



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 15, 2017 – 03:12 am GMT

PDB ID : 2PFD
Title : Anisotropically refined structure of FTCD
Authors : Poon, B.K.; Chen, X.; Lu, M.; Quioco, F.A.; Wang, Q.; Ma, J.
Deposited on : 2007-04-04
Resolution : 3.42 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

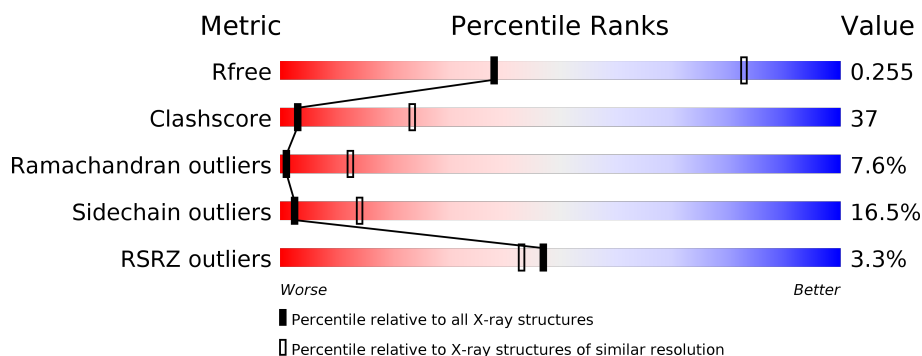
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.42 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	1074 (3.50-3.34)
Clashscore	112137	1179 (3.50-3.34)
Ramachandran outliers	110173	1147 (3.50-3.34)
Sidechain outliers	110143	1148 (3.50-3.34)
RSRZ outliers	101464	1100 (3.50-3.34)

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	541	<div> <div>3%</div> <div> <div></div> <div>47%</div> <div>39%</div> <div>12%</div> <div>.</div> </div> </div>
1	B	541	<div> <div>2%</div> <div> <div></div> <div>45%</div> <div>40%</div> <div>13%</div> <div>.</div> </div> </div>
1	C	541	<div> <div>4%</div> <div> <div></div> <div>47%</div> <div>38%</div> <div>13%</div> <div>.</div> </div> </div>
1	D	541	<div> <div>4%</div> <div> <div></div> <div>48%</div> <div>38%</div> <div>12%</div> <div>.</div> </div> </div>

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 16524 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.

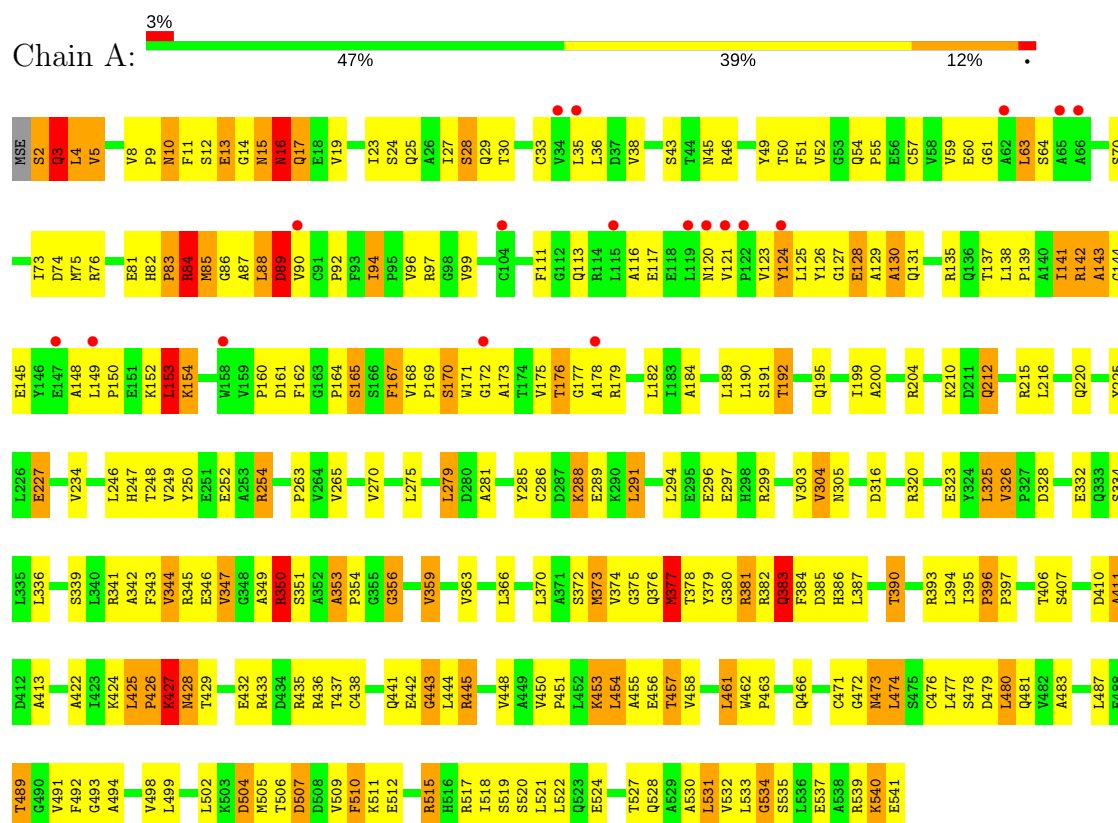
- Molecule 1 is a protein called Formimidoyltransferase-cyclodeaminase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	540	Total 4131	C 2602	N 731	O 779	S 11	Se 8	0	0	0
1	B	540	Total 4131	C 2602	N 731	O 779	S 11	Se 8	0	0	0
1	C	540	Total 4131	C 2602	N 731	O 779	S 11	Se 8	0	0	0
1	D	540	Total 4131	C 2602	N 731	O 779	S 11	Se 8	0	0	0

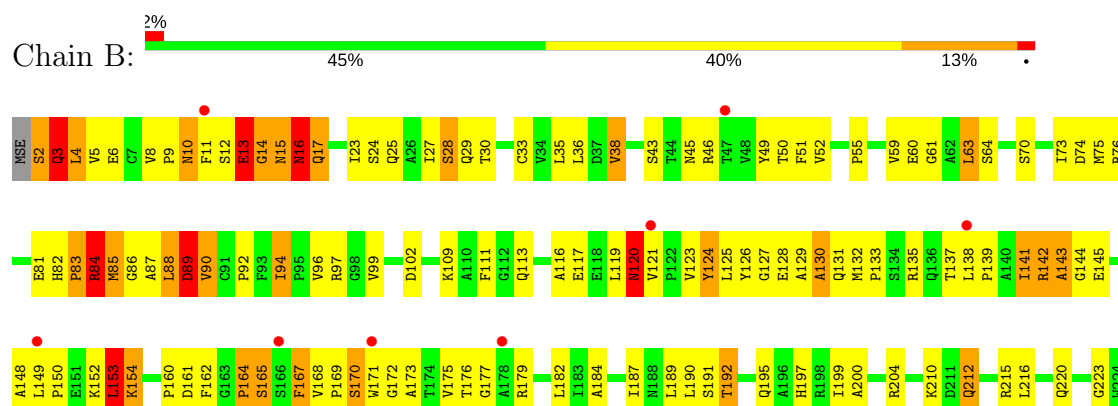
3 Residue-property plots

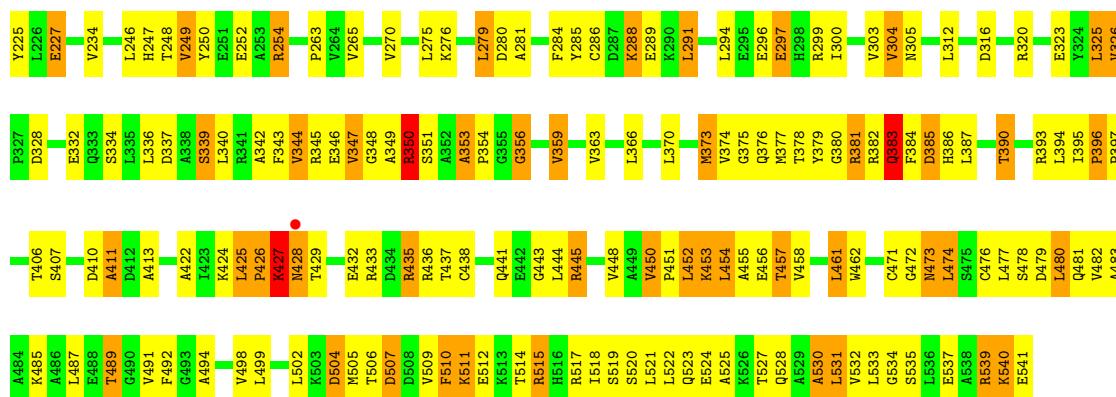
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are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

• Molecule 1: Formimidoyltransferase-cyclodeaminase

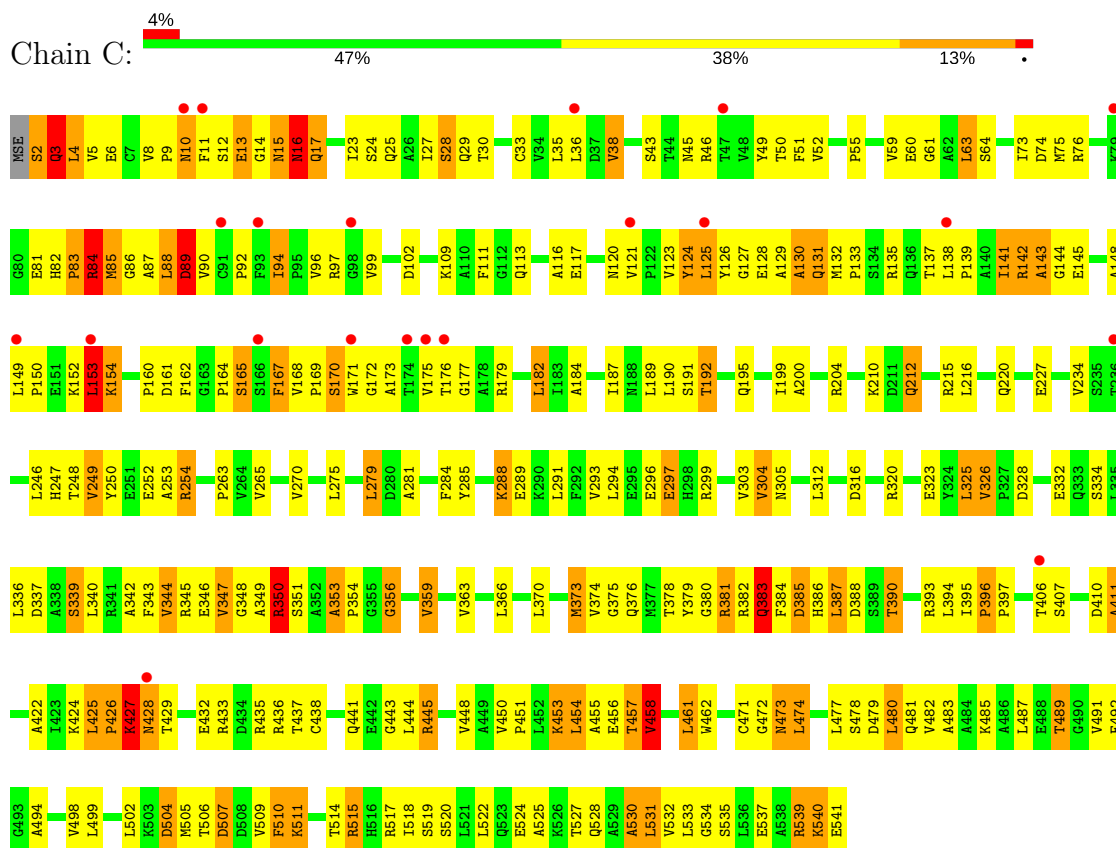


• Molecule 1: Formimidoyltransferase-cyclodeaminase

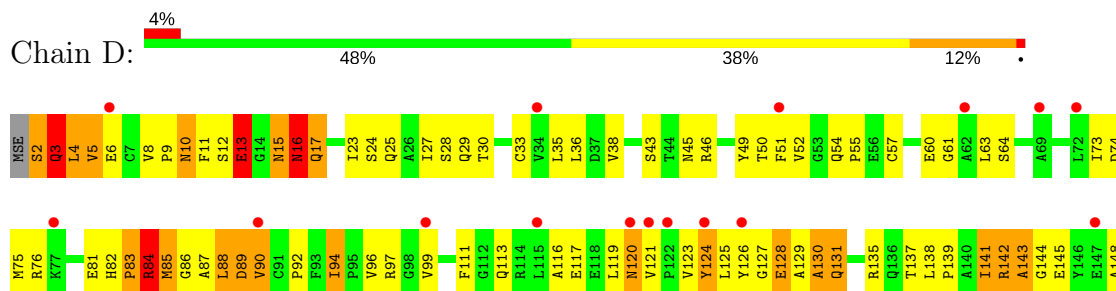




• Molecule 1: Formimidoyltransferase-cyclodeaminase



• Molecule 1: Formimidoyltransferase-cyclodeaminase



F492	L502	L149	E227	L336	A422
G493	K503	P150	E227	L336	A422
A494	D504	E151	V234	S339	A423
	M505	K152	L246	L340	A424
V498	T506	L153	A342	R341	L425
L499	D507	K154	T248	F343	P426
	L502	E157	V249	V344	K427
K503	D508	P160	V250	V345	M428
M504	V509	D161	E251	R346	T429
M505	T506	F162	E252	V347	E432
D507	D507	G163	A253	G348	R433
D508	V509	P164	R254	A349	D434
V509	F510	S165	L250	R350	R435
F510	K511	S166	L250	S351	R436
K511	E512	F167	P263	A352	T437
E512	K513	V168	V264	A353	C438
K513	T514	P169	V265	P354	
T514	R515	G172	V270	G355	D441
R515	H516	A173	P274	G356	E442
H516	L517	T174		V359	G443
L517	I518	G176		V363	L444
I518	S519	T177		L366	R445
S519	S520	A178	L279	L370	V448
S520	L521	R179	D280	L370	A449
L521	Q523	G177	A281	M373	V450
Q523	E524	R177	F284	V374	K453
E524		G178	Y285	C286	L454
	T527	T182	C286	G375	A455
T527	Q528	L183	D287	Q376	E456
Q528	A529	A184	K288	M377	T457
A529	L530	I187	E289	K290	V458
L530	V531	N188	L291	Y379	
V531	V532	L189	L291	G380	L461
V532	L533	L190	L294	R381	W462
L533	G534	S191		R382	P463
G534	S535	T192		F384	Q466
S535	L536	Q195	R299	D385	
L536	E537	R198	V303	H386	C471
E537	A538	I199	Y304	L387	G472
A538	R539	A200	N305	T390	M473
R539	K540	R204	D316	R393	L474
K540	E541	I204	R320	L394	S475
E541		K210	E323	I395	G476
		D211	Y324	P396	L477
		Q212	L325	P397	S478
		R215	V326	T406	D479
		L216	D328	S407	L480
		Q220	E332	D410	Q481
		Y225	Q333	A411	V482
		L226	S334	D412	A483
			L335	A413	L487
					E488
					T489
					G490
					Y491

4 Data and refinement statistics

Property	Value	Source
Space group	P 4	Depositor
Cell constants a, b, c, α , β , γ	134.85Å 134.85Å 156.37Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 3.42 47.75 – 3.42	Depositor EDS
% Data completeness (in resolution range)	94.0 (10.00-3.42) 96.0 (47.75-3.42)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.33 (at 3.40Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.240 , 0.249 0.242 , 0.255	Depositor DCC
R_{free} test set	1797 reflections (5.21%)	DCC
Wilson B-factor (Å ²)	57.0	Xtriage
Anisotropy	0.563	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 18.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.40$, $\langle L^2 \rangle = 0.22$	Xtriage
Estimated twinning fraction	0.367 for h,-k,-l	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	16524	wwPDB-VP
Average B, all atoms (Å ²)	74.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.09% 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	0.58	1/4195 (0.0%)	0.76	5/5674 (0.1%)
1	B	0.59	2/4195 (0.0%)	0.82	8/5674 (0.1%)
1	C	0.52	1/4195 (0.0%)	0.75	5/5674 (0.1%)
1	D	0.60	3/4195 (0.1%)	0.75	5/5674 (0.1%)
All	All	0.57	7/16780 (0.0%)	0.77	23/22696 (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
1	B	0	1
1	C	0	1
1	D	0	1
All	All	0	4

