ND2	2.17	0.58
1:A:14:SER:HA	1:A:71:ILE:HB	1.85	0.58
1:A:183:ARG:HG3	1:A:206:ARG:HH22	1.69	0.58
1:A:191:LYS:O	1:A:195:GLU:HG3	2.04	0.58
1:B:48:GLY:O	1:B:49:GLN:HG2	2.04	0.58
1:A:367:PRO:C	1:A:369:ILE:H	2.06	0.58
1:B:257:CYS:HB3	1:B:258:PRO:CD	2.33	0.58
1:B:298:VAL:CG2	1:B:330:ILE:HB	2.25	0.58
1:A:303:THR:O	1:A:303:THR:HG22	2.03	0.58
1:A:347:ALA:HA	1:A:352:PHE:CD2	2.39	0.58
1:B:142:LEU:HD22	1:B:165:ILE:HD12	1.86	0.57
1:A:14:SER:HB3	1:A:71:ILE:HG22	1.84	0.57
1:B:218:TYR:HH	1:B:255:PHE:HD1	1.53	0.57
1:B:39:ARG:HG2	1:B:66:THR:OG1	2.04	0.57
2:D:436:ALA:HA	2:D:439:ASP:HB2	1.85	0.57
1:A:140:LEU:HD13	1:A:343:GLY:CA	2.34	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:334:GLU:CD	1:B:334:GLU:H	2.08	0.57
1:A:145:SER:HB2	1:A:147:ARG:NH1	2.19	0.57
1:A:53:TYR:HD2	1:A:65:LEU:HD21	1.70	0.57
1:B:41:GLN:O	1:B:43:VAL:N	2.38	0.57
2:D:450:VAL:CG1	2:D:451:ALA:H	2.18	0.56
1:A:294:TYR:CD1	1:A:327:ILE:HD11	2.40	0.56
1:B:330:ILE:HD12	1:B:330:ILE:N	2.20	0.56
1:A:155:SER:HB3	1:A:304:THR:HG23	1.87	0.56
1:A:152:VAL:N	1:A:163:VAL:O	2.37	0.56
1:B:189:LEU:HD22	1:B:213:LYS:HB2	1.88	0.56
1:B:29:ALA:HB1	1:B:93:GLU:OE1	2.05	0.56
1:B:14:SER:HA	1:B:71:ILE:HB	1.86	0.56
1:B:294:TYR:CE1	1:B:321:ALA:HB2	2.40	0.56
1:A:294:TYR:HB3	1:A:327:ILE:CD1	2.36	0.56
1:B:303:THR:O	1:B:303:THR:HG22	2.05	0.56
1:B:216:LEU:O	1:B:254:ARG:HG2	2.05	0.56
1:B:335:ARG:HB3	1:B:335:ARG:NH1	2.21	0.56
2:D:434:ARG:O	2:D:437:LEU:HB3	2.05	0.56
1:A:59:GLN:O	1:A:61:LYS:N	2.39	0.55
1:A:90:PHE:CG	1:A:98:PRO:HG3	2.41	0.55
1:B:208:ILE:HG21	1:B:242:LEU:HD22	1.87	0.55
1:B:189:LEU:HD12	1:B:192:ILE:HD11	1.89	0.55
1:B:316:GLU:O	1:B:320:LEU:HG	2.06	0.55
2:D:450:VAL:CG1	2:D:451:ALA:N	2.69	0.55
1:B:200:PHE:HD1	1:B:205:GLU:HB3	1.70	0.55
1:A:15:GLY:O	1:A:16:LEU:HD23	2.07	0.55
1:B:104:LEU:HD23	1:B:343:GLY:O	2.07	0.55
1:A:190:MET:HG2	1:A:209:VAL:HG21	1.89	0.55
1:B:14:SER:OG	3:B:1376:ATP:O2G	2.23	0.55
1:A:62:ARG:NH1	1:A:203:THR:HB	2.22	0.55
1:A:292:ASP:O	1:A:296:ASN:ND2	2.40	0.55
1:B:187:ASP:O	1:B:190:MET:HB2	2.07	0.54
1:B:183:ARG:HG3	1:B:206:ARG:HH22	1.72	0.54
1:B:62:ARG:HH12	1:B:203:THR:HB	1.71	0.54
1:B:358:THR:HG23	1:B:361:GLU:OE1	2.08	0.54
1:A:107:GLU:OE2	1:A:116:ARG:NH2	2.41	0.54
1:B:13:GLY:HA2	3:B:1376:ATP:O1G	2.07	0.54
1:B:13:GLY:C	1:B:15:GLY:H	2.09	0.54
1:A:330:ILE:HD12	1:A:330:ILE:N	2.22	0.54
1:B:327:ILE:HG22	1:B:328:LYS:N	2.22	0.54
1:A:129:VAL:HB	1:A:130:PRO:HD2	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:227:MET:HG2	1:A:255:PHE:HE2	1.73	0.54
1:B:136:ILE:HG22	1:B:138:ALA:H	1.72	0.54
1:B:140:LEU:HD13	1:B:343:GLY:N	2.23	0.54
1:A:165:ILE:HG23	1:A:169:TYR:O	2.07	0.53
1:A:189:LEU:HD12	1:A:192:ILE:HD11	1.91	0.53
1:B:104:LEU:CD2	1:B:346:LEU:HD23	2.36	0.53
1:B:39:ARG:CZ	1:B:63:GLY:O	2.56	0.53
1:A:29:ALA:HB1	1:A:93:GLU:OE1	2.07	0.53
1:A:304:THR:OG1	1:A:335:ARG:HD2	2.08	0.53
1:A:261:LEU:HB3	1:A:274:ILE:CD1	2.37	0.53
1:B:79:TRP:O	1:B:82:MET:N	2.39	0.53
1:A:70:PRO:HG3	1:A:85:ILE:HD12	1.89	0.53
1:A:257:CYS:HB3	1:A:258:PRO:CD	2.38	0.53
1:A:110:LEU:HD11	1:A:175:ILE:HG21	1.91	0.53
1:A:335:ARG:HA	1:A:338:SER:OG	2.09	0.53
1:B:306:TYR:O	1:B:309:ILE:HG22	2.09	0.53
1:A:201:VAL:CG2	1:A:202:THR:N	2.72	0.53
1:A:189:LEU:HD13	1:A:257:CYS:HB2	1.91	0.53
1:B:367:PRO:C	1:B:369:ILE:H	2.11	0.53
1:B:113:LYS:HG3	1:B:114:ALA:H	1.74	0.52
1:B:238:LYS:O	1:B:249:THR:HG23	2.09	0.52
1:B:105:LEU:HD11	1:B:123:MET:HG3	1.89	0.52
1:A:140:LEU:HD13	1:A:343:GLY:H	1.71	0.52
1:B:148:THR:OG1	2:E:442:ARG:CZ	2.58	0.52
1:B:275:HIS:CG	1:B:276:GLU:N	2.78	0.52
1:A:164:PRO:HG3	1:A:174:ALA:HB3	1.91	0.52
1:A:294:TYR:CD1	1:A:327:ILE:CD1	2.92	0.52
1:B:217:CYS:O	1:B:307:PRO:HD2	2.09	0.52
1:A:218:TYR:HE1	1:A:254:ARG:HB3	1.73	0.52
1:A:33:SER:O	1:A:70:PRO:HD2	2.10	0.52
1:B:185:LEU:CD1	1:B:261:LEU:HD11	2.37	0.52
1:A:102:PRO:HA	1:A:131:ALA:O	2.09	0.52
1:A:193:LEU:HD23	1:A:253:GLU:HG2	1.92	0.52
1:B:160:THR:HG21	1:B:178:LEU:HD23	1.92	0.52
1:A:53:TYR:HA	1:B:49:GLN:NE2	2.24	0.52
1:A:128:ASN:OD1	1:A:128:ASN:O	2.28	0.51
1:A:53:TYR:HA	1:B:49:GLN:HE22	1.74	0.51
1:A:261:LEU:O	1:A:274:ILE:HG12	2.10	0.51
1:B:141:SER:O	1:B:144:ALA:HB3	2.10	0.51
1:B:189:LEU:HD13	1:B:257:CYS:CB	2.40	0.51
1:B:321:ALA:HB1	1:B:322:PRO:CD	2.40	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:160:THR:HB	1:B:178:LEU:HB3	1.93	0.51
1:B:53:TYR:HD2	1:B:65:LEU:HD21	1.75	0.51
1:B:136:ILE:O	1:B:138:ALA:N	2.44	0.51
1:B:191:LYS:O	1:B:195:GLU:HG3	2.11	0.51
1:B:90:PHE:CB	1:B:98:PRO:HG3	2.41	0.51
1:B:355:MET:SD	2:E:437:LEU:HD22	2.50	0.51
1:A:105:LEU:HD11	1:A:123:MET:HG3	1.93	0.51
1:A:166:TYR:CE1	1:A:167:GLU:HG3	2.45	0.51