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	13	GLU	CD-OE1	14.62	1.41	1.25
1	D	153	LEU	CG-CD2	-8.97	1.18	1.51
1	B	153	LEU	CG-CD2	-7.96	1.22	1.51
1	A	153	LEU	CG-CD2	-7.45	1.24	1.51
1	C	153	LEU	CG-CD2	-7.37	1.24	1.51
1	B	13	GLU	C-O	-5.96	1.12	1.23
1	D	13	GLU	CD-OE2	5.05	1.31	1.25

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	435	ARG	NE-CZ-NH2	-14.22	113.19	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	435	ARG	NE-CZ-NH1	13.88	127.24	120.30
1	D	153	LEU	CB-CG-CD1	11.02	129.73	111.00
1	B	153	LEU	CB-CG-CD1	10.56	128.95	111.00
1	A	153	LEU	CB-CG-CD1	9.31	126.83	111.00
1	A	153	LEU	CB-CG-CD2	-9.16	95.43	111.00
1	C	153	LEU	CB-CG-CD1	8.85	126.04	111.00
1	B	153	LEU	CB-CG-CD2	-8.11	97.21	111.00
1	C	153	LEU	CB-CG-CD2	-7.59	98.10	111.00
1	D	153	LEU	CB-CG-CD2	-7.08	98.96	111.00
1	B	13	GLU	CA-C-N	6.94	130.07	116.20
1	B	435	ARG	CD-NE-CZ	6.68	132.96	123.60
1	A	377	MSE	CB-CG-SE	6.67	132.70	112.70
1	D	153	LEU	CA-CB-CG	6.66	130.61	115.30
1	D	153	LEU	CD1-CG-CD2	-6.54	90.86	110.50
1	A	377	MSE	CG-SE-CE	6.44	113.06	98.90
1	B	153	LEU	CD1-CG-CD2	-6.04	92.37	110.50
1	C	458	VAL	CG1-CB-CG2	-5.94	101.39	110.90
1	A	435	ARG	NE-CZ-NH1	-5.57	117.52	120.30
1	C	435	ARG	NE-CZ-NH1	-5.38	117.61	120.30
1	D	435	ARG	NE-CZ-NH1	-5.21	117.69	120.30
1	B	452	LEU	CA-CB-CG	5.09	127.01	115.30
1	C	125	LEU	CA-CB-CG	5.05	126.91	115.30

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	427	LYS	Peptide
1	B	427	LYS	Peptide
1	C	427	LYS	Peptide
1	D	427	LYS	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	4131	0	4175	325	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	4131	0	4175	333	0
1	C	4131	0	4175	322	0
1	D	4131	0	4175	315	0
All	All	16524	0	16700	1227	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 37.

All (1227) 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:C:351:SER:O	1:D:373:MSE:HE2	1.37	1.22
1:A:373:MSE:HE2	1:B:351:SER:O	1.44	1.18
1:C:427:LYS:HE3	1:C:436:ARG:NH1	1.63	1.14
1:B:426:PRO:O	1:B:427:LYS:HB2	1.48	1.13
1:B:2:SER:N	1:B:328:ASP:HB2	1.63	1.13
1:B:427:LYS:HE3	1:B:436:ARG:NH1	1.66	1.11
1:A:27:ILE:HD11	1:A:51:PHE:CD1	1.86	1.11
1:C:2:SER:N	1:C:328:ASP:HB2	1.64	1.11
1:A:427:LYS:HE3	1:A:436:ARG:HH12	1.16	1.11
1:C:347:VAL:O	1:D:373:MSE:HE3	1.52	1.10
1:C:489:THR:HG21	1:D:489:THR:HG21	1.11	1.10
1:A:2:SER:N	1:A:328:ASP:HB2	1.67	1.10
1:C:149:LEU:CD2	1:C:153:LEU:HD23	1.81	1.09
1:B:27:ILE:HD11	1:B:51:PHE:CD1	1.87	1.09
1:A:427:LYS:HE3	1:A:436:ARG:NH1	1.66	1.09
1:A:373:MSE:HE3	1:B:347:VAL:O	1.52	1.09
1:D:2:SER:N	1:D:328:ASP:HB2	1.67	1.09
1:C:427:LYS:HE3	1:C:436:ARG:HH12	1.10	1.08
1:B:359:VAL:O	1:B:363:VAL:HG23	1.54	1.08
1:D:427:LYS:HE3	1:D:436:ARG:NH1	1.67	1.07
1:C:359:VAL:O	1:C:363:VAL:HG23	1.54	1.07
1:C:425:LEU:HD22	1:C:426:PRO:HD2	1.35	1.07
1:C:149:LEU:HD22	1:C:153:LEU:HD23	1.16	1.07
1:C:27:ILE:HD11	1:C:51:PHE:CD1	1.89	1.07
1:D:27:ILE:HD11	1:D:51:PHE:CD1	1.90	1.06
1:C:426:PRO:O	1:C:427:LYS:HB2	1.50	1.06
1:D:426:PRO:O	1:D:427:LYS:HB2	1.52	1.06
1:D:531:LEU:H	1:D:531:LEU:HD23	1.20	1.06
1:A:426:PRO:O	1:A:427:LYS:HB2	1.52	1.06
1:D:427:LYS:HE3	1:D:436:ARG:HH12	1.16	1.05