1:A:289:ILE:O	1:A:291:LYS:N	2.44	0.51
1:B:189:LEU:HD23	1:B:209:VAL:CG1	2.41	0.51
1:B:358:THR:OG1	1:B:361:GLU:HG3	2.10	0.51
1:A:91:TYR:HB3	1:B:45:VAL:HA	1.93	0.51
1:A:204:ALA:O	1:A:208:ILE:HG13	2.11	0.50
1:B:204:ALA:O	1:B:208:ILE:HG13	2.11	0.50
1:B:145:SER:HB2	1:B:147:ARG:NH1	2.26	0.50
1:B:185:LEU:HD11	1:B:261:LEU:CD1	2.41	0.50
1:B:18:LYS:HG3	1:B:30:VAL:HG13	1.93	0.50
1:B:90:PHE:CD1	1:B:98:PRO:HG3	2.45	0.50
1:B:332:PRO:O	1:B:335:ARG:NH1	2.45	0.50
1:B:90:PHE:HB3	1:B:98:PRO:HG3	1.94	0.50
1:B:218:TYR:N	1:B:218:TYR:CD1	2.80	0.50
1:B:224:GLU:HA	1:B:227:MET:HB2	1.93	0.50
1:B:152:VAL:HA	1:B:298:VAL:O	2.11	0.50
1:A:234:SER:O	1:A:237:GLU:HG2	2.12	0.50
1:A:174:ALA:HA	1:A:284:LYS:CD	2.42	0.50
1:A:294:TYR:CE1	1:A:321:ALA:HB2	2.47	0.50
1:B:257:CYS:N	1:B:258:PRO:HD2	2.27	0.50
1:A:12:ASN:O	1:A:137:GLN:NE2	2.45	0.50
1:B:145:SER:HB2	1:B:147:ARG:HH12	1.77	0.50
1:B:153:LEU:CD2	1:B:299:MET:HG2	2.40	0.49
1:A:164:PRO:C	1:A:165:ILE:HG13	2.33	0.49
1:A:303:THR:O	1:A:303:THR:CG2	2.60	0.49
1:A:367:PRO:C	1:A:369:ILE:N	2.65	0.49
1:B:124:PHE:CZ	1:B:132:MET:HG3	2.47	0.49
1:B:151:ILE:HG13	1:B:163:VAL:O	2.12	0.49
2:E:438:LEU:O	2:E:439:ASP:C	2.51	0.49
1:B:102:PRO:HA	1:B:131:ALA:O	2.13	0.49
1:B:189:LEU:HD13	1:B:257:CYS:SG	2.53	0.49
1:B:335:ARG:HH11	1:B:335:ARG:HB3	1.77	0.49
1:A:273:GLY:O	1:A:276:GLU:N	2.45	0.49
1:B:215:LYS:C	1:B:216:LEU:HD23	2.33	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:240:TYR:CE2	1:B:242:LEU:HD23	2.46	0.49
1:A:14:SER:OG	3:A:1376:ATP:O2G	2.31	0.49
1:B:117:GLU:OE2	1:B:371:HIS:NE2	2.44	0.49
1:A:334:GLU:CD	1:A:334:GLU:H	2.16	0.49
1:B:110:LEU:HD11	1:B:175:ILE:CG2	2.43	0.49
1:A:79:TRP:O	1:A:82:MET:N	2.40	0.48
1:B:274:ILE:HG13	1:B:275:HIS:N	2.28	0.48
1:B:279:TYR:C	1:B:279:TYR:CD2	2.86	0.48
1:A:185:LEU:HD21	1:A:260:THR:HB	1.95	0.48
1:A:31:PHE:CE2	1:A:93:GLU:HG3	2.48	0.48
1:A:41:GLN:O	1:A:43:VAL:N	2.47	0.48
1:A:174:ALA:HA	1:A:284:LYS:HD2	1.95	0.48
1:B:338:SER:O	1:B:339:VAL:C	2.52	0.48
1:A:328:LYS:O	1:A:330:ILE:HD12	2.14	0.48
1:B:160:THR:HB	1:B:178:LEU:O	2.13	0.48
1:B:182:GLY:O	1:B:183:ARG:C	2.52	0.48
1:A:51:ASP:CG	1:A:52:SER:H	2.16	0.48
1:B:176:MET:CE	1:B:280:ASN:HB3	2.43	0.48
1:A:18:LYS:HD3	1:A:18:LYS:N	2.29	0.48
1:A:344:SER:OG	1:A:345:ILE:N	2.42	0.48
1:A:44:MET:HA	1:A:47:MET:HG3	1.94	0.48
1:B:107:GLU:C	1:B:137:GLN:HG3	2.34	0.48
1:B:303:THR:CG2	1:B:303:THR:O	2.61	0.48
1:B:304:THR:OG1	1:B:335:ARG:HD2	2.13	0.48
1:B:14:SER:HB3	1:B:71:ILE:CG2	2.43	0.48
1:A:208:ILE:O	1:A:212:ILE:HG13	2.14	0.48
1:B:46:GLY:O	1:B:48:GLY:N	2.46	0.48
1:B:151:ILE:CA	1:B:163:VAL:O	2.59	0.48
1:B:188:TYR:CE2	1:B:192:ILE:CG2	2.97	0.48
1:B:273:GLY:HA3	1:B:275:HIS:CD2	2.48	0.48
1:A:205:GLU:O	1:A:208:ILE:HB	2.14	0.47
1:A:90:PHE:HB3	1:A:98:PRO:HG3	1.97	0.47
1:B:159:VAL:HG21	1:B:161:HIS:CE1	2.48	0.47
1:B:159:VAL:HG23	1:B:177:ARG:HD2	1.95	0.47
1:B:227:MET:HG2	1:B:255:PHE:HE2	1.79	0.47
1:B:321:ALA:HB1	1:B:322:PRO:HD2	1.96	0.47
1:B:143:TYR:CG	2:E:441:ILE:HD13	2.49	0.47
1:B:143:TYR:CD2	2:E:441:ILE:HD13	2.50	0.47
1:A:218:TYR:CE1	1:A:254:ARG:HB3	2.49	0.47
1:A:375:PHE:HB3	2:D:434:ARG:HH12	1.79	0.47
1:B:303:THR:HG23	1:B:306:TYR:HE2	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:107:GLU:C	1:A:137:GLN:HG3	2.34	0.47
1:B:173:HIS:C	1:B:173:HIS:CD2	2.86	0.47
1:B:250:ILE:HD11	1:B:254:ARG:CA	2.43	0.47
1:B:178:LEU:HD11	1:B:180:LEU:HB3	1.97	0.47
2:D:438:LEU:O	2:D:439:ASP:C	2.53	0.47
1:A:250:ILE:HD11	1:A:254:ARG:HA	1.97	0.47
1:A:44:MET:CA	1:A:47:MET:HG2	2.37	0.47
1:B:90:PHE:HE2	1:B:123:MET:HE1	1.79	0.47
1:B:153:LEU:HB3	1:B:299:MET:HG2	1.97	0.47
1:B:212:ILE:HG12	1:B:240:TYR:CD2	2.49	0.47
1:A:112:PRO:HB2	1:A:115:ASN:OD1	2.15	0.47
1:A:88:HIS:O	1:A:92:ASN:HB2	2.15	0.47
1:B:185:LEU:HD21	1:B:260:THR:HB	1.97	0.47
1:B:274:ILE:HA	1:B:277:THR:OG1	2.14	0.46
1:A:51:ASP:CG	1:A:52:SER:N	2.69	0.46
1:B:367:PRO:C	1:B:369:ILE:N	2.69	0.46
1:A:355:MET:SD	2:D:437:LEU:HD22	2.55	0.46
2:D:450:VAL:O	2:D:452:ASP:N	2.48	0.46
1:A:289:ILE:O	1:A:290:ARG:C	2.53	0.46
1:A:70:PRO:HA	1:A:78:ASN:HB3	1.96	0.46
1:B:272:ALA:HB3	1:B:277:THR:HG23	1.96	0.46
1:B:282:ILE:HG21	1:B:294:TYR:CZ	2.50	0.46
1:B:31:PHE:HB2	1:B:32:PRO:CD	2.46	0.46
1:A:185:LEU:O	1:A:186:THR:C	2.54	0.46
1:A:283:MET:C	1:A:285:CYS:H	2.19	0.46
1:A:335:ARG:NH1	1:A:335:ARG:HB3	2.27	0.46
1:A:337:TYR:O	1:A:341:ILE:HG13	2.15	0.46
1:B:250:ILE:CD1	1:B:254:ARG:HG3	2.44	0.46
1:B:335:ARG:HA	1:B:338:SER:OG	2.16	0.46
1:A:186:THR:O	1:A:189:LEU:HB3	2.16	0.46
1:A:257:CYS:HB3	1:A:258:PRO:HD3	1.97	0.46
1:A:188:TYR:O	1:A:189:LEU:C	2.53	0.46
1:A:187:ASP:O	1:A:190:MET:HB2	2.15	0.46
1:A:312:ARG:HG2	1:A:312:ARG:HH11	1.81	0.46