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:425:LEU:HD22	1:D:426:PRO:HD2	1.37	1.05
1:A:359:VAL:O	1:A:363:VAL:HG23	1.56	1.05
1:D:359:VAL:O	1:D:363:VAL:HG23	1.55	1.05
1:A:5:VAL:HG23	1:A:99:VAL:HG11	1.34	1.05
1:D:5:VAL:HG23	1:D:99:VAL:HG11	1.34	1.05
1:A:489:THR:CG2	1:B:489:THR:HG21	1.88	1.04
1:B:425:LEU:HD22	1:B:426:PRO:HD2	1.33	1.04
1:D:149:LEU:O	1:D:153:LEU:HD12	1.57	1.04
1:A:425:LEU:HD22	1:A:426:PRO:HD2	1.37	1.02
1:B:5:VAL:HG23	1:B:99:VAL:HG11	1.38	1.02
1:A:351:SER:O	1:B:373:MSE:HE2	1.58	1.02
1:C:5:VAL:HG23	1:C:99:VAL:HG11	1.38	1.01
1:A:531:LEU:H	1:A:531:LEU:HD23	1.21	1.01
1:A:27:ILE:HD11	1:A:51:PHE:CE1	1.96	1.01
1:B:27:ILE:HD11	1:B:51:PHE:CE1	1.95	1.00
1:D:153:LEU:HD23	1:D:165:SER:O	1.61	1.00
1:B:427:LYS:HE3	1:B:436:ARG:HH12	1.14	0.99
1:C:502:LEU:HA	1:C:505:MSE:HG3	1.42	0.99
1:B:531:LEU:H	1:B:531:LEU:HD23	1.27	0.98
1:C:27:ILE:HD11	1:C:51:PHE:CE1	1.97	0.98
1:A:489:THR:HG21	1:B:489:THR:HG21	1.00	0.98
1:C:458:VAL:HG11	1:C:491:VAL:HG22	1.42	0.98
1:C:531:LEU:H	1:C:531:LEU:HD23	1.27	0.97
1:A:489:THR:HG21	1:B:489:THR:CG2	1.95	0.96
1:D:502:LEU:HA	1:D:505:MSE:HG3	1.48	0.95
1:C:373:MSE:HE2	1:D:351:SER:O	1.67	0.94
1:B:13:GLU:HG2	1:B:13:GLU:O	1.68	0.94
1:C:489:THR:HG21	1:D:489:THR:CG2	1.97	0.94
1:D:27:ILE:HD11	1:D:51:PHE:CE1	2.01	0.94
1:C:445:ARG:HG3	1:C:445:ARG:HH11	1.32	0.93
1:A:373:MSE:HE1	1:B:354:PRO:O	1.68	0.93
1:A:502:LEU:HA	1:A:505:MSE:HG3	1.51	0.93
1:A:422:ALA:O	1:A:425:LEU:HB2	1.69	0.93
1:D:153:LEU:CD2	1:D:165:SER:O	2.17	0.93
1:B:502:LEU:HA	1:B:505:MSE:HG3	1.48	0.93
1:A:149:LEU:CD2	1:A:153:LEU:HD23	1.99	0.92
1:D:422:ALA:O	1:D:425:LEU:HB2	1.69	0.92
1:B:422:ALA:O	1:B:425:LEU:HB2	1.69	0.92
1:C:15:ASN:O	1:C:16:ASN:HB3	1.70	0.91
1:A:363:VAL:HG13	1:B:363:VAL:HG13	1.50	0.91
1:D:227:GLU:HA	1:D:227:GLU:OE1	1.70	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:15:ASN:O	1:D:16:ASN:HB3	1.71	0.91
1:D:445:ARG:HG3	1:D:445:ARG:HH11	1.35	0.91
1:B:483:ALA:O	1:B:487:LEU:HD12	1.71	0.90
1:A:370:LEU:HD11	1:B:359:VAL:HG11	1.52	0.90
1:B:445:ARG:HH11	1:B:445:ARG:HG3	1.36	0.90
1:B:15:ASN:O	1:B:16:ASN:HB3	1.70	0.90
1:C:422:ALA:O	1:C:425:LEU:HB2	1.69	0.89
1:A:15:ASN:O	1:A:16:ASN:HB3	1.70	0.89
1:D:149:LEU:O	1:D:153:LEU:CD1	2.21	0.89
1:A:390:THR:HG22	1:A:393:ARG:HH21	1.37	0.88
1:A:149:LEU:HB3	1:A:153:LEU:HD21	1.56	0.88
1:A:356:GLY:H	1:B:370:LEU:HD21	1.38	0.88
1:C:113:GLN:O	1:C:117:GLU:HG2	1.74	0.87
1:C:149:LEU:HD22	1:C:153:LEU:CD2	2.05	0.87
1:C:359:VAL:HG11	1:D:370:LEU:HD11	1.55	0.87
1:C:483:ALA:O	1:C:487:LEU:HD12	1.75	0.86
1:B:113:GLN:O	1:B:117:GLU:HG2	1.75	0.85
1:C:445:ARG:CG	1:C:445:ARG:HH11	1.89	0.85
1:A:445:ARG:HH11	1:A:445:ARG:HG3	1.38	0.85
1:C:390:THR:HG22	1:C:393:ARG:HH21	1.42	0.85
1:D:445:ARG:CG	1:D:445:ARG:HH11	1.89	0.84
1:A:370:LEU:HD21	1:B:356:GLY:H	1.40	0.84
1:A:113:GLN:O	1:A:117:GLU:HG2	1.78	0.83
1:D:483:ALA:O	1:D:487:LEU:HD12	1.78	0.83
1:C:354:PRO:O	1:D:373:MSE:HE1	1.78	0.83
1:A:227:GLU:HA	1:A:227:GLU:OE1	1.76	0.83
1:A:149:LEU:HB3	1:A:153:LEU:CD2	2.08	0.83
1:C:349:ALA:C	1:C:351:SER:H	1.79	0.83
1:A:349:ALA:C	1:A:351:SER:H	1.81	0.82
1:C:345:ARG:HH21	1:D:406:THR:HB	1.43	0.82
1:D:390:THR:HG22	1:D:393:ARG:HH21	1.41	0.82
1:A:373:MSE:CE	1:B:351:SER:OG	2.27	0.82
1:A:90:VAL:HA	1:A:175:VAL:HG23	1.60	0.82
1:C:227:GLU:OE1	1:C:227:GLU:HA	1.79	0.82
1:C:351:SER:OG	1:D:373:MSE:CE	2.26	0.82
1:A:445:ARG:HH11	1:A:445:ARG:CG	1.92	0.81
1:B:445:ARG:HH11	1:B:445:ARG:CG	1.93	0.81
1:D:15:ASN:HB2	1:D:45:ASN:OD1	1.80	0.81
1:C:2:SER:N	1:C:328:ASP:CB	2.43	0.81
1:A:15:ASN:HB2	1:A:45:ASN:OD1	1.81	0.81
1:B:15:ASN:HB2	1:B:45:ASN:OD1	1.80	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:153:LEU:HG	1:B:165:SER:O	1.80	0.81
1:B:227:GLU:HA	1:B:227:GLU:OE1	1.80	0.81
1:B:390:THR:HG22	1:B:393:ARG:HH21	1.46	0.81
1:B:2:SER:N	1:B:328:ASP:CB	2.43	0.81
1:C:90:VAL:HA	1:C:175:VAL:HG23	1.62	0.81
1:D:113:GLN:O	1:D:117:GLU:HG2	1.80	0.81
1:B:458:VAL:HG11	1:B:491:VAL:HG22	1.61	0.81
1:A:483:ALA:O	1:A:487:LEU:HD12	1.81	0.80
1:A:97:ARG:NH2	1:A:328:ASP:HB3	1.96	0.80
1:D:427:LYS:HB3	1:D:428:ASN:HD22	1.46	0.80
1:D:90:VAL:HA	1:D:175:VAL:HG23	1.62	0.80
1:C:15:ASN:HB2	1:C:45:ASN:OD1	1.81	0.80
1:A:427:LYS:HB3	1:A:428:ASN:HD22	1.47	0.80
1:A:149:LEU:HD22	1:A:153:LEU:CD2	2.11	0.79
1:B:149:LEU:HD23	1:B:153:LEU:HB3	1.64	0.79
1:B:149:LEU:CD2	1:B:153:LEU:HB3	2.11	0.79
1:B:153:LEU:C	1:B:153:LEU:HD23	2.03	0.79
1:D:97:ARG:NH2	1:D:328:ASP:HB3	1.98	0.79
1:D:515:ARG:O	1:D:518:ILE:HG22	1.83	0.78
1:B:471:CYS:SG	1:B:472:GLY:N	2.55	0.78
1:B:90:VAL:HA	1:B:175:VAL:HG23	1.63	0.78
1:B:349:ALA:C	1:B:351:SER:H	1.84	0.78
1:A:363:VAL:CG1	1:B:363:VAL:HG13	2.14	0.77
1:D:149:LEU:HD23	1:D:153:LEU:HB3	1.66	0.77
1:B:190:LEU:HB2	1:B:263:PRO:HG2	1.67	0.77
1:A:2:SER:N	1:A:328:ASP:CB	2.46	0.77
1:D:149:LEU:HD22	1:D:153:LEU:HG	1.66	0.77
1:D:2:SER:N	1:D:328:ASP:CB	2.47	0.77
1:A:515:ARG:O	1:A:518:ILE:HG22	1.84	0.77
1:C:373:MSE:HE3	1:D:347:VAL:O	1.84	0.77
1:C:370:LEU:HD21	1:D:356:GLY:H	1.50	0.76
1:C:351:SER:OG	1:D:373:MSE:HE2	1.85	0.76
1:B:13:GLU:O	1:B:15:ASN:N	2.18	0.76
1:C:363:VAL:HG13	1:D:363:VAL:HG13	1.66	0.76
1:B:97:ARG:NH2	1:B:328:ASP:HB3	2.00	0.76
1:D:494:ALA:O	1:D:498:VAL:HG23	1.84	0.76
1:C:97:ARG:NH2	1:C:328:ASP:HB3	2.00	0.76
1:D:349:ALA:C	1:D:351:SER:H	1.88	0.75
1:C:458:VAL:HG11	1:C:491:VAL:CG2	2.17	0.75
1:D:25:GLN:HB3	1:D:29:GLN:NE2	2.01	0.75
1:A:342:ALA:O	1:A:346:GLU:HB2	1.87	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:25:GLN:HB3	1:C:29:GLN:NE2	2.01	0.74
1:C:471:CYS:SG	1:C:472:GLY:N	2.60	0.74
1:A:494:ALA:O	1:A:498:VAL:HG23	1.86	0.74
1:C:356:GLY:H	1:D:370:LEU:HD21	1.53	0.74
1:D:473:ASN:O	1:D:474:LEU:HB2	1.87	0.74
1:B:25:GLN:HB3	1:B:29:GLN:NE2	2.03	0.73
1:B:396:PRO:HB2	1:B:397:PRO:CD	2.18	0.73
1:C:116:ALA:HB2	1:C:123:VAL:HG12	1.69	0.73
1:C:454:LEU:O	1:C:454:LEU:HD12	1.87	0.73
1:D:116:ALA:HB2	1:D:123:VAL:HG12	1.71	0.73
1:A:116:ALA:HB2	1:A:123:VAL:HG12	1.70	0.73
1:C:494:ALA:O	1:C:498:VAL:HG23	1.88	0.73
1:A:25:GLN:HB3	1:A:29:GLN:NE2	2.04	0.72
1:D:216:LEU:HD21	1:D:252:GLU:HG2	1.71	0.72
1:D:342:ALA:O	1:D:346:GLU:HB2	1.88	0.72
1:B:116:ALA:HB2	1:B:123:VAL:HG12	1.69	0.72
1:D:382:ARG:O	1:D:383:GLN:HB3	1.88	0.72
1:A:458:VAL:HG11	1:A:491:VAL:HG22	1.71	0.72
1:A:373:MSE:HE3	1:B:351:SER:OG	1.89	0.71
1:A:347:VAL:O	1:B:373:MSE:HE3	1.90	0.71
1:C:190:LEU:HB2	1:C:263:PRO:HG2	1.72	0.71
1:C:427:LYS:HB3	1:C:428:ASN:HD22	1.54	0.71
1:B:494:ALA:O	1:B:498:VAL:HG23	1.89	0.71
1:D:149:LEU:CD2	1:D:153:LEU:HB3	2.20	0.71
1:B:342:ALA:O	1:B:346:GLU:HB2	1.91	0.71
1:C:342:ALA:O	1:C:346:GLU:HB2	1.90	0.71
1:C:396:PRO:HB2	1:C:397:PRO:CD	2.20	0.71
1:C:515:ARG:O	1:C:518:ILE:HG22	1.91	0.71
1:A:135:ARG:HG2	1:A:141:ILE:HD11	1.73	0.71
1:A:406:THR:HB	1:B:345:ARG:HH21	1.55	0.71
1:B:135:ARG:HG2	1:B:141:ILE:HD11	1.73	0.71
1:B:149:LEU:HB3	1:B:153:LEU:HD13	1.73	0.71
1:C:382:ARG:O	1:C:383:GLN:HB3	1.90	0.71
1:D:11:PHE:CE1	1:D:88:LEU:HD12	2.26	0.71
1:C:135:ARG:HG2	1:C:141:ILE:HD11	1.72	0.70
1:B:427:LYS:HB3	1:B:428:ASN:HD22	1.55	0.70
1:C:13:GLU:HG2	1:C:15:ASN:N	2.06	0.70
1:A:386:HIS:CD2	1:A:387:LEU:HD12	2.26	0.70
1:A:13:GLU:HG2	1:A:15:ASN:N	2.06	0.70
1:C:473:ASN:O	1:C:474:LEU:HB2	1.91	0.70
1:D:190:LEU:HB2	1:D:263:PRO:HG2	1.74	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:116:ALA:HB2	1:C:123:VAL:CG1	2.22	0.70
1:A:149:LEU:CD2	1:A:153:LEU:CD2	2.68	0.70
1:A:149:LEU:HD23	1:A:153:LEU:HD23	1.72	0.70
1:D:458:VAL:HG11	1:D:491:VAL:HG22	1.73	0.70
1:A:216:LEU:HD21	1:A:252:GLU:HG2	1.72	0.69
1:B:454:LEU:O	1:B:454:LEU:HD12	1.91	0.69
1:A:190:LEU:HB2	1:A:263:PRO:HG2	1.74	0.69
1:D:76:ARG:NH2	1:D:169:PRO:HB3	2.08	0.69
1:B:515:ARG:O	1:B:518:ILE:HG22	1.92	0.69
1:A:471:CYS:SG	1:A:472:GLY:N	2.65	0.69
1:D:424:LYS:HG3	1:D:424:LYS:O	1.93	0.69
1:D:458:VAL:HG23	1:D:487:LEU:HD23	1.74	0.69
1:D:13:GLU:H	1:D:46:ARG:HA	1.57	0.69
1:B:176:THR:CG2	1:B:177:GLY:N	2.56	0.69
1:C:148:ALA:N	1:C:150:PRO:HD2	2.08	0.69
1:C:76:ARG:NH2	1:C:169:PRO:HB3	2.08	0.68
1:A:473:ASN:O	1:A:474:LEU:HB2	1.93	0.68
1:B:76:ARG:NH2	1:B:169:PRO:HB3	2.08	0.68
1:B:116:ALA:HB2	1:B:123:VAL:CG1	2.23	0.68
1:A:382:ARG:O	1:A:383:GLN:HB3	1.92	0.68
1:D:148:ALA:C	1:D:150:PRO:HD2	2.14	0.68
1:D:13:GLU:HG2	1:D:15:ASN:N	2.08	0.68
1:D:25:GLN:HB3	1:D:29:GLN:HE21	1.59	0.68
1:C:148:ALA:C	1:C:150:PRO:HD2	2.13	0.68
1:A:424:LYS:HG3	1:A:424:LYS:O	1.94	0.68
1:A:396:PRO:HB2	1:A:397:PRO:CD	2.24	0.68
1:A:427:LYS:HB3	1:A:428:ASN:ND2	2.09	0.68
1:B:473:ASN:O	1:B:474:LEU:HB2	1.92	0.68
1:C:489:THR:CG2	1:D:489:THR:HG21	2.07	0.68
1:C:445:ARG:HG3	1:C:445:ARG:NH1	2.07	0.68
1:D:471:CYS:SG	1:D:472:GLY:N	2.67	0.68
1:A:116:ALA:HB2	1:A:123:VAL:CG1	2.24	0.67
1:A:373:MSE:HE2	1:B:351:SER:OG	1.93	0.67
1:B:374:VAL:HG21	1:B:480:LEU:HD22	1.76	0.67
1:D:11:PHE:CZ	1:D:88:LEU:HD11	2.29	0.67
1:B:148:ALA:C	1:B:150:PRO:HD2	2.14	0.67
1:D:116:ALA:HB2	1:D:123:VAL:CG1	2.24	0.67
1:B:148:ALA:N	1:B:150:PRO:HD2	2.09	0.67
1:C:427:LYS:HG3	1:C:436:ARG:HH11	1.60	0.67
1:D:316:ASP:O	1:D:320:ARG:HG2	1.95	0.67
1:C:374:VAL:HG21	1:C:480:LEU:HD22	1.77	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:11:PHE:CE1	1:A:88:LEU:HD12	2.29	0.67
1:A:531:LEU:H	1:A:531:LEU:CD2	2.01	0.67
1:D:427:LYS:HB3	1:D:428:ASN:ND2	2.08	0.67
1:A:148:ALA:C	1:A:150:PRO:HD2	2.15	0.67
1:A:111:PHE:HD2	1:A:176:THR:HG1	1.40	0.67
1:A:176:THR:CG2	1:A:177:GLY:N	2.58	0.67
1:B:299:ARG:O	1:B:303:VAL:HG12	1.95	0.67
1:D:8:VAL:O	1:D:8:VAL:HG12	1.95	0.67
1:A:76:ARG:NH2	1:A:169:PRO:HB3	2.10	0.67
1:C:386:HIS:CD2	1:C:387:LEU:HD12	2.30	0.67
1:D:299:ARG:O	1:D:303:VAL:HG12	1.95	0.67
1:C:351:SER:OG	1:D:373:MSE:HE3	1.95	0.67
1:D:396:PRO:HB2	1:D:397:PRO:CD	2.25	0.67
1:C:25:GLN:HB3	1:C:29:GLN:HE21	1.58	0.66
1:A:149:LEU:HD22	1:A:153:LEU:HD22	1.75	0.66
1:C:299:ARG:O	1:C:303:VAL:HG12	1.95	0.66
1:D:148:ALA:N	1:D:150:PRO:HD2	2.10	0.66
1:A:373:MSE:CE	1:B:354:PRO:O	2.43	0.66
1:C:76:ARG:CZ	1:C:169:PRO:HB2	2.24	0.66
1:B:13:GLU:CG	1:B:13:GLU:O	2.36	0.66
1:A:76:ARG:CZ	1:A:169:PRO:HB2	2.26	0.66
1:D:386:HIS:CD2	1:D:387:LEU:HD12	2.31	0.66
1:B:76:ARG:CZ	1:B:169:PRO:HB2	2.25	0.66
1:B:386:HIS:CD2	1:B:387:LEU:HD12	2.30	0.66
1:B:382:ARG:O	1:B:383:GLN:HB3	1.96	0.66
1:B:427:LYS:HG3	1:B:436:ARG:HH11	1.61	0.66
1:B:531:LEU:H	1:B:531:LEU:CD2	2.05	0.66
1:D:531:LEU:CD2	1:D:531:LEU:H	1.99	0.66
1:A:13:GLU:H	1:A:46:ARG:HA	1.61	0.66
1:A:374:VAL:HG21	1:A:480:LEU:CD2	2.26	0.66
1:A:148:ALA:N	1:A:150:PRO:HD2	2.10	0.65
1:A:374:VAL:HG21	1:A:480:LEU:HD22	1.78	0.65
1:B:25:GLN:HB3	1:B:29:GLN:HE21	1.61	0.65
1:C:13:GLU:H	1:C:46:ARG:HA	1.60	0.65
1:D:76:ARG:CZ	1:D:169:PRO:HB2	2.25	0.65
1:D:46:ARG:CZ	1:D:82:HIS:HD2	2.10	0.65
1:A:299:ARG:O	1:A:303:VAL:HG12	1.97	0.65
1:B:458:VAL:CG1	1:B:491:VAL:HG22	2.27	0.65
1:B:502:LEU:HA	1:B:505:MSE:CG	2.26	0.65
1:C:8:VAL:HG12	1:C:8:VAL:O	1.96	0.65
1:D:374:VAL:HG21	1:D:480:LEU:HD22	1.78	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:189:LEU:HD12	1:A:234:VAL:HG23	1.79	0.65
1:A:247:HIS:CD2	1:A:281:ALA:HA	2.32	0.65
1:A:316:ASP:O	1:A:320:ARG:HG2	1.97	0.65
1:C:46:ARG:CZ	1:C:82:HIS:HD2	2.10	0.65
1:A:25:GLN:HB3	1:A:29:GLN:HE21	1.61	0.64
1:A:344:VAL:HG22	1:A:345:ARG:HG2	1.78	0.64
1:C:11:PHE:CZ	1:C:88:LEU:HD11	2.32	0.64
1:C:502:LEU:HA	1:C:505:MSE:CG	2.24	0.64
1:D:189:LEU:HD12	1:D:234:VAL:HG23	1.79	0.64
1:D:247:HIS:CD2	1:D:281:ALA:HA	2.31	0.64
1:B:374:VAL:HG21	1:B:480:LEU:CD2	2.27	0.64
1:C:247:HIS:CD2	1:C:281:ALA:HA	2.32	0.64
1:D:176:THR:CG2	1:D:177:GLY:N	2.60	0.64
1:B:46:ARG:CZ	1:B:82:HIS:HD2	2.10	0.64
1:C:189:LEU:HD12	1:C:234:VAL:HG23	1.80	0.64
1:C:316:ASP:O	1:C:320:ARG:HG2	1.98	0.64
1:D:351:SER:HB2	1:D:354:PRO:HD2	1.80	0.64
1:A:46:ARG:CZ	1:A:82:HIS:HD2	2.10	0.64
1:C:374:VAL:HG21	1:C:480:LEU:CD2	2.27	0.64
1:D:149:LEU:C	1:D:153:LEU:HD12	2.18	0.64
1:B:426:PRO:O	1:B:427:LYS:CB	2.35	0.64
1:D:11:PHE:CE1	1:D:88:LEU:CD1	2.81	0.64
1:D:441:GLN:OE1	1:D:505:MSE:HA	1.97	0.64
1:A:11:PHE:CZ	1:A:88:LEU:HD11	2.33	0.64
1:A:386:HIS:CD2	1:A:387:LEU:CD1	2.81	0.64
1:A:458:VAL:HG23	1:A:487:LEU:HD23	1.80	0.64
1:A:441:GLN:OE1	1:A:505:MSE:HA	1.98	0.64
1:B:13:GLU:HG2	1:B:15:ASN:N	2.13	0.64
1:A:373:MSE:CE	1:B:351:SER:O	2.36	0.64
1:D:502:LEU:HA	1:D:505:MSE:CG	2.25	0.63
1:B:441:GLN:OE1	1:B:505:MSE:HA	1.99	0.63
1:B:8:VAL:HG12	1:B:8:VAL:O	1.97	0.63
1:C:285:TYR:O	1:C:289:GLU:HB2	1.98	0.63
1:B:247:HIS:CD2	1:B:281:ALA:HA	2.33	0.63
1:C:427:LYS:HB3	1:C:428:ASN:ND2	2.12	0.63
1:D:454:LEU:O	1:D:454:LEU:HD12	1.98	0.63
1:C:424:LYS:O	1:C:424:LYS:HG3	1.97	0.63
1:C:363:VAL:HG13	1:D:363:VAL:CG1	2.27	0.63
1:C:427:LYS:CE	1:C:436:ARG:HH12	2.00	0.63
1:D:425:LEU:HB3	1:D:436:ARG:HG3	1.80	0.63
1:D:285:TYR:O	1:D:289:GLU:HB2	1.98	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:176:THR:CG2	1:C:177:GLY:N	2.61	0.63
1:B:424:LYS:O	1:B:424:LYS:HG3	1.98	0.63
1:D:382:ARG:O	1:D:383:GLN:CB	2.46	0.63
1:A:111:PHE:HD2	1:A:176:THR:OG1	1.82	0.62
1:A:200:ALA:HB2	1:A:234:VAL:HG13	1.81	0.62
1:A:8:VAL:O	1:A:8:VAL:HG12	1.97	0.62
1:D:374:VAL:HG21	1:D:480:LEU:CD2	2.30	0.62
1:C:111:PHE:HD2	1:C:176:THR:OG1	1.83	0.62
1:C:425:LEU:HB3	1:C:436:ARG:HG3	1.81	0.62
1:A:425:LEU:HB3	1:A:436:ARG:HG3	1.81	0.62