1:A:298:VAL:HG22	1:A:330:ILE:CB	2.36	0.46
1:B:350:SER:C	1:B:352:PHE:H	2.20	0.46
1:B:38:PRO:HA	1:B:64:ILE:O	2.16	0.46
1:A:218:TYR:HH	1:A:255:PHE:HD1	1.61	0.45
1:A:306:TYR:O	1:A:309:ILE:HG22	2.16	0.45
1:B:261:LEU:O	1:B:274:ILE:HG23	2.16	0.45
1:B:54:VAL:HG12	1:B:55:GLY:N	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:142:LEU:CD2	1:A:165:ILE:HD12	2.38	0.45
1:A:106:THR:HA	1:A:135:ALA:O	2.17	0.45
1:B:305:MET:HA	1:B:335:ARG:HE	1.82	0.45
2:D:449:SER:OG	2:D:450:VAL:N	2.50	0.45
1:A:297:ASN:HD22	1:A:329:ILE:HD12	1.82	0.45
1:A:37:ARG:O	1:A:66:THR:N	2.50	0.45
1:B:140:LEU:HB3	1:B:342:GLY:HA3	1.98	0.45
1:B:335:ARG:O	1:B:335:ARG:HG3	2.16	0.45
2:E:437:LEU:O	2:E:441:ILE:HG13	2.16	0.45
1:A:17:VAL:O	1:A:30:VAL:HA	2.16	0.45
1:B:140:LEU:HD13	1:B:343:GLY:CA	2.47	0.45
1:B:251:GLY:N	1:B:253:GLU:OE1	2.48	0.45
1:A:106:THR:OG1	1:A:137:GLN:HG2	2.17	0.45
1:A:216:LEU:HD12	1:A:250:ILE:HG21	1.98	0.45
1:A:180:LEU:HD13	1:A:267:ILE:HD13	1.99	0.45
1:B:31:PHE:CE2	1:B:93:GLU:HG3	2.52	0.45
1:B:189:LEU:HD23	1:B:209:VAL:HG13	1.99	0.44
1:B:344:SER:O	1:B:345:ILE:C	2.55	0.44
1:A:38:PRO:HA	1:A:64:ILE:O	2.18	0.44
1:B:176:MET:HE3	1:B:280:ASN:HB3	1.99	0.44
1:B:188:TYR:O	1:B:189:LEU:C	2.56	0.44
1:B:282:ILE:CD1	1:B:294:TYR:CD1	3.00	0.44
1:B:186:THR:O	1:B:189:LEU:HB3	2.17	0.44
1:B:282:ILE:HD12	1:B:294:TYR:CD1	2.53	0.44
1:B:85:ILE:HG22	1:B:86:TRP:N	2.32	0.44
1:B:117:GLU:O	1:B:120:THR:HB	2.17	0.44
1:A:135:ALA:CB	1:A:140:LEU:HD21	2.47	0.44
1:A:14:SER:HB3	1:A:71:ILE:CG2	2.46	0.44
1:A:274:ILE:HA	1:A:277:THR:OG1	2.17	0.44
1:A:34:ILE:HD12	1:A:67:LEU:HD13	2.00	0.44
1:B:357:ILE:HD11	1:B:373:LYS:HB2	1.99	0.44
1:A:148:THR:OG1	2:D:442:ARG:NH2	2.51	0.44
1:A:205:GLU:HA	1:A:208:ILE:CD1	2.32	0.44
1:A:289:ILE:C	1:A:291:LYS:N	2.70	0.44
1:B:330:ILE:O	1:B:332:PRO:HD3	2.17	0.44
1:B:36:GLY:CA	1:B:65:LEU:HD13	2.45	0.44
1:A:117:GLU:OE2	1:A:371:HIS:NE2	2.47	0.43
1:A:13:GLY:C	1:A:15:GLY:H	2.21	0.43
1:A:208:ILE:HG21	1:A:242:LEU:HD22	2.00	0.43
1:B:159:VAL:CG2	1:B:160:THR:H	2.28	0.43
1:A:107:GLU:O	1:A:137:GLN:HG3	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:312:ARG:HG2	1:A:312:ARG:NH1	2.33	0.43
1:B:208:ILE:HG21	1:B:242:LEU:CD2	2.47	0.43
1:B:185:LEU:HD11	1:B:261:LEU:HD21	2.00	0.43
1:B:46:GLY:O	1:B:47:MET:C	2.56	0.43
1:A:193:LEU:O	1:A:196:ARG:CB	2.62	0.43