1:B:427:LYS:HB3	1:B:428:ASN:ND2	2.13	0.62
1:B:453:LYS:O	1:B:457:THR:HG22	1.99	0.62
1:C:149:LEU:HB3	1:C:153:LEU:CD2	2.30	0.62
1:C:458:VAL:HG22	1:C:487:LEU:HD23	1.82	0.62
1:D:200:ALA:HB2	1:D:234:VAL:HG13	1.80	0.62
1:B:189:LEU:HD11	1:B:199:ILE:HD12	1.82	0.62
1:B:425:LEU:HB3	1:B:436:ARG:HG3	1.81	0.62
1:A:370:LEU:HD11	1:B:359:VAL:CG1	2.27	0.62
1:B:200:ALA:HB2	1:B:234:VAL:HG13	1.82	0.62
1:B:285:TYR:O	1:B:289:GLU:HB2	1.99	0.62
1:B:506:THR:O	1:B:507:ASP:CB	2.46	0.62
1:A:427:LYS:HG3	1:A:436:ARG:HH11	1.65	0.62
1:C:254:ARG:HH11	1:C:254:ARG:HB3	1.65	0.62
1:C:351:SER:O	1:D:373:MSE:CE	2.30	0.62
1:C:386:HIS:CD2	1:C:387:LEU:CD1	2.83	0.62
1:C:200:ALA:HB2	1:C:234:VAL:HG13	1.81	0.61
1:D:111:PHE:HD2	1:D:176:THR:OG1	1.83	0.61
1:B:11:PHE:CE1	1:B:88:LEU:HD12	2.34	0.61
1:D:111:PHE:HD2	1:D:176:THR:HG1	1.47	0.61
1:A:11:PHE:CE1	1:A:88:LEU:CD1	2.83	0.61
1:C:149:LEU:HB3	1:C:153:LEU:HD21	1.82	0.61
1:C:441:GLN:OE1	1:C:505:MSE:HA	2.00	0.61
1:B:189:LEU:HD12	1:B:234:VAL:HG23	1.82	0.61
1:B:386:HIS:CD2	1:B:387:LEU:CD1	2.83	0.61
1:B:458:VAL:HG23	1:B:487:LEU:HD23	1.82	0.61
1:C:9:PRO:HG2	1:C:49:TYR:HB2	1.83	0.61
1:D:82:HIS:O	1:D:84:ARG:N	2.34	0.61
1:B:111:PHE:HD2	1:B:176:THR:OG1	1.84	0.61
1:A:2:SER:O	1:A:3:GLN:HB2	2.01	0.61
1:B:349:ALA:C	1:B:351:SER:N	2.54	0.61
1:C:506:THR:O	1:C:507:ASP:CB	2.49	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:478:SER:OG	1:D:479:ASP:N	2.33	0.61
1:A:390:THR:HG22	1:A:393:ARG:NH2	2.14	0.61
1:A:458:VAL:CG2	1:A:487:LEU:HD23	2.31	0.61
1:B:458:VAL:CG2	1:B:487:LEU:HD23	2.31	0.61
1:C:462:TRP:HB3	1:C:528:GLN:HG2	1.83	0.61
1:A:35:LEU:HD12	1:A:51:PHE:HB3	1.83	0.61
1:D:254:ARG:HB3	1:D:254:ARG:HH11	1.65	0.61
1:B:11:PHE:CZ	1:B:88:LEU:HD11	2.36	0.60
1:C:215:ARG:CZ	1:C:252:GLU:OE2	2.49	0.60
1:A:382:ARG:O	1:A:383:GLN:CB	2.49	0.60
1:A:454:LEU:O	1:A:454:LEU:HD12	2.01	0.60
1:A:349:ALA:C	1:A:351:SER:N	2.54	0.60
1:B:9:PRO:HG2	1:B:49:TYR:HB2	1.83	0.60
1:C:11:PHE:CE1	1:C:88:LEU:HD12	2.35	0.60
1:D:506:THR:O	1:D:507:ASP:CB	2.48	0.60
1:A:502:LEU:HA	1:A:505:MSE:CG	2.28	0.60
1:A:506:THR:O	1:A:507:ASP:CB	2.49	0.60
1:C:453:LYS:O	1:C:457:THR:HG22	2.00	0.60
1:A:82:HIS:O	1:A:84:ARG:N	2.34	0.60
1:D:135:ARG:HH11	1:D:135:ARG:HG3	1.66	0.60
1:A:149:LEU:CB	1:A:153:LEU:CD2	2.78	0.60
1:A:215:ARG:CZ	1:A:252:GLU:OE2	2.49	0.60
1:C:351:SER:HB2	1:C:354:PRO:HD2	1.84	0.60
1:D:189:LEU:HD11	1:D:199:ILE:HD12	1.84	0.60
1:D:386:HIS:CD2	1:D:387:LEU:CD1	2.84	0.60
1:A:326:VAL:O	1:A:326:VAL:CG2	2.49	0.60
1:A:478:SER:OG	1:A:479:ASP:N	2.34	0.60
1:C:354:PRO:O	1:D:373:MSE:CE	2.50	0.60
1:A:499:LEU:CD2	1:A:515:ARG:HH11	2.14	0.60
1:D:427:LYS:HG3	1:D:436:ARG:HH11	1.67	0.60
1:D:453:LYS:O	1:D:457:THR:HG22	2.02	0.60
1:A:153:LEU:HD12	1:A:165:SER:O	2.02	0.60
1:A:363:VAL:HG13	1:B:363:VAL:CG1	2.27	0.60
1:B:351:SER:HB2	1:B:354:PRO:HD2	1.83	0.59
1:B:82:HIS:O	1:B:84:ARG:N	2.36	0.59
1:C:382:ARG:O	1:C:383:GLN:CB	2.50	0.59
1:A:353:ALA:HB3	1:A:354:PRO:HD2	1.84	0.59
1:C:248:THR:O	1:C:252:GLU:HB2	2.03	0.59
1:C:10:ASN:OD1	1:C:46:ARG:NH1	2.35	0.59
1:D:135:ARG:HG2	1:D:141:ILE:HD11	1.84	0.59
1:A:499:LEU:HD21	1:A:515:ARG:HH11	1.68	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:316:ASP:O	1:B:320:ARG:HG2	2.02	0.59
1:C:141:ILE:O	1:C:143:ALA:N	2.34	0.59
1:D:2:SER:O	1:D:3:GLN:HB2	2.01	0.59
1:C:142:ARG:O	1:C:144:GLY:N	2.35	0.59
1:C:349:ALA:O	1:C:351:SER:N	2.35	0.59
1:A:138:LEU:HD21	1:A:142:ARG:HH12	1.68	0.59
1:A:142:ARG:O	1:A:144:GLY:N	2.36	0.59
1:B:135:ARG:HG3	1:B:135:ARG:HH11	1.67	0.59
1:B:215:ARG:CZ	1:B:252:GLU:OE2	2.50	0.59
1:D:35:LEU:HD12	1:D:51:PHE:HB3	1.85	0.59
1:B:13:GLU:O	1:B:14:GLY:C	2.36	0.59
1:B:27:ILE:CD1	1:B:51:PHE:CE1	2.81	0.59
1:D:143:ALA:O	1:D:152:LYS:NZ	2.35	0.59
1:D:248:THR:O	1:D:252:GLU:HB2	2.02	0.59
1:C:359:VAL:CG1	1:D:370:LEU:HD11	2.31	0.59
1:C:138:LEU:HD21	1:C:142:ARG:HH12	1.68	0.59
1:C:11:PHE:CE1	1:C:88:LEU:CD1	2.86	0.59
1:D:215:ARG:CZ	1:D:252:GLU:OE2	2.51	0.59
1:A:248:THR:O	1:A:252:GLU:HB2	2.03	0.58
1:A:363:VAL:CG1	1:B:363:VAL:CG1	2.80	0.58
1:A:127:GLY:C	1:A:129:ALA:H	2.06	0.58
1:B:141:ILE:O	1:B:143:ALA:N	2.34	0.58
1:B:138:LEU:HD21	1:B:142:ARG:HH12	1.68	0.58
1:D:326:VAL:CG2	1:D:326:VAL:O	2.50	0.58
1:B:142:ARG:O	1:B:144:GLY:N	2.34	0.58
1:B:499:LEU:CD2	1:B:515:ARG:HH11	2.17	0.58
1:C:35:LEU:HD12	1:C:51:PHE:HB3	1.83	0.58
1:C:43:SER:O	1:C:81:GLU:HB2	2.04	0.58
1:D:445:ARG:NH1	1:D:445:ARG:HG3	2.10	0.58
1:A:12:SER:HB2	1:A:87:ALA:HA	1.85	0.58
1:A:351:SER:HB2	1:A:354:PRO:HD2	1.85	0.58
1:A:4:LEU:HD12	1:A:52:VAL:HB	1.85	0.58
1:B:153:LEU:HD22	1:B:153:LEU:H	1.68	0.58
1:B:248:THR:O	1:B:252:GLU:HB2	2.04	0.58
1:D:83:PRO:HA	1:D:145:GLU:OE1	2.03	0.58
1:A:376:GLN:HG2	1:A:395:ILE:HD13	1.85	0.58
1:A:453:LYS:O	1:A:457:THR:HG22	2.03	0.58
1:D:12:SER:HB2	1:D:87:ALA:HA	1.86	0.58
1:D:462:TRP:HB3	1:D:528:GLN:HG2	1.84	0.58
1:A:458:VAL:CG1	1:A:491:VAL:HG22	2.34	0.58
1:D:376:GLN:HG2	1:D:395:ILE:HD13	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:189:LEU:HD11	1:A:199:ILE:HD12	1.86	0.58
1:B:304:VAL:HG12	1:B:305:ASN:N	2.18	0.58
1:C:82:HIS:O	1:C:84:ARG:N	2.36	0.58
1:D:527:THR:O	1:D:531:LEU:HD23	2.03	0.58
1:B:216:LEU:HD21	1:B:252:GLU:HG2	1.85	0.58
1:B:254:ARG:HH11	1:B:254:ARG:HB3	1.69	0.58
1:B:382:ARG:O	1:B:383:GLN:CB	2.52	0.58
1:B:2:SER:O	1:B:3:GLN:HB2	2.03	0.58
1:D:138:LEU:HD21	1:D:142:ARG:HH12	1.69	0.58
1:D:9:PRO:HG2	1:D:49:TYR:HB2	1.86	0.58
1:B:462:TRP:HB3	1:B:528:GLN:HG2	1.86	0.57
1:C:15:ASN:O	1:C:16:ASN:CB	2.49	0.57
1:A:427:LYS:CE	1:A:436:ARG:HH12	2.04	0.57
1:B:373:MSE:O	1:B:373:MSE:HG2	1.95	0.57
1:D:499:LEU:HD21	1:D:515:ARG:HH11	1.69	0.57
1:A:254:ARG:HH11	1:A:254:ARG:HB3	1.69	0.57
1:C:189:LEU:HD11	1:C:199:ILE:HD12	1.86	0.57
1:B:143:ALA:O	1:B:152:LYS:NZ	2.38	0.57
1:B:35:LEU:HD12	1:B:51:PHE:HB3	1.84	0.57
1:D:4:LEU:HD12	1:D:52:VAL:HB	1.86	0.57
1:C:2:SER:O	1:C:3:GLN:HB2	2.03	0.57
1:C:458:VAL:CG1	1:C:491:VAL:HG22	2.27	0.57
1:D:127:GLY:C	1:D:129:ALA:H	2.08	0.57
1:D:142:ARG:O	1:D:144:GLY:N	2.37	0.57
1:A:462:TRP:HB3	1:A:528:GLN:HG2	1.85	0.57
1:A:9:PRO:HG2	1:A:49:TYR:HB2	1.86	0.57
1:C:4:LEU:HD23	1:C:97:ARG:NH2	2.19	0.57
1:A:143:ALA:O	1:A:152:LYS:NZ	2.37	0.57
1:A:285:TYR:O	1:A:289:GLU:HB2	2.04	0.57
1:A:343:PHE:O	1:A:346:GLU:HB3	2.05	0.57
1:D:458:VAL:CG1	1:D:491:VAL:HG22	2.34	0.57
1:B:149:LEU:HD22	1:B:153:LEU:HB3	1.86	0.57
1:B:10:ASN:OD1	1:B:46:ARG:NH1	2.38	0.57
1:B:376:GLN:HG2	1:B:395:ILE:HD13	1.87	0.57
1:C:135:ARG:HH11	1:C:135:ARG:HG3	1.68	0.57
1:C:143:ALA:O	1:C:152:LYS:NZ	2.38	0.57
1:C:4:LEU:HB3	1:C:96:VAL:HB	1.87	0.57
1:D:344:VAL:HG22	1:D:345:ARG:HG2	1.85	0.57
1:D:458:VAL:CG2	1:D:487:LEU:HD23	2.34	0.57
1:A:527:THR:O	1:A:531:LEU:HD23	2.05	0.56
1:B:13:GLU:H	1:B:46:ARG:HA	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:11:PHE:CE1	1:B:88:LEU:CD1	2.88	0.56
1:C:487:LEU:O	1:C:491:VAL:HG23	2.04	0.56
1:A:141:ILE:HG21	1:A:175:VAL:HG11	1.88	0.56
1:A:326:VAL:O	1:A:326:VAL:HG22	2.05	0.56
1:A:534:GLY:O	1:A:535:SER:C	2.43	0.56
1:A:83:PRO:HA	1:A:145:GLU:OE1	2.04	0.56
1:B:425:LEU:CD2	1:B:426:PRO:HD2	2.23	0.56
1:A:149:LEU:CB	1:A:153:LEU:HD23	2.36	0.56
1:C:376:GLN:HG2	1:C:395:ILE:HD13	1.88	0.56
1:D:191:SER:HB2	1:D:195:GLN:OE1	2.06	0.56
1:C:12:SER:HB2	1:C:87:ALA:HA	1.88	0.56
1:C:348:GLY:HA2	1:D:373:MSE:HB2	1.88	0.56
1:B:30:THR:HG21	1:B:61:GLY:N	2.21	0.56
1:D:498:VAL:HG12	1:D:502:LEU:CD1	2.35	0.56
1:D:499:LEU:CD2	1:D:515:ARG:HH11	2.19	0.56
1:B:153:LEU:N	1:B:153:LEU:CD2	2.68	0.56
1:C:390:THR:HG22	1:C:393:ARG:NH2	2.17	0.56
1:B:127:GLY:C	1:B:129:ALA:H	2.09	0.56
1:B:344:VAL:HG22	1:B:345:ARG:HG2	1.86	0.56
1:B:43:SER:O	1:B:81:GLU:HB2	2.06	0.56
1:B:4:LEU:HB3	1:B:96:VAL:HB	1.87	0.56
1:C:517:ARG:O	1:C:520:SER:OG	2.23	0.56
1:A:304:VAL:HG12	1:A:305:ASN:N	2.20	0.56
1:A:36:LEU:HD22	1:A:325:LEU:HD22	1.87	0.56
1:A:428:ASN:H	1:A:433:ARG:HB2	1.71	0.55
1:B:498:VAL:HG12	1:B:502:LEU:CD1	2.36	0.55
1:B:4:LEU:HD12	1:B:52:VAL:HB	1.88	0.55
1:C:111:PHE:HD2	1:C:176:THR:HG1	1.52	0.55
1:B:390:THR:HG22	1:B:393:ARG:NH2	2.18	0.55
1:C:326:VAL:CG2	1:C:326:VAL:O	2.53	0.55
1:D:36:LEU:HD22	1:D:325:LEU:HD22	1.88	0.55
1:A:135:ARG:HG3	1:A:135:ARG:HH11	1.70	0.55
1:A:141:ILE:O	1:A:143:ALA:N	2.38	0.55
1:C:4:LEU:HD12	1:C:52:VAL:HB	1.89	0.55
1:D:15:ASN:O	1:D:16:ASN:CB	2.49	0.55
1:A:349:ALA:O	1:A:351:SER:N	2.39	0.55
1:A:492:PHE:CD2	1:A:522:LEU:HD11	2.42	0.55
1:B:499:LEU:HD21	1:B:515:ARG:HH11	1.71	0.55
1:A:517:ARG:O	1:A:520:SER:OG	2.24	0.55
1:B:111:PHE:HD2	1:B:176:THR:HG1	1.54	0.55
1:D:141:ILE:O	1:D:143:ALA:N	2.38	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:353:ALA:HB3	1:D:354:PRO:HD2	1.87	0.55
1:B:76:ARG:NH2	1:B:169:PRO:CB	2.69	0.55
1:B:4:LEU:HD23	1:B:97:ARG:NH2	2.21	0.55
1:A:124:TYR:HD2	1:A:160:PRO:HA	1.71	0.55
1:B:216:LEU:HD13	1:B:249:VAL:HG22	1.89	0.55
1:B:8:VAL:HG22	1:B:50:THR:HG23	1.89	0.55
1:D:4:LEU:HB3	1:D:96:VAL:HB	1.89	0.55
1:A:498:VAL:HG12	1:A:502:LEU:CD1	2.36	0.55
1:C:138:LEU:N	1:C:139:PRO:HD2	2.22	0.55
1:A:84:ARG:O	1:A:145:GLU:HB2	2.06	0.55
1:B:176:THR:HG22	1:B:177:GLY:N	2.22	0.55
1:D:445:ARG:NH1	1:D:445:ARG:CG	2.60	0.55
1:A:27:ILE:CD1	1:A:51:PHE:CE1	2.81	0.55
1:B:124:TYR:HD2	1:B:160:PRO:HA	1.72	0.55
1:D:428:ASN:H	1:D:433:ARG:HB2	1.72	0.55
1:D:84:ARG:O	1:D:145:GLU:HB2	2.07	0.55
1:B:343:PHE:O	1:B:347:VAL:HG13	2.07	0.54
1:C:425:LEU:CD2	1:C:426:PRO:HD2	2.24	0.54
1:C:477:LEU:O	1:C:481:GLN:HG3	2.07	0.54
1:C:76:ARG:NH2	1:C:169:PRO:CB	2.70	0.54
1:D:390:THR:HG22	1:D:393:ARG:NH2	2.17	0.54
1:A:359:VAL:HG11	1:B:370:LEU:HD11	1.88	0.54
1:C:124:TYR:HD2	1:C:160:PRO:HA	1.72	0.54
1:C:215:ARG:NH2	1:C:252:GLU:OE2	2.39	0.54
1:B:102:ASP:CG	1:C:109:LYS:HZ1	2.09	0.54
1:C:141:ILE:HG21	1:C:175:VAL:HG11	1.88	0.54
1:C:499:LEU:HD21	1:C:515:ARG:HH11	1.72	0.54
1:A:10:ASN:OD1	1:A:46:ARG:NH1	2.39	0.54
1:B:12:SER:HB2	1:B:87:ALA:HA	1.89	0.54
1:B:141:ILE:HG21	1:B:175:VAL:HG11	1.89	0.54
1:C:216:LEU:HD21	1:C:252:GLU:HG2	1.89	0.54
1:C:498:VAL:HG12	1:C:502:LEU:CD1	2.36	0.54
1:D:76:ARG:NH2	1:D:169:PRO:CB	2.70	0.54
1:D:304:VAL:HG12	1:D:305:ASN:N	2.22	0.54
1:D:534:GLY:O	1:D:535:SER:C	2.46	0.54
1:A:148:ALA:H	1:A:150:PRO:HD2	1.73	0.54
1:B:143:ALA:HB1	1:B:152:LYS:NZ	2.23	0.54
1:D:125:LEU:O	1:D:130:ALA:HB2	2.07	0.54
1:D:4:LEU:HD23	1:D:97:ARG:NH2	2.23	0.54
1:B:149:LEU:N	1:B:150:PRO:HD2	2.23	0.54
1:B:445:ARG:NH1	1:B:445:ARG:HG3	2.11	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:323:GLU:N	1:C:323:GLU:OE1	2.41	0.54
1:D:10:ASN:OD1	1:D:46:ARG:NH1	2.41	0.54
1:D:531:LEU:N	1:D:531:LEU:HD23	2.05	0.54
1:A:215:ARG:NH2	1:A:252:GLU:OE2	2.40	0.54
1:C:30:THR:HG21	1:C:61:GLY:N	2.22	0.54
1:C:326:VAL:HG22	1:C:326:VAL:O	2.07	0.54
1:C:83:PRO:HA	1:C:145:GLU:OE1	2.08	0.54
1:D:141:ILE:HG21	1:D:175:VAL:HG11	1.89	0.54
1:D:30:THR:HG21	1:D:61:GLY:N	2.23	0.54
1:D:326:VAL:HG22	1:D:326:VAL:O	2.07	0.54
1:A:191:SER:HB2	1:A:195:GLN:OE1	2.07	0.54
1:B:455:ALA:O	1:B:456:GLU:C	2.46	0.54
1:C:125:LEU:O	1:C:130:ALA:HB2	2.08	0.54
1:D:143:ALA:HB1	1:D:152:LYS:NZ	2.23	0.54
1:A:531:LEU:N	1:A:531:LEU:HD23	2.06	0.53
1:B:527:THR:O	1:B:531:LEU:HD23	2.08	0.53
1:C:143:ALA:HB1	1:C:152:LYS:NZ	2.23	0.53
1:D:382:ARG:HG2	1:D:383:GLN:N	2.23	0.53
1:D:427:LYS:CE	1:D:436:ARG:HH12	2.05	0.53
1:D:8:VAL:HG22	1:D:50:THR:HG23	1.90	0.53
1:B:349:ALA:O	1:B:351:SER:N	2.42	0.53
1:A:125:LEU:O	1:A:130:ALA:HB2	2.08	0.53
1:A:30:THR:HG21	1:A:61:GLY:N	2.23	0.53
1:A:4:LEU:HB3	1:A:96:VAL:HB	1.89	0.53
1:C:345:ARG:HH21	1:D:406:THR:CB	2.18	0.53
1:B:138:LEU:N	1:B:139:PRO:HD2	2.22	0.53
1:D:215:ARG:NH2	1:D:252:GLU:OE2	2.40	0.53
1:D:343:PHE:O	1:D:347:VAL:HG13	2.09	0.53
1:B:36:LEU:HD22	1:B:325:LEU:HD22	1.91	0.53
1:C:148:ALA:H	1:C:150:PRO:HD2	1.72	0.53
1:A:149:LEU:N	1:A:150:PRO:HD2	2.24	0.53
1:A:373:MSE:O	1:A:373:MSE:HG2	2.08	0.53
1:A:13:GLU:HB2	1:A:46:ARG:C	2.28	0.53
1:B:427:LYS:CE	1:B:436:ARG:HH12	2.03	0.53
1:A:143:ALA:HB1	1:A:152:LYS:NZ	2.23	0.53
1:C:124:TYR:CD2	1:C:160:PRO:HA	2.44	0.53
1:D:43:SER:O	1:D:81:GLU:HB2	2.09	0.53
1:D:11:PHE:CZ	1:D:88:LEU:CD1	2.90	0.53
1:A:124:TYR:CD2	1:A:160:PRO:HA	2.44	0.53
1:B:124:TYR:CD2	1:B:160:PRO:HA	2.44	0.53
1:D:477:LEU:O	1:D:481:GLN:HG3	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:127:GLY:C	1:C:129:ALA:H	2.11	0.53
1:B:83:PRO:HA	1:B:145:GLU:OE1	2.09	0.52
1:D:323:GLU:OE1	1:D:323:GLU:N	2.41	0.52
1:B:428:ASN:H	1:B:433:ARG:HB2	1.74	0.52
1:D:149:LEU:N	1:D:150:PRO:HD2	2.24	0.52
1:D:487:LEU:O	1:D:491:VAL:HG23	2.09	0.52
1:A:353:ALA:HB3	1:A:354:PRO:CD	2.38	0.52
1:B:125:LEU:O	1:B:130:ALA:HB2	2.09	0.52
1:B:527:THR:O	1:B:530:ALA:HB3	2.09	0.52
1:C:36:LEU:HD22	1:C:325:LEU:HD22	1.90	0.52
1:A:138:LEU:N	1:A:139:PRO:HD2	2.25	0.52
1:A:445:ARG:CG	1:A:445:ARG:NH1	2.61	0.52
1:B:126:TYR:O	1:B:129:ALA:HB3	2.10	0.52
1:C:17:GLN:HA	1:C:17:GLN:OE1	2.09	0.52
1:C:531:LEU:H	1:C:531:LEU:CD2	2.06	0.52
1:A:8:VAL:HG22	1:A:50:THR:HG23	1.92	0.52
1:A:510:PHE:C	1:A:510:PHE:CD2	2.83	0.52
1:B:326:VAL:CG2	1:B:326:VAL:O	2.57	0.52
1:C:149:LEU:N	1:C:150:PRO:HD2	2.24	0.52
1:C:8:VAL:HG22	1:C:50:THR:HG23	1.92	0.52
1:D:527:THR:O	1:D:530:ALA:HB3	2.10	0.52
1:A:445:ARG:NH1	1:A:445:ARG:HG3	2.12	0.52
1:A:487:LEU:O	1:A:491:VAL:HG23	2.09	0.52
1:B:153:LEU:H	1:B:153:LEU:CD2	2.22	0.52
1:B:517:ARG:O	1:B:520:SER:OG	2.28	0.52
1:A:76:ARG:NH2	1:A:169:PRO:CB	2.71	0.52
1:B:382:ARG:HA	1:B:385:ASP:OD1	2.09	0.52
1:D:425:LEU:CD2	1:D:426:PRO:HD2	2.26	0.52
1:B:478:SER:OG	1:B:479:ASP:N	2.43	0.52
1:B:506:THR:O	1:B:507:ASP:HB2	2.10	0.52
1:C:13:GLU:HG2	1:C:15:ASN:CA	2.40	0.52
1:C:36:LEU:HD22	1:C:325:LEU:CD2	2.40	0.52
1:D:124:TYR:HD2	1:D:160:PRO:HA	1.74	0.52
1:B:176:THR:HG23	1:B:177:GLY:H	1.75	0.52
1:D:148:ALA:H	1:D:150:PRO:HD2	1.72	0.52
1:A:11:PHE:CZ	1:A:88:LEU:CD1	2.93	0.52
1:A:176:THR:HG22	1:A:177:GLY:N	2.25	0.52
1:A:43:SER:O	1:A:81:GLU:HB2	2.10	0.52
1:C:216:LEU:HD13	1:C:249:VAL:HG22	1.91	0.52
1:C:499:LEU:CD2	1:C:515:ARG:HH11	2.22	0.52
1:C:13:GLU:HG2	1:C:15:ASN:H	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:227:GLU:OE1	1:D:227:GLU:CA	2.50	0.51
1:D:13:GLU:OE1	1:D:45:ASN:HA	2.10	0.51
1:A:176:THR:HG23	1:A:177:GLY:H	1.76	0.51
1:D:123:VAL:HG13	1:D:162:PHE:HB2	1.92	0.51
1:D:27:ILE:CD1	1:D:51:PHE:CE1	2.87	0.51
1:A:265:VAL:HG23	1:A:265:VAL:O	2.10	0.51
1:A:506:THR:O	1:A:507:ASP:HB2	2.11	0.51
1:B:148:ALA:H	1:B:150:PRO:HD2	1.73	0.51
1:C:13:GLU:HB2	1:C:46:ARG:C	2.31	0.51
1:C:84:ARG:O	1:C:145:GLU:HB2	2.10	0.51
1:B:353:ALA:HB3	1:B:354:PRO:HD2	1.92	0.51
1:B:84:ARG:O	1:B:145:GLU:HB2	2.10	0.51
1:A:4:LEU:HD23	1:A:97:ARG:NH2	2.26	0.51
1:B:382:ARG:HG2	1:B:383:GLN:N	2.25	0.51
1:C:396:PRO:HB2	1:C:397:PRO:HD2	1.92	0.51
1:D:124:TYR:CD2	1:D:160:PRO:HA	2.46	0.51
1:D:216:LEU:HD13	1:D:249:VAL:HG22	1.92	0.51
1:A:84:ARG:O	1:A:145:GLU:CB	2.59	0.51
1:A:378:THR:HG22	1:A:378:THR:O	2.11	0.51
1:A:455:ALA:O	1:A:456:GLU:C	2.49	0.51
1:B:378:THR:O	1:B:378:THR:HG22	2.10	0.51
1:B:487:LEU:O	1:B:491:VAL:HG23	2.10	0.51
1:C:382:ARG:HA	1:C:385:ASP:OD1	2.10	0.51
1:C:528:GLN:O	1:C:532:VAL:HG23	2.11	0.51
1:D:373:MSE:O	1:D:373:MSE:HG2	2.09	0.51
1:A:123:VAL:HG13	1:A:162:PHE:HB2	1.93	0.51
1:A:376:GLN:HB3	1:B:350:ARG:HD2	1.91	0.51
1:C:76:ARG:CZ	1:C:169:PRO:CB	2.89	0.51
1:C:350:ARG:HD2	1:D:376:GLN:O	2.11	0.51
1:C:382:ARG:HG2	1:C:383:GLN:N	2.25	0.51
1:C:304:VAL:HG12	1:C:305:ASN:N	2.27	0.51
1:C:444:LEU:HD11	1:C:504:ASP:HB2	1.93	0.51
1:D:149:LEU:CA	1:D:153:LEU:HD12	2.40	0.51
1:A:249:VAL:HG12	1:A:250:TYR:N	2.25	0.50
1:A:382:ARG:HG2	1:A:383:GLN:N	2.25	0.50
1:B:191:SER:HB2	1:B:195:GLN:OE1	2.10	0.50
1:D:97:ARG:HH21	1:D:328:ASP:HB3	1.74	0.50
1:C:373:MSE:HG2	1:C:373:MSE:O	2.03	0.50
1:A:373:MSE:HB2	1:B:348:GLY:HA2	1.93	0.50
1:B:395:ILE:N	1:B:396:PRO:CD	2.74	0.50
1:B:76:ARG:CZ	1:B:169:PRO:CB	2.89	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:11:PHE:CZ	1:C:88:LEU:CD1	2.94	0.50
1:C:428:ASN:H	1:C:433:ARG:HB2	1.76	0.50
1:C:510:PHE:C	1:C:510:PHE:CD2	2.85	0.50
1:C:534:GLY:O	1:C:535:SER:C	2.49	0.50
1:C:60:GLU:O	1:C:64:SER:N	2.35	0.50
1:D:192:THR:HG22	1:D:195:GLN:OE1	2.10	0.50
1:D:383:GLN:HG3	1:D:384:PHE:N	2.26	0.50
1:A:379:TYR:CG	1:A:380:GLY:N	2.80	0.50
1:B:444:LEU:HD11	1:B:504:ASP:HB2	1.93	0.50
1:C:478:SER:OG	1:C:479:ASP:N	2.43	0.50
1:D:353:ALA:HB3	1:D:354:PRO:CD	2.41	0.50
1:D:73:ILE:HG21	1:D:75:MSE:HE3	1.93	0.50
1:A:25:GLN:O	1:A:28:SER:N	2.45	0.50
1:C:378:THR:HG22	1:C:378:THR:O	2.11	0.50
1:A:126:TYR:O	1:A:129:ALA:HB3	2.12	0.50
1:A:425:LEU:CD2	1:A:426:PRO:HD2	2.27	0.50
1:D:138:LEU:N	1:D:139:PRO:HD2	2.27	0.50
1:D:84:ARG:O	1:D:145:GLU:CB	2.59	0.50
1:D:454:LEU:HG	1:D:494:ALA:HB2	1.94	0.50
1:A:15:ASN:O	1:A:16:ASN:CB	2.48	0.50
1:B:326:VAL:HG22	1:B:326:VAL:O	2.12	0.50
1:C:455:ALA:O	1:C:456:GLU:C	2.48	0.50
1:C:527:THR:O	1:C:531:LEU:HD23	2.11	0.50
1:D:76:ARG:CZ	1:D:169:PRO:CB	2.90	0.50
1:A:73:ILE:HG21	1:A:75:MSE:HE3	1.92	0.50
1:B:192:THR:HG22	1:B:195:GLN:OE1	2.10	0.50
1:B:510:PHE:CD2	1:B:510:PHE:C	2.85	0.50
1:C:383:GLN:HG3	1:C:384:PHE:N	2.27	0.50
1:D:530:ALA:O	1:D:533:LEU:HB2	2.12	0.50
1:B:17:GLN:HA	1:B:17:GLN:OE1	2.11	0.50
1:B:36:LEU:HD22	1:B:325:LEU:CD2	2.41	0.50
1:C:153:LEU:HD13	1:C:165:SER:O	2.12	0.50
1:D:506:THR:O	1:D:507:ASP:HB2	2.12	0.50
1:B:323:GLU:N	1:B:323:GLU:OE1	2.44	0.49
1:C:395:ILE:N	1:C:396:PRO:CD	2.75	0.49
1:D:510:PHE:CD2	1:D:510:PHE:C	2.85	0.49
1:A:13:GLU:HG2	1:A:15:ASN:CA	2.41	0.49
1:C:506:THR:O	1:C:507:ASP:HB2	2.11	0.49
1:B:383:GLN:HG3	1:B:384:PHE:N	2.26	0.49
1:D:176:THR:HG22	1:D:177:GLY:N	2.27	0.49
1:D:25:GLN:O	1:D:28:SER:N	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:97:ARG:CZ	1:A:328:ASP:HB3	2.42	0.49
1:B:124:TYR:HD1	1:B:175:VAL:HG12	1.76	0.49
1:B:97:ARG:HH21	1:B:328:ASP:HB3	1.77	0.49
1:B:60:GLU:O	1:B:64:SER:N	2.34	0.49
1:D:247:HIS:HD2	1:D:281:ALA:HA	1.77	0.49
1:A:537:GLU:O	1:A:540:LYS:HB2	2.13	0.49
1:A:54:GLN:HB2	1:A:57:CYS:SG	2.52	0.49
1:A:76:ARG:CZ	1:A:169:PRO:CB	2.90	0.49
1:B:215:ARG:NH2	1:B:252:GLU:OE2	2.44	0.49
1:B:379:TYR:CG	1:B:380:GLY:N	2.81	0.49
1:B:380:GLY:O	1:B:381:ARG:C	2.51	0.49
1:C:353:ALA:HB3	1:C:354:PRO:HD2	1.93	0.49
1:C:448:VAL:HG13	1:C:498:VAL:HG13	1.94	0.49
1:A:124:TYR:HD1	1:A:175:VAL:HG12	1.78	0.49
1:C:344:VAL:HG22	1:C:345:ARG:HG2	1.94	0.49
1:D:265:VAL:HG23	1:D:265:VAL:O	2.13	0.49
1:A:84:ARG:HG2	1:A:85:MSE:N	2.28	0.49
1:B:249:VAL:HG12	1:B:250:TYR:N	2.27	0.49
1:B:427:LYS:O	1:B:428:ASN:HB2	2.12	0.49
1:C:191:SER:HB2	1:C:195:GLN:OE1	2.13	0.49
1:C:247:HIS:HD2	1:C:281:ALA:HA	1.76	0.49
1:A:13:GLU:HG2	1:A:15:ASN:H	1.76	0.49
1:B:511:LYS:O	1:B:514:THR:N	2.46	0.49
1:C:370:LEU:HD11	1:D:359:VAL:HG11	1.95	0.49
1:A:323:GLU:OE1	1:A:323:GLU:N	2.42	0.48
1:B:477:LEU:O	1:B:481:GLN:HG3	2.13	0.48
1:C:124:TYR:HD1	1:C:175:VAL:HG12	1.77	0.48
1:D:303:VAL:O	1:D:303:VAL:HG22	2.12	0.48
1:D:349:ALA:C	1:D:351:SER:N	2.59	0.48
1:A:353:ALA:CB	1:A:354:PRO:CD	2.91	0.48
1:A:527:THR:O	1:A:530:ALA:HB3	2.13	0.48
1:D:84:ARG:HG2	1:D:85:MSE:N	2.29	0.48
1:A:345:ARG:HH21	1:B:406:THR:HB	1.77	0.48
1:C:192:THR:HG22	1:C:195:GLN:OE1	2.12	0.48
1:C:530:ALA:O	1:C:533:LEU:HB2	2.12	0.48
1:A:192:THR:HG22	1:A:195:GLN:OE1	2.13	0.48
1:A:383:GLN:N	1:A:385:ASP:OD1	2.47	0.48
1:B:149:LEU:O	1:B:153:LEU:HD22	2.13	0.48
1:B:530:ALA:O	1:B:533:LEU:HB2	2.13	0.48
1:C:126:TYR:O	1:C:129:ALA:HB3	2.13	0.48
1:C:427:LYS:O	1:C:428:ASN:HB2	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:127:GLY:C	1:A:129:ALA:N	2.67	0.48
1:B:383:GLN:N	1:B:385:ASP:OD1	2.46	0.48
1:C:176:THR:HG22	1:C:177:GLY:N	2.29	0.48
1:C:343:PHE:O	1:C:347:VAL:HG13	2.13	0.48
1:D:135:ARG:CG	1:D:135:ARG:HH11	2.26	0.48
1:D:527:THR:O	1:D:531:LEU:CD2	2.60	0.48
1:A:374:VAL:HA	1:A:377:MSE:HB2	1.95	0.48
1:A:390:THR:CG2	1:A:393:ARG:HH21	2.19	0.48
1:A:410:ASP:O	1:A:413:ALA:N	2.46	0.48
1:A:510:PHE:C	1:A:510:PHE:HD2	2.16	0.48
1:B:13:GLU:HB3	1:B:46:ARG:HA	1.96	0.48
1:A:97:ARG:HH21	1:A:328:ASP:HB3	1.74	0.48
1:B:353:ALA:HB3	1:B:354:PRO:CD	2.44	0.48
1:B:97:ARG:CZ	1:B:328:ASP:HB3	2.44	0.48
1:C:84:ARG:O	1:C:145:GLU:CB	2.62	0.48
1:C:527:THR:O	1:C:530:ALA:HB3	2.14	0.48
1:D:13:GLU:HG2	1:D:15:ASN:CA	2.44	0.48
1:D:492:PHE:CD2	1:D:522:LEU:HD11	2.49	0.48
1:B:25:GLN:O	1:B:28:SER:N	2.47	0.48
1:D:379:TYR:CG	1:D:380:GLY:N	2.81	0.48
1:A:303:VAL:HG22	1:A:303:VAL:O	2.14	0.48
1:A:383:GLN:HG3	1:A:384:PHE:N	2.29	0.48
1:A:444:LEU:CD1	1:A:504:ASP:HB2	2.44	0.48
1:B:11:PHE:CZ	1:B:88:LEU:CD1	2.96	0.48
1:D:90:VAL:HG11	1:D:138:LEU:HD21	1.95	0.48
1:D:427:LYS:O	1:D:428:ASN:HB2	2.13	0.48
1:C:76:ARG:HH21	1:C:169:PRO:HB3	1.79	0.48
1:A:216:LEU:HD13	1:A:249:VAL:HG22	1.95	0.47
1:A:454:LEU:HG	1:A:494:ALA:HB2	1.96	0.47
1:C:510:PHE:C	1:C:510:PHE:HD2	2.17	0.47
1:D:13:GLU:HB2	1:D:46:ARG:C	2.33	0.47
1:A:530:ALA:O	1:A:533:LEU:HB2	2.14	0.47
1:B:10:ASN:HB2	1:B:90:VAL:O	2.14	0.47
1:C:27:ILE:CD1	1:C:51:PHE:CE1	2.83	0.47
1:D:76:ARG:NE	1:D:169:PRO:HB2	2.29	0.47
1:C:288:LYS:HG3	1:C:289:GLU:N	2.29	0.47
1:C:13:GLU:HB2	1:C:46:ARG:CA	2.44	0.47
1:B:528:GLN:O	1:B:532:VAL:HG23	2.15	0.47
1:B:84:ARG:O	1:B:145:GLU:CB	2.63	0.47
1:D:97:ARG:CZ	1:D:328:ASP:HB3	2.44	0.47
1:A:350:ARG:HD2	1:B:376:GLN:HB3	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:126:TYR:O	1:D:129:ALA:HB3	2.14	0.47
1:A:463:PRO:O	1:A:466:GLN:HB3	2.13	0.47
1:A:90:VAL:HG11	1:A:138:LEU:HD21	1.96	0.47
1:B:343:PHE:O	1:B:346:GLU:HB3	2.14	0.47
1:A:370:LEU:CD1	1:B:359:VAL:HG11	2.36	0.47
1:C:171:TRP:CD1	1:C:172:GLY:N	2.83	0.47
1:A:153:LEU:CD1	1:A:165:SER:O	2.62	0.47
1:A:76:ARG:NE	1:A:169:PRO:HB2	2.29	0.47
1:B:445:ARG:NH1	1:B:445:ARG:CG	2.62	0.47
1:C:97:ARG:HH21	1:C:328:ASP:HB3	1.79	0.47
1:C:406:THR:HB	1:D:345:ARG:HH21	1.79	0.47
1:D:124:TYR:HD1	1:D:175:VAL:HG12	1.78	0.47
1:D:378:THR:O	1:D:378:THR:HG22	2.14	0.47
1:D:74:ASP:OD1	1:D:170:SER:HB3	2.15	0.47
1:A:17:GLN:HA	1:A:17:GLN:OE1	2.14	0.47
1:B:76:ARG:HH21	1:B:169:PRO:HB3	1.79	0.47
1:B:410:ASP:O	1:B:413:ALA:N	2.47	0.47
1:B:510:PHE:C	1:B:510:PHE:HD2	2.18	0.47
1:C:90:VAL:HG11	1:C:138:LEU:HD21	1.96	0.47
1:D:60:GLU:O	1:D:64:SER:N	2.36	0.47
1:B:90:VAL:HG11	1:B:138:LEU:HD21	1.96	0.47
1:B:176:THR:HG23	1:B:177:GLY:N	2.29	0.47
1:A:74:ASP:OD1	1:A:170:SER:HB3	2.14	0.47
1:B:347:VAL:HA	1:B:354:PRO:HG2	1.96	0.47
1:C:347:VAL:HA	1:C:354:PRO:HG2	1.96	0.47
1:A:395:ILE:N	1:A:396:PRO:CD	2.78	0.47
1:B:396:PRO:HB2	1:B:397:PRO:HD2	1.93	0.47
1:C:76:ARG:NE	1:C:169:PRO:HB2	2.29	0.47
1:D:176:THR:HG23	1:D:177:GLY:H	1.80	0.47
1:B:476:CYS:O	1:B:477:LEU:C	2.54	0.46
1:C:265:VAL:O	1:C:265:VAL:HG23	2.14	0.46
1:C:351:SER:OG	1:C:351:SER:O	2.32	0.46
1:D:76:ARG:HH21	1:D:169:PRO:HB3	1.79	0.46
1:D:94:ILE:HG22	1:D:179:ARG:O	2.15	0.46
1:D:426:PRO:O	1:D:427:LYS:CB	2.39	0.46
1:A:13:GLU:HB2	1:A:46:ARG:CA	2.45	0.46
1:A:60:GLU:O	1:A:64:SER:N	2.34	0.46
1:B:374:VAL:HG11	1:B:480:LEU:HD23	1.97	0.46
1:C:97:ARG:CZ	1:C:328:ASP:HB3	2.44	0.46
1:C:454:LEU:HG	1:C:494:ALA:HB2	1.97	0.46
1:B:410:ASP:O	1:B:411:ALA:C	2.53	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:10:ASN:HB2	1:C:90:VAL:O	2.15	0.46
1:D:129:ALA:O	1:D:130:ALA:C	2.53	0.46
1:D:288:LYS:HG3	1:D:289:GLU:N	2.30	0.46
1:B:123:VAL:HG13	1:B:162:PHE:HB2	1.96	0.46
1:B:537:GLU:O	1:B:540:LYS:HB2	2.16	0.46
1:B:76:ARG:NE	1:B:169:PRO:HB2	2.30	0.46
1:B:84:ARG:HG2	1:B:85:MSE:N	2.30	0.46
1:C:123:VAL:HG13	1:C:162:PHE:HB2	1.96	0.46
1:C:522:LEU:O	1:C:525:ALA:HB3	2.16	0.46
1:D:353:ALA:CB	1:D:354:PRO:CD	2.93	0.46
1:A:46:ARG:CZ	1:A:82:HIS:CD2	2.96	0.46
1:A:527:THR:O	1:A:531:LEU:CD2	2.64	0.46
1:A:8:VAL:O	1:A:92:PRO:HD2	2.15	0.46
1:D:349:ALA:O	1:D:351:SER:N	2.49	0.46
1:D:380:GLY:O	1:D:381:ARG:C	2.53	0.46
1:D:455:ALA:O	1:D:456:GLU:C	2.51	0.46
1:B:296:GLU:O	1:B:297:GLU:C	2.51	0.46
1:B:534:GLY:O	1:B:535:SER:C	2.52	0.46
1:C:353:ALA:HB3	1:C:354:PRO:CD	2.46	0.46
1:C:380:GLY:O	1:C:381:ARG:C	2.53	0.46
1:C:383:GLN:N	1:C:385:ASP:OD1	2.45	0.46
1:C:537:GLU:O	1:C:540:LYS:HB2	2.16	0.46
1:D:127:GLY:C	1:D:129:ALA:N	2.68	0.46
1:D:387:LEU:CD2	1:D:471:CYS:SG	3.04	0.46
1:A:448:VAL:O	1:A:451:PRO:HD2	2.16	0.46
1:C:84:ARG:HG2	1:C:85:MSE:N	2.30	0.46
1:D:131:GLN:HE21	1:D:131:GLN:HB2	1.58	0.46
1:A:111:PHE:CD2	1:A:176:THR:OG1	2.67	0.46
1:A:176:THR:HG23	1:A:177:GLY:N	2.30	0.46
1:A:347:VAL:HA	1:A:354:PRO:HG2	1.98	0.46
1:A:427:LYS:O	1:A:428:ASN:HB2	2.15	0.46
1:B:132:MSE:HA	1:B:133:PRO:HD3	1.76	0.46
1:C:379:TYR:CG	1:C:380:GLY:N	2.84	0.46
1:C:4:LEU:HD23	1:C:97:ARG:HH21	1.80	0.46
1:D:517:ARG:O	1:D:520:SER:OG	2.33	0.46
1:A:184:ALA:HB3	1:A:270:VAL:HB	1.98	0.46
1:A:343:PHE:O	1:A:347:VAL:HG13	2.15	0.46
1:B:167:PHE:HD1	1:B:168:VAL:N	2.14	0.46
1:B:530:ALA:O	1:B:533:LEU:N	2.48	0.46
1:C:281:ALA:O	1:C:284:PHE:HB3	2.16	0.46
1:D:334:SER:OG	1:D:336:LEU:HB2	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:463:PRO:O	1:D:466:GLN:HB3	2.16	0.46
1:A:531:LEU:O	1:A:535:SER:N	2.44	0.46
1:B:190:LEU:HA	1:B:190:LEU:HD23	1.80	0.46
1:B:13:GLU:HB3	1:B:46:ARG:CA	2.46	0.46
1:B:531:LEU:O	1:B:535:SER:N	2.44	0.46
1:C:129:ALA:O	1:C:130:ALA:C	2.54	0.46
1:C:13:GLU:HB3	1:C:45:ASN:C	2.36	0.46
1:D:17:GLN:HA	1:D:17:GLN:OE1	2.15	0.46
1:D:249:VAL:HG12	1:D:250:TYR:N	2.29	0.46
1:D:510:PHE:HD2	1:D:510:PHE:C	2.18	0.46
1:A:334:SER:OG	1:A:336:LEU:HB2	2.16	0.45
1:A:10:ASN:HB2	1:A:90:VAL:O	2.16	0.45
1:B:171:TRP:CD1	1:B:172:GLY:N	2.82	0.45
1:B:265:VAL:O	1:B:265:VAL:HG23	2.16	0.45
1:C:167:PHE:HD1	1:C:168:VAL:N	2.14	0.45
1:C:343:PHE:O	1:C:346:GLU:HB3	2.17	0.45
1:D:448:VAL:HG13	1:D:498:VAL:HG13	1.99	0.45
1:B:444:LEU:CD1	1:B:504:ASP:HB2	2.47	0.45
1:C:303:VAL:HG22	1:C:303:VAL:O	2.16	0.45
1:D:143:ALA:HB1	1:D:152:LYS:HZ3	1.80	0.45
1:B:247:HIS:HD2	1:B:281:ALA:HA	1.77	0.45
1:C:227:GLU:OE1	1:C:227:GLU:CA	2.58	0.45
1:D:537:GLU:O	1:D:540:LYS:HB2	2.16	0.45
1:B:127:GLY:C	1:B:129:ALA:N	2.70	0.45
1:C:337:ASP:OD1	1:D:341:ARG:NH1	2.28	0.45
1:C:448:VAL:O	1:C:451:PRO:HD2	2.16	0.45
1:C:90:VAL:HG23	1:C:92:PRO:HD3	1.99	0.45
1:D:524:GLU:O	1:D:528:GLN:HB2	2.16	0.45
1:D:10:ASN:HB2	1:D:90:VAL:O	2.17	0.45
1:A:76:ARG:HH21	1:A:169:PRO:HB3	1.81	0.45
1:A:74:ASP:HA	1:A:170:SER:CB	2.46	0.45
1:D:167:PHE:HD1	1:D:168:VAL:N	2.14	0.45
1:D:347:VAL:HA	1:D:354:PRO:HG2	1.99	0.45
1:A:354:PRO:O	1:B:373:MSE:HE1	2.17	0.45
1:B:450:VAL:HG22	1:B:451:PRO:HD3	1.99	0.45
1:D:410:ASP:O	1:D:413:ALA:N	2.49	0.45
1:D:444:LEU:CD1	1:D:504:ASP:HB2	2.47	0.45
1:A:184:ALA:CB	1:A:270:VAL:HB	2.47	0.45
1:A:531:LEU:O	1:A:532:VAL:C	2.55	0.45
1:B:303:VAL:O	1:B:303:VAL:HG22	2.14	0.45