1:A:200:PHE:CD1	1:A:205:GLU:HB3	2.44	0.43
1:A:117:GLU:O	1:A:120:THR:HB	2.19	0.43
1:A:90:PHE:CB	1:A:98:PRO:HG3	2.48	0.43
1:B:31:PHE:HZ	1:B:89:THR:OG1	2.02	0.43
1:B:13:GLY:C	1:B:15:GLY:N	2.72	0.43
1:A:289:ILE:HG13	1:A:290:ARG:N	2.34	0.43
1:B:145:SER:CB	1:B:147:ARG:NH1	2.82	0.43
1:B:216:LEU:HD12	1:B:250:ILE:CG2	2.49	0.43
1:B:294:TYR:O	1:B:327:ILE:HA	2.19	0.43
1:B:51:ASP:CG	1:B:52:SER:N	2.72	0.43
1:A:104:LEU:HD13	1:A:133:TYR:HB3	2.00	0.43
1:B:165:ILE:HG23	1:B:169:TYR:O	2.19	0.43
1:A:273:GLY:HA3	1:A:275:HIS:CE1	2.54	0.43
1:B:140:LEU:HD23	1:B:140:LEU:N	2.34	0.43
1:A:313:MET:O	1:A:314:GLN:C	2.57	0.42
1:B:151:ILE:HG13	1:B:163:VAL:C	2.40	0.42
1:A:53:TYR:CD2	1:A:65:LEU:HD21	2.54	0.42
1:B:34:ILE:O	1:B:54:VAL:HG13	2.20	0.42
1:B:298:VAL:HG22	1:B:330:ILE:CG2	2.49	0.42
1:A:149:THR:HG23	1:A:165:ILE:O	2.19	0.42
1:A:43:VAL:CG1	1:A:64:ILE:HB	2.50	0.42
1:B:39:ARG:NH2	1:B:63:GLY:O	2.52	0.42
1:B:8:LEU:HD22	1:B:94:LEU:CD1	2.30	0.42
1:A:275:HIS:CD2	1:A:276:GLU:N	2.88	0.42
1:B:178:LEU:C	1:B:180:LEU:H	2.23	0.42
1:B:208:ILE:O	1:B:212:ILE:CG1	2.65	0.42
1:B:21:PHE:CE1	1:B:96:VAL:HG11	2.55	0.42
1:A:39:ARG:CZ	1:A:63:GLY:O	2.68	0.42
1:B:210:ARG:O	1:B:214:GLU:CG	2.50	0.42
1:B:35:VAL:HG11	1:B:81:ASP:OD1	2.19	0.42
1:B:51:ASP:CG	1:B:52:SER:H	2.23	0.42
1:A:278:THR:HB	1:A:317:ILE:HD11	2.02	0.42
1:A:46:GLY:O	1:A:47:MET:C	2.58	0.42
1:B:31:PHE:CD2	1:B:31:PHE:N	2.88	0.42
1:A:110:LEU:HD11	1:A:175:ILE:CG2	2.49	0.42
1:A:252:ASN:C	1:A:254:ARG:N	2.72	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:293:LEU:O	1:A:294:TYR:C	2.56	0.42
1:B:257:CYS:H	1:B:258:PRO:HD2	1.85	0.42
1:A:192:ILE:HB	1:A:256:ARG:HH21	1.84	0.41
1:B:297:ASN:HB3	1:B:329:ILE:HD13	2.02	0.41
1:A:293:LEU:O	1:A:296:ASN:N	2.53	0.41
1:B:188:TYR:CZ	1:B:192:ILE:CG2	3.03	0.41
1:B:240:TYR:CD1	1:B:241:GLU:N	2.88	0.41
1:A:70:PRO:HG3	1:A:85:ILE:CD1	2.49	0.41
1:B:221:LEU:HD12	1:B:221:LEU:HA	1.88	0.41
1:B:70:PRO:HG3	1:B:85:ILE:HD12	2.02	0.41
1:A:48:GLY:O	1:A:49:GLN:CG	2.67	0.41
1:A:223:PHE:O	1:A:227:MET:HB2	2.21	0.41
1:B:61:LYS:O	1:B:64:ILE:HG12	2.20	0.41
1:A:295:ALA:O	1:A:328:LYS:O	2.38	0.41
1:B:314:GLN:O	1:B:315:LYS:C	2.59	0.41
1:B:88:HIS:O	1:B:92:ASN:HB2	2.21	0.41
1:A:104:LEU:CD1	1:A:133:TYR:HD2	2.33	0.41
1:A:275:HIS:CG	1:A:276:GLU:N	2.88	0.41
1:A:44:MET:O	1:A:47:MET:HB2	2.20	0.41
1:B:185:LEU:HD23	1:B:185:LEU:HA	1.88	0.41
1:A:160:THR:HB	1:A:178:LEU:HB3	2.03	0.41
1:B:128:ASN:O	1:B:128:ASN:OD1	2.38	0.41
2:D:449:SER:C	2:D:450:VAL:HG23	2.41	0.41
1:A:109:PRO:O	1:A:110:LEU:HB2	2.21	0.41
1:A:11:ASP:OD2	1:A:339:VAL:CG1	2.69	0.41
1:B:166:TYR:CE1	1:B:167:GLU:HG3	2.56	0.41
1:B:53:TYR:CD2	1:B:65:LEU:HD11	2.56	0.41
1:A:145:SER:CB	1:A:147:ARG:NH1	2.84	0.41
1:A:67:LEU:HD23	1:A:67:LEU:N	2.36	0.41
1:B:130:PRO:HG2	1:B:131:ALA:H	1.86	0.41
1:B:140:LEU:O	1:B:141:SER:C	2.58	0.41
1:B:16:LEU:HD12	3:B:1376:ATP:O2A	2.21	0.41
1:B:29:ALA:C	1:B:30:VAL:HG23	2.42	0.41
1:B:97:ALA:O	1:B:98:PRO:C	2.60	0.41
1:A:124:PHE:CZ	1:A:132:MET:HG3	2.55	0.40
1:A:72:GLU:OE1	1:A:77:THR:HG21	2.21	0.40
1:A:264:PRO:HB3	1:A:269:MET:HB2	2.03	0.40
1:B:44:MET:HA	1:B:47:MET:HG3	2.01	0.40
1:B:107:GLU:OE2	1:B:116:ARG:NH2	2.55	0.40
1:A:188:TYR:HH	1:A:266:PHE:HD2	1.66	0.40
1:A:286:ASP:C	1:A:286:ASP:OD1	2.60	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:87:HIS:O	1:A:91:TYR:HD1	2.05	0.40
1:B:116:ARG:HG2	1:B:370:VAL:CG2	2.48	0.40
1:B:48:GLY:O	1:B:49:GLN:CG	2.67	0.40
1:A:375:PHE:CB	2:D:434:ARG:HH12	2.34	0.40
2:D:449:SER:O	2:D:450:VAL:CG2	2.70	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	368/375 (98%)	298 (81%)	61 (17%)	9 (2%)	7	39
1	B	368/375 (98%)	287 (78%)	71 (19%)	10 (3%)	6	35
2	D	18/93 (19%)	14 (78%)	4 (22%)	0	100	100
2	E	18/93 (19%)	16 (89%)	2 (11%)	0	100	100
All	All	772/936 (82%)	615 (80%)	138 (18%)	19 (2%)	6	38

All (19) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	42	GLY
1	A	60	SER
1	B	42	GLY
1	B	60	SER
1	B	137	GLN
1	A	202	THR
1	B	47	MET
1	B	179	ASP
1	A	99	GLU
1	A	179	ASP

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Mol	Chain	Res	Type
1	A	290	ARG
1	A	47	MET
1	A	315	LYS
1	B	356	TRP
1	A	45	VAL
1	B	345	ILE
1	B	15	GLY
1	B	45	VAL
1	B	339	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	313/317 (99%)	303 (97%)	10 (3%)	44	78
1	B	313/317 (99%)	298 (95%)	15 (5%)	30	68
2	D	15/76 (20%)	15 (100%)	0	100	100
2	E	15/76 (20%)	14 (93%)	1 (7%)	19	56
All	All	656/786 (84%)	630 (96%)	26 (4%)	36	73

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	221	LEU
1	A	225	ASN
1	A	244	ASP
1	A	265	SER
1	A	267	ILE
1	A	318	THR
1	A	334	GLU
1	A	335	ARG
1	A	344	SER
1	A	364	GLU
1	B	173	HIS
1	B	176	MET