1:B:448:VAL:HG13	1:B:498:VAL:HG13	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:12:SER:O	1:B:73:ILE:HD13	2.16	0.45
1:C:350:ARG:HD2	1:D:376:GLN:HB3	1.98	0.45
1:C:374:VAL:HG11	1:C:480:LEU:HD23	1.99	0.45
1:D:184:ALA:CB	1:D:270:VAL:HB	2.46	0.45
1:D:184:ALA:HB3	1:D:270:VAL:HB	1.99	0.45
1:A:86:GLY:HA3	1:A:173:ALA:O	2.16	0.45
1:A:89:ASP:HB3	1:A:90:VAL:H	1.64	0.45
1:D:395:ILE:N	1:D:396:PRO:CD	2.79	0.45
1:D:474:LEU:HD23	1:D:477:LEU:HD13	1.98	0.45
1:A:444:LEU:HD11	1:A:504:ASP:HB2	1.99	0.45
1:C:25:GLN:O	1:C:28:SER:N	2.49	0.45
1:A:127:GLY:O	1:A:129:ALA:N	2.50	0.45
1:B:129:ALA:O	1:B:130:ALA:C	2.55	0.45
1:B:94:ILE:HG22	1:B:179:ARG:O	2.17	0.45
1:C:179:ARG:HH12	1:C:182:LEU:HB3	1.82	0.45
1:C:23:ILE:O	1:C:27:ILE:HG22	2.17	0.45
1:C:445:ARG:CG	1:C:445:ARG:NH1	2.58	0.45
1:C:458:VAL:CG2	1:C:487:LEU:HD23	2.47	0.45
1:C:531:LEU:O	1:C:535:SER:N	2.42	0.45
1:D:531:LEU:O	1:D:535:SER:N	2.44	0.45
1:B:74:ASP:OD1	1:B:170:SER:HB3	2.17	0.44
1:B:6:GLU:OE1	1:B:94:ILE:HG13	2.17	0.44
1:D:444:LEU:HD11	1:D:504:ASP:HB2	1.99	0.44
1:A:167:PHE:HD1	1:A:168:VAL:N	2.15	0.44
1:B:111:PHE:CD2	1:B:176:THR:OG1	2.69	0.44
1:B:454:LEU:HG	1:B:494:ALA:HB2	1.98	0.44
1:C:179:ARG:NH1	1:C:182:LEU:HB3	2.32	0.44
1:D:129:ALA:O	1:D:130:ALA:O	2.35	0.44
1:D:13:GLU:HB3	1:D:45:ASN:C	2.37	0.44
1:D:383:GLN:N	1:D:385:ASP:OD1	2.47	0.44
1:A:382:ARG:HA	1:A:385:ASP:OD1	2.18	0.44
1:A:474:LEU:HD11	1:A:541:GLU:OE2	2.17	0.44
1:A:73:ILE:CG2	1:A:75:MSE:HE3	2.47	0.44
1:B:3:GLN:OE1	1:B:3:GLN:HA	2.17	0.44
1:C:249:VAL:HG12	1:C:250:TYR:N	2.32	0.44
1:A:462:TRP:CE3	1:A:462:TRP:HA	2.53	0.44
1:C:176:THR:HG23	1:C:177:GLY:H	1.81	0.44
1:C:379:TYR:CE1	1:C:388:ASP:OD2	2.70	0.44
1:C:539:ARG:O	1:C:541:GLU:N	2.51	0.44
1:A:12:SER:O	1:A:73:ILE:HD13	2.18	0.44
1:B:444:LEU:O	1:B:445:ARG:C	2.56	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:86:GLY:HA3	1:B:173:ALA:O	2.17	0.44
1:A:477:LEU:O	1:A:481:GLN:HG3	2.18	0.44
1:B:23:ILE:O	1:B:27:ILE:HG22	2.17	0.44
1:B:458:VAL:HA	1:B:461:LEU:HD22	2.00	0.44
1:C:461:LEU:N	1:C:461:LEU:CD1	2.79	0.44
1:D:198:ARG:HD3	1:D:260:LEU:HD11	2.00	0.44
1:D:8:VAL:O	1:D:92:PRO:HD2	2.16	0.44
1:A:492:PHE:CE2	1:A:522:LEU:HD11	2.53	0.44
1:B:281:ALA:O	1:B:284:PHE:HB3	2.17	0.44
1:B:492:PHE:CD2	1:B:522:LEU:HD11	2.53	0.44
1:C:6:GLU:OE1	1:C:94:ILE:HG13	2.17	0.44
1:D:171:TRP:CD1	1:D:172:GLY:N	2.84	0.44
1:D:46:ARG:CZ	1:D:82:HIS:CD2	2.95	0.44
1:D:86:GLY:HA3	1:D:173:ALA:O	2.17	0.44
1:A:247:HIS:HD2	1:A:281:ALA:HA	1.79	0.44
1:B:149:LEU:O	1:B:153:LEU:CD2	2.66	0.44
1:C:73:ILE:HG21	1:C:75:MSE:HE3	1.99	0.44
1:D:74:ASP:HA	1:D:170:SER:CB	2.47	0.44
1:D:187:ILE:HD11	1:D:249:VAL:HG12	1.99	0.44
1:D:377:MSE:HE3	1:D:377:MSE:HA	2.00	0.44
1:A:171:TRP:CD1	1:A:172:GLY:N	2.85	0.44
1:A:128:GLU:HB2	1:A:178:ALA:O	2.17	0.44
1:A:336:LEU:O	1:B:339:SER:HB2	2.18	0.44
1:B:184:ALA:CB	1:B:270:VAL:HB	2.48	0.44
1:B:25:GLN:O	1:B:29:GLN:N	2.50	0.44
1:C:38:VAL:HG22	1:C:38:VAL:O	2.18	0.44
1:C:74:ASP:OD1	1:C:170:SER:HB3	2.18	0.44
1:C:86:GLY:HA3	1:C:173:ALA:O	2.18	0.44
1:C:94:ILE:HG22	1:C:179:ARG:O	2.18	0.44
1:D:128:GLU:HB2	1:D:178:ALA:O	2.17	0.44
1:D:374:VAL:HG11	1:D:480:LEU:HD23	2.00	0.44
1:B:15:ASN:O	1:B:16:ASN:CB	2.49	0.43
1:A:341:ARG:NH1	1:B:337:ASP:OD1	2.34	0.43
1:A:493:GLY:HA2	1:B:482:VAL:HG22	2.00	0.43
1:B:46:ARG:CZ	1:B:82:HIS:CD2	2.95	0.43
1:B:8:VAL:O	1:B:92:PRO:HD2	2.18	0.43
1:D:176:THR:HG23	1:D:177:GLY:N	2.33	0.43
1:A:288:LYS:HG3	1:A:289:GLU:N	2.33	0.43
1:B:276:LYS:HE2	1:B:280:ASP:OD1	2.19	0.43
1:C:349:ALA:C	1:C:351:SER:N	2.51	0.43
1:D:127:GLY:O	1:D:129:ALA:N	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:4:LEU:HD23	1:B:97:ARG:HH21	1.82	0.43
1:C:13:GLU:HG2	1:C:15:ASN:HA	2.01	0.43
1:D:153:LEU:HD22	1:D:153:LEU:C	2.38	0.43
1:D:351:SER:OG	1:D:351:SER:O	2.35	0.43
1:A:458:VAL:HA	1:A:461:LEU:HD22	2.00	0.43
1:B:13:GLU:HG2	1:B:15:ASN:H	1.83	0.43
1:B:461:LEU:CD1	1:B:461:LEU:N	2.81	0.43
1:B:73:ILE:HG21	1:B:75:MSE:HE3	1.99	0.43
1:C:59:VAL:O	1:C:63:LEU:HG	2.18	0.43
1:D:3:GLN:HA	1:D:3:GLN:OE1	2.18	0.43
1:D:462:TRP:CE3	1:D:462:TRP:HA	2.54	0.43
1:D:76:ARG:HG3	1:D:76:ARG:H	1.48	0.43
1:A:13:GLU:HB3	1:A:45:ASN:C	2.38	0.43
1:B:288:LYS:HG3	1:B:289:GLU:N	2.33	0.43
1:C:113:GLN:O	1:C:117:GLU:CG	2.57	0.43
1:C:13:GLU:C	1:C:15:ASN:H	2.21	0.43
1:C:531:LEU:N	1:C:531:LEU:HD23	2.12	0.43
1:D:23:ILE:O	1:D:27:ILE:HG22	2.18	0.43
1:A:14:GLY:O	1:A:15:ASN:HB3	2.18	0.43
1:B:396:PRO:CB	1:B:397:PRO:CD	2.92	0.43
1:C:184:ALA:CB	1:C:270:VAL:HB	2.48	0.43
1:C:444:LEU:O	1:C:445:ARG:C	2.56	0.43
1:C:458:VAL:HA	1:C:461:LEU:HD22	2.00	0.43
1:A:432:GLU:HG2	1:A:432:GLU:O	2.19	0.43
1:C:482:VAL:HG22	1:D:493:GLY:HA2	2.01	0.43
1:D:111:PHE:CD2	1:D:176:THR:OG1	2.68	0.43
1:D:432:GLU:O	1:D:432:GLU:HG2	2.17	0.43
1:A:448:VAL:HG13	1:A:498:VAL:HG13	2.01	0.43
1:B:478:SER:HA	1:B:481:GLN:HE21	1.83	0.43
1:B:524:GLU:O	1:B:528:GLN:HB2	2.18	0.43
1:C:127:GLY:C	1:C:129:ALA:N	2.71	0.43
1:C:378:THR:OG1	1:C:473:ASN:N	2.47	0.43
1:D:382:ARG:HA	1:D:385:ASP:OD1	2.19	0.43
1:C:46:ARG:CZ	1:C:82:HIS:CD2	2.95	0.43
1:A:154:LYS:HE2	1:A:154:LYS:HB3	1.70	0.43
1:A:286:CYS:HA	1:A:291:LEU:CD1	2.49	0.43
1:C:135:ARG:CG	1:C:135:ARG:HH11	2.31	0.43
1:D:12:SER:O	1:D:73:ILE:HD13	2.19	0.43
1:A:380:GLY:O	1:A:381:ARG:C	2.58	0.42
1:B:74:ASP:HA	1:B:170:SER:CB	2.49	0.42
1:C:375:GLY:HA3	1:C:395:ILE:HG12	1.99	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:3:GLN:HA	1:C:3:GLN:OE1	2.18	0.42
1:C:444:LEU:CD1	1:C:504:ASP:HB2	2.49	0.42
1:C:8:VAL:O	1:C:92:PRO:HD2	2.18	0.42
1:D:461:LEU:N	1:D:461:LEU:CD1	2.82	0.42
1:A:377:MSE:CE	1:A:377:MSE:HA	2.49	0.42
1:A:406:THR:CB	1:B:345:ARG:HH21	2.27	0.42
1:C:12:SER:HB3	1:C:75:MSE:HE1	2.00	0.42
1:D:36:LEU:HD22	1:D:325:LEU:CD2	2.49	0.42
1:A:375:GLY:HA3	1:A:395:ILE:HG12	2.00	0.42
1:A:524:GLU:O	1:A:528:GLN:HB2	2.19	0.42
1:B:12:SER:HB3	1:B:75:MSE:HE1	2.00	0.42
1:B:432:GLU:O	1:B:432:GLU:HG2	2.18	0.42
1:B:518:ILE:HD12	1:B:518:ILE:HA	1.89	0.42
1:C:425:LEU:O	1:C:426:PRO:C	2.58	0.42
1:D:13:GLU:CB	1:D:46:ARG:HA	2.50	0.42
1:A:94:ILE:HG22	1:A:179:ARG:O	2.19	0.42
1:B:312:LEU:HA	1:B:312:LEU:HD23	1.81	0.42
1:D:498:VAL:HG12	1:D:502:LEU:HD13	2.01	0.42
1:D:82:HIS:ND1	1:D:83:PRO:HD2	2.35	0.42
1:A:190:LEU:HD23	1:A:190:LEU:HA	1.89	0.42
1:A:346:GLU:HG3	1:A:354:PRO:HG3	2.01	0.42
1:B:59:VAL:O	1:B:63:LEU:HG	2.19	0.42
1:C:187:ILE:HD11	1:C:249:VAL:HG12	2.01	0.42
1:D:73:ILE:CG2	1:D:75:MSE:HE3	2.50	0.42
1:A:149:LEU:CD2	1:A:153:LEU:HB3	2.49	0.42
1:A:275:LEU:HG	1:A:279:LEU:HD12	2.01	0.42
1:A:3:GLN:HA	1:A:3:GLN:OE1	2.18	0.42
1:B:520:SER:O	1:B:523:GLN:HB3	2.19	0.42
1:B:522:LEU:O	1:B:525:ALA:HB3	2.19	0.42
1:C:74:ASP:HA	1:C:170:SER:CB	2.49	0.42
1:C:275:LEU:HG	1:C:279:LEU:HD12	2.01	0.42
1:C:511:LYS:O	1:C:514:THR:N	2.53	0.42
1:C:524:GLU:O	1:C:528:GLN:HB2	2.19	0.42
1:C:82:HIS:ND1	1:C:83:PRO:HD2	2.35	0.42
1:D:149:LEU:HB3	1:D:153:LEU:HD12	2.00	0.42
1:A:36:LEU:HD22	1:A:325:LEU:CD2	2.50	0.42
1:A:443:GLY:O	1:A:444:LEU:C	2.58	0.42
1:A:90:VAL:HG12	1:A:138:LEU:HD11	2.01	0.42
1:B:113:GLN:HA	1:B:162:PHE:CD2	2.55	0.42
1:B:425:LEU:O	1:B:426:PRO:C	2.58	0.42
1:B:520:SER:HG	1:B:521:LEU:H	1.67	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:461:LEU:CD1	1:A:461:LEU:N	2.82	0.42
1:B:154:LYS:HE2	1:B:154:LYS:HB3	1.80	0.42
1:B:373:MSE:O	1:B:377:MSE:HB2	2.19	0.42
1:B:480:LEU:O	1:B:483:ALA:HB3	2.20	0.42
1:C:14:GLY:O	1:C:15:ASN:HB3	2.20	0.42
1:C:190:LEU:CB	1:C:263:PRO:HG2	2.47	0.42
1:C:339:SER:HB2	1:D:336:LEU:O	2.19	0.42
1:D:343:PHE:O	1:D:346:GLU:HB3	2.20	0.42
1:D:54:GLN:HB2	1:D:57:CYS:SG	2.60	0.42
1:A:344:VAL:HG21	1:B:406:THR:OG1	2.20	0.42
1:A:13:GLU:CB	1:A:46:ARG:HA	2.50	0.42
1:B:353:ALA:CB	1:B:354:PRO:CD	2.97	0.42
1:B:38:VAL:HG22	1:B:38:VAL:O	2.20	0.42
1:C:132:MSE:HA	1:C:133:PRO:HD3	1.76	0.42
1:C:13:GLU:O	1:C:15:ASN:N	2.51	0.42
1:C:334:SER:OG	1:C:336:LEU:HB2	2.19	0.42
1:A:23:ILE:O	1:A:27:ILE:HG22	2.19	0.42
1:B:275:LEU:HG	1:B:279:LEU:HD12	2.01	0.42
1:B:539:ARG:O	1:B:541:GLU:N	2.53	0.42
1:C:25:GLN:O	1:C:29:GLN:N	2.52	0.42
1:C:492:PHE:CD2	1:C:522:LEU:HD11	2.55	0.42
1:B:13:GLU:HG2	1:B:15:ASN:CA	2.50	0.41
1:B:184:ALA:HB3	1:B:270:VAL:HB	2.01	0.41
1:C:176:THR:HG23	1:C:177:GLY:N	2.34	0.41
1:D:25:GLN:O	1:D:29:GLN:N	2.51	0.41
1:D:4:LEU:HD23	1:D:97:ARG:HH21	1.85	0.41
1:B:119:LEU:O	1:B:120:ASN:CB	2.68	0.41
1:C:154:LYS:HB3	1:C:154:LYS:HE2	1.79	0.41
1:C:353:ALA:CB	1:C:354:PRO:CD	2.98	0.41
1:C:390:THR:CG2	1:C:393:ARG:HH21	2.23	0.41
1:A:129:ALA:O	1:A:130:ALA:C	2.57	0.41
1:A:444:LEU:O	1:A:445:ARG:C	2.57	0.41
1:A:12:SER:HB3	1:A:75:MSE:HE1	2.02	0.41
1:A:376:GLN:O	1:B:350:ARG:HD2	2.20	0.41
1:B:82:HIS:ND1	1:B:83:PRO:HD2	2.34	0.41
1:C:254:ARG:HH11	1:C:254:ARG:CB	2.32	0.41
1:A:227:GLU:OE1	1:A:227:GLU:CA	2.54	0.41
1:B:127:GLY:O	1:B:129:ALA:N	2.53	0.41
1:B:135:ARG:CG	1:B:135:ARG:HH11	2.29	0.41
1:B:13:GLU:OE1	1:B:45:ASN:HA	2.20	0.41
1:C:129:ALA:O	1:C:130:ALA:O	2.39	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:474:LEU:HD23	1:C:477:LEU:HD13	2.02	0.41
1:D:153:LEU:HD23	1:D:165:SER:C	2.35	0.41
1:D:154:LYS:HE2	1:D:154:LYS:HB3	1.78	0.41
1:A:518:ILE:HA	1:A:521:LEU:HD12	2.02	0.41
1:A:82:HIS:ND1	1:A:83:PRO:HD2	2.35	0.41
1:B:375:GLY:HA3	1:B:395:ILE:HG12	2.02	0.41
1:C:13:GLU:CB	1:C:46:ARG:HA	2.50	0.41
1:A:14:GLY:O	1:A:15:ASN:CB	2.69	0.41
1:A:150:PRO:HD3	1:A:167:PHE:CE2	2.56	0.41
1:B:135:ARG:CG	1:B:141:ILE:HD11	2.48	0.41
1:B:187:ILE:HD11	1:B:249:VAL:HG12	2.02	0.41
1:C:12:SER:O	1:C:73:ILE:HD13	2.19	0.41
1:C:111:PHE:CD2	1:C:176:THR:OG1	2.67	0.41
1:C:340:LEU:O	1:C:344:VAL:HG12	2.21	0.41
1:C:432:GLU:O	1:C:432:GLU:HG2	2.20	0.41
1:D:113:GLN:HA	1:D:162:PHE:CD2	2.55	0.41
1:D:149:LEU:CD2	1:D:153:LEU:HG	2.45	0.41
1:D:375:GLY:HA3	1:D:395:ILE:HG12	2.01	0.41
1:A:135:ARG:CG	1:A:135:ARG:HH11	2.32	0.41
1:A:351:SER:OG	1:A:351:SER:O	2.38	0.41
1:B:70:SER:HA	1:B:171:TRP:HZ3	1.85	0.41
1:C:410:ASP:O	1:C:411:ALA:C	2.59	0.41
1:D:6:GLU:OE1	1:D:94:ILE:HG13	2.20	0.41
1:A:13:GLU:OE1	1:A:45:ASN:HA	2.21	0.41
1:A:25:GLN:O	1:A:29:GLN:N	2.51	0.41
1:A:303:VAL:CG2	1:A:303:VAL:O	2.69	0.41
1:A:476:CYS:O	1:A:477:LEU:C	2.59	0.41
1:B:149:LEU:N	1:B:150:PRO:CD	2.84	0.41
1:B:197:HIS:HB2	1:B:223:GLY:HA3	2.02	0.41
1:B:4:LEU:HB2	1:B:97:ARG:HG2	2.03	0.41
1:D:498:VAL:O	1:D:499:LEU:C	2.58	0.41
1:B:153:LEU:N	1:B:153:LEU:HD23	2.23	0.41
1:B:164:PRO:HB2	1:B:165:SER:H	1.60	0.41
1:B:498:VAL:O	1:B:499:LEU:C	2.58	0.41
1:C:113:GLN:HA	1:C:162:PHE:CD2	2.55	0.41
1:C:296:GLU:O	1:C:297:GLU:C	2.59	0.41
1:C:426:PRO:O	1:C:427:LYS:CB	2.37	0.41
1:C:461:LEU:N	1:C:461:LEU:HD13	2.36	0.41
1:C:89:ASP:HB3	1:C:90:VAL:H	1.63	0.41
1:D:119:LEU:O	1:D:120:ASN:CB	2.69	0.41
1:C:363:VAL:CG1	1:D:363:VAL:CG1	2.97	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:373:MSE:O	1:D:377:MSE:HB2	2.21	0.41
1:D:458:VAL:HA	1:D:461:LEU:HD22	2.02	0.41
1:D:502:LEU:HD21	1:D:514:THR:HB	2.03	0.41
1:D:531:LEU:O	1:D:532:VAL:C	2.57	0.41
1:A:406:THR:OG1	1:B:344:VAL:HG21	2.21	0.41
1:C:149:LEU:HB3	1:C:153:LEU:HD23	2.03	0.41
1:C:187:ILE:HD12	1:C:253:ALA:CB	2.51	0.41
1:C:184:ALA:HB3	1:C:270:VAL:HB	2.02	0.41
1:C:76:ARG:HG3	1:C:76:ARG:H	1.48	0.41
1:D:90:VAL:HG12	1:D:138:LEU:HD11	2.03	0.41
1:D:13:GLU:C	1:D:15:ASN:H	2.24	0.41
1:D:378:THR:OG1	1:D:473:ASN:N	2.49	0.41
1:A:113:GLN:HA	1:A:162:PHE:CD2	2.56	0.41
1:A:372:SER:O	1:A:376:GLN:HG3	2.21	0.41
1:A:498:VAL:O	1:A:499:LEU:C	2.59	0.41
1:B:339:SER:O	1:B:340:LEU:C	2.59	0.41
1:C:131:GLN:HB2	1:C:131:GLN:HE21	1.59	0.41
1:C:312:LEU:HD23	1:C:312:LEU:HA	1.81	0.41
1:C:485:LYS:HD3	1:C:485:LYS:HA	1.96	0.41
1:D:164:PRO:HB2	1:D:165:SER:H	1.59	0.41
1:A:124:TYR:N	1:A:124:TYR:CD1	2.89	0.40
1:B:286:CYS:HA	1:B:291:LEU:CD1	2.52	0.40
1:C:425:LEU:HD23	1:C:425:LEU:HA	1.89	0.40
1:A:396:PRO:O	1:A:397:PRO:C	2.58	0.40
1:B:474:LEU:HD23	1:B:477:LEU:HD13	2.02	0.40
1:B:485:LYS:HD3	1:B:485:LYS:HA	1.97	0.40
1:D:125:LEU:HD12	1:D:129:ALA:HB1	2.04	0.40
1:D:303:VAL:CG2	1:D:303:VAL:O	2.70	0.40
1:D:518:ILE:HA	1:D:518:ILE:HD12	1.89	0.40
1:D:12:SER:HB3	1:D:75:MSE:HE1	2.02	0.40
1:A:395:ILE:HB	1:A:396:PRO:HD3	2.04	0.40
1:A:410:ASP:O	1:A:411:ALA:C	2.59	0.40
1:A:70:SER:HA	1:A:171:TRP:HZ3	1.86	0.40
1:B:89:ASP:HB3	1:B:90:VAL:H	1.63	0.40
1:C:135:ARG:HG2	1:C:141:ILE:CD1	2.47	0.40
1:D:281:ALA:O	1:D:284:PHE:HB3	2.21	0.40
1:D:2:SER:HA	1:D:97:ARG:HE	1.86	0.40
1:A:377:MSE:HA	1:A:377:MSE:HE3	2.03	0.40
1:B:109:LYS:HZ3	1:C:102:ASP:CG	2.24	0.40
1:B:334:SER:OG	1:B:336:LEU:HB2	2.22	0.40
1:B:351:SER:OG	1:B:351:SER:O	2.38	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:149:LEU:N	1:C:150:PRO:CD	2.85	0.40
1:D:124:TYR:N	1:D:124:TYR:CD1	2.88	0.40
1:D:286:CYS:HA	1:D:291:LEU:CD1	2.52	0.40
1:A:296:GLU:O	1:A:297:GLU:C	2.59	0.40
1:A:498:VAL:HG12	1:A:502:LEU:HD13	2.03	0.40
1:A:59:VAL:O	1:A:63:LEU:HG	2.21	0.40
1:A:19:VAL:HG11	1:A:73:ILE:HD11	2.03	0.40
1:C:125:LEU:HD12	1:C:129:ALA:HB1	2.04	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	538/541 (99%)	401 (74%)	97 (18%)	40 (7%)	1	13
1	B	538/541 (99%)	407 (76%)	88 (16%)	43 (8%)	1	11
1	C	538/541 (99%)	404 (75%)	94 (18%)	40 (7%)	1	13
1	D	538/541 (99%)	404 (75%)	94 (18%)	40 (7%)	1	13
All	All	2152/2164 (99%)	1616 (75%)	373 (17%)	163 (8%)	1	12

All (163) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	16	ASN
1	A	89	ASP
1	A	142	ARG
1	A	164	PRO
1	A	350	ARG
1	A	353	ALA
1	A	383	GLN

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Mol	Chain	Res	Type
1	A	426	PRO
1	A	427	LYS
1	A	428	ASN
1	A	473	ASN
1	A	507	ASP
1	A	511	LYS
1	A	540	LYS
1	B	13	GLU
1	B	14	GLY
1	B	16	ASN
1	B	89	ASP
1	B	142	ARG
1	B	143	ALA
1	B	164	PRO
1	B	350	ARG
1	B	383	GLN
1	B	426	PRO
1	B	427	LYS
1	B	428	ASN
1	B	473	ASN
1	B	507	ASP
1	B	511	LYS
1	B	540	LYS
1	C	16	ASN
1	C	89	ASP
1	C	130	ALA
1	C	142	ARG
1	C	143	ALA
1	C	164	PRO
1	C	350	ARG
1	C	353	ALA
1	C	383	GLN
1	C	426	PRO
1	C	427	LYS
1	C	428	ASN
1	C	473	ASN
1	C	507	ASP
1	C	511	LYS
1	C	540	LYS
1	D	16	ASN
1	D	89	ASP
1	D	130	ALA

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Mol	Chain	Res	Type
1	D	142	ARG
1	D	143	ALA
1	D	164	PRO
1	D	350	ARG
1	D	353	ALA
1	D	383	GLN
1	D	426	PRO
1	D	427	LYS
1	D	428	ASN
1	D	473	ASN
1	D	507	ASP
1	D	511	LYS
1	D	540	LYS
1	A	13	GLU
1	A	83	PRO
1	A	128	GLU
1	A	130	ALA
1	A	143	ALA
1	A	210	LYS
1	A	356	GLY
1	A	381	ARG
1	A	411	ALA
1	A	474	LEU
1	B	83	PRO
1	B	128	GLU
1	B	130	ALA
1	B	165	SER
1	B	210	LYS
1	B	304	VAL
1	B	353	ALA
1	B	356	GLY
1	B	381	ARG
1	B	411	ALA
1	B	474	LEU
1	C	13	GLU
1	C	83	PRO
1	C	128	GLU
1	C	165	SER
1	C	210	LYS
1	C	356	GLY
1	C	381	ARG
1	C	411	ALA