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Mol	Chain	Res	Type
1	B	177	ARG
1	B	211	ASP
1	B	216	LEU
1	B	221	LEU
1	B	225	ASN
1	B	267	ILE
1	B	279	TYR
1	B	318	THR
1	B	334	GLU
1	B	335	ARG
1	B	344	SER
1	B	364	GLU
1	B	370	VAL
2	E	435	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	59	GLN
1	A	92	ASN
1	A	162	ASN
1	A	173	HIS
1	A	246	GLN
1	A	280	ASN
1	A	296	ASN
1	A	354	GLN
1	B	59	GLN
1	B	92	ASN
1	B	246	GLN
1	B	275	HIS
1	B	280	ASN
1	B	354	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues are modelled in this entry.

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	$\# Z > 2$
1	HIC	A	73	1	9,11,12	0.93	1 (11%)	7,14,16	1.02	0
1	HIC	B	73	1	9,11,12	0.67	0	7,14,16	1.04	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
1	HIC	A	73	1	-	0/4/6/8	0/1/1/1
1	HIC	B	73	1	-	0/4/6/8	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	73	HIC	CA-C	2.13	1.53	1.50

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

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	ATP	A	1376	4	27,33,33	1.21	4 (14%)	25,52,52	0.88	0
3	ATP	B	1376	4	27,33,33	1.04	1 (3%)	25,52,52	1.04	2 (8%)

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	ATP	A	1376	4	-	0/18/38/38	0/3/3/3
3	ATP	B	1376	4	-	0/18/38/38	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1376	ATP	C8-N7	-2.09	1.30	1.34
3	A	1376	ATP	PG-O2G	-2.01	1.46	1.54
3	A	1376	ATP	C4-N3	2.12	1.38	1.35
3	A	1376	ATP	C2-N3	2.38	1.36	1.32
3	B	1376	ATP	O4'-C1'	2.64	1.44	1.41

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1376	ATP	C4-C5-N7	2.04	111.39	109.41
3	B	1376	ATP	O3G-PG-O2G	2.16	116.33	107.61

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1376	ATP	1	0
3	B	1376	ATP	3	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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	370/375 (98%)	0.16	12 (3%) 48 32	10, 24, 59, 75	0
1	B	370/375 (98%)	0.36	13 (3%) 44 29	9, 24, 59, 75	0
2	D	20/93 (21%)	0.29	2 (10%) 8 5	18, 35, 67, 68	0
2	E	20/93 (21%)	0.63	2 (10%) 8 5	17, 35, 58, 59	0
All	All	780/936 (83%)	0.27	29 (3%) 42 27	9, 24, 59, 75	0

All (29) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	248	ILE	4.3
1	A	244	ASP	3.3
1	A	234	SER	3.3
1	A	40	HIS	2.8
1	B	246	GLN	2.7
1	B	47	MET	2.7
1	B	179	ASP	2.7
1	A	231	ALA	2.7
1	A	41	GLN	2.6
1	A	366	GLY	2.4
1	B	368	SER	2.4
1	A	230	ALA	2.4
2	E	440	GLN	2.3
1	A	237	GLU	2.3
2	D	451	ALA	2.3
1	A	49	GLN	2.3
1	A	51	ASP	2.3
1	B	168	GLY	2.2
1	A	229	THR	2.2
1	B	358	THR	2.2
1	B	173	HIS	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	367	PRO	2.1
1	A	363	ASP	2.1
1	B	232	SER	2.1
2	E	445	ILE	2.1
1	B	231	ALA	2.1
1	B	240	TYR	2.0
2	D	450	VAL	2.0
1	B	106	THR	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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, 95th 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 ²)	Q<0.9
1	HIC	B	73	11/12	0.82	0.27	-	26,40,40,40	0
1	HIC	A	73	11/12	0.95	0.25	-	27,40,40,40	0

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, 95th 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 ²)	Q<0.9
3	ATP	A	1376	31/31	0.95	0.22	-0.03	12,12,12,12	0
3	ATP	B	1376	31/31	0.92	0.19	-1.19	13,13,13,13	0
4	CA	B	1377	1/1	0.88	0.18	-1.61	11,11,11,11	0
4	CA	A	1377	1/1	0.97	0.16	-1.82	7,7,7,7	0

6.5 Other polymers [i](#)

There are no such residues in this entry.