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Mol	Chain	Res	Type
1	C	474	LEU
1	D	13	GLU
1	D	83	PRO
1	D	128	GLU
1	D	210	LYS
1	D	356	GLY
1	D	381	ARG
1	D	411	ALA
1	D	474	LEU
1	A	3	GLN
1	A	17	GLN
1	A	165	SER
1	A	304	VAL
1	A	339	SER
1	B	3	GLN
1	C	3	GLN
1	C	17	GLN
1	D	3	GLN
1	D	17	GLN
1	D	165	SER
1	D	332	GLU
1	D	336	LEU
1	D	339	SER
1	A	15	ASN
1	A	212	GLN
1	B	17	GLN
1	B	512	GLU
1	C	15	ASN
1	C	304	VAL
1	C	332	GLU
1	C	339	SER
1	D	15	ASN
1	D	212	GLN
1	D	304	VAL
1	D	512	GLU
1	A	84	ARG
1	A	85	MSE
1	A	332	GLU
1	A	396	PRO
1	A	512	GLU
1	B	15	ASN
1	B	55	PRO

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Mol	Chain	Res	Type
1	B	84	ARG
1	B	85	MSE
1	B	212	GLN
1	B	332	GLU
1	B	339	SER
1	B	530	ALA
1	C	84	ARG
1	C	85	MSE
1	C	212	GLN
1	C	530	ALA
1	D	84	ARG
1	D	85	MSE
1	D	509	VAL
1	A	55	PRO
1	A	443	GLY
1	A	509	VAL
1	B	120	ASN
1	B	396	PRO
1	C	55	PRO
1	C	396	PRO
1	C	509	VAL
1	D	55	PRO
1	D	396	PRO
1	D	443	GLY
1	B	249	VAL
1	B	443	GLY
1	C	443	GLY
1	B	509	VAL
1	C	249	VAL
1	A	534	GLY

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	437/429 (102%)	365 (84%)	72 (16%)	2 14

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	437/429 (102%)	363 (83%)	74 (17%)	2	13
1	C	437/429 (102%)	366 (84%)	71 (16%)	3	15
1	D	437/429 (102%)	365 (84%)	72 (16%)	2	14
All	All	1748/1716 (102%)	1459 (84%)	289 (16%)	2	14

All (289) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	SER
1	A	3	GLN
1	A	4	LEU
1	A	5	VAL
1	A	10	ASN
1	A	16	ASN
1	A	24	SER
1	A	28	SER
1	A	33	CYS
1	A	38	VAL
1	A	63	LEU
1	A	84	ARG
1	A	88	LEU
1	A	89	ASP
1	A	94	ILE
1	A	120	ASN
1	A	121	VAL
1	A	124	TYR
1	A	131	GLN
1	A	137	THR
1	A	141	ILE
1	A	153	LEU
1	A	154	LYS
1	A	161	ASP
1	A	167	PHE
1	A	170	SER
1	A	176	THR
1	A	182	LEU
1	A	192	THR
1	A	204	ARG
1	A	212	GLN
1	A	220	GLN
1	A	225	TYR

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Mol	Chain	Res	Type
1	A	227	GLU
1	A	246	LEU
1	A	254	ARG
1	A	279	LEU
1	A	288	LYS
1	A	291	LEU
1	A	294	LEU
1	A	325	LEU
1	A	326	VAL
1	A	344	VAL
1	A	347	VAL
1	A	350	ARG
1	A	359	VAL
1	A	366	LEU
1	A	373	MSE
1	A	377	MSE
1	A	383	GLN
1	A	390	THR
1	A	394	LEU
1	A	407	SER
1	A	425	LEU
1	A	429	THR
1	A	437	THR
1	A	438	CYS
1	A	442	GLU
1	A	445	ARG
1	A	450	VAL
1	A	453	LYS
1	A	454	LEU
1	A	457	THR
1	A	461	LEU
1	A	480	LEU
1	A	489	THR
1	A	504	ASP
1	A	510	PHE
1	A	515	ARG
1	A	519	SER
1	A	531	LEU
1	A	539	ARG
1	B	2	SER
1	B	3	GLN
1	B	4	LEU

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Mol	Chain	Res	Type
1	B	10	ASN
1	B	16	ASN
1	B	24	SER
1	B	28	SER
1	B	33	CYS
1	B	38	VAL
1	B	63	LEU
1	B	84	ARG
1	B	88	LEU
1	B	89	ASP
1	B	90	VAL
1	B	94	ILE
1	B	120	ASN
1	B	121	VAL
1	B	124	TYR
1	B	131	GLN
1	B	137	THR
1	B	141	ILE
1	B	153	LEU
1	B	154	LYS
1	B	161	ASP
1	B	167	PHE
1	B	170	SER
1	B	182	LEU
1	B	192	THR
1	B	204	ARG
1	B	212	GLN
1	B	220	GLN
1	B	225	TYR
1	B	227	GLU
1	B	246	LEU
1	B	254	ARG
1	B	279	LEU
1	B	288	LYS
1	B	291	LEU
1	B	294	LEU
1	B	297	GLU
1	B	300	ILE
1	B	325	LEU
1	B	326	VAL
1	B	344	VAL
1	B	347	VAL

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Mol	Chain	Res	Type
1	B	350	ARG
1	B	359	VAL
1	B	366	LEU
1	B	373	MSE
1	B	383	GLN
1	B	385	ASP
1	B	390	THR
1	B	394	LEU
1	B	407	SER
1	B	425	LEU
1	B	429	THR
1	B	435	ARG
1	B	437	THR
1	B	438	CYS
1	B	445	ARG
1	B	450	VAL
1	B	452	LEU
1	B	453	LYS
1	B	454	LEU
1	B	457	THR
1	B	461	LEU
1	B	480	LEU
1	B	489	THR
1	B	504	ASP
1	B	510	PHE
1	B	515	ARG
1	B	519	SER
1	B	531	LEU
1	B	539	ARG
1	C	2	SER
1	C	3	GLN
1	C	4	LEU
1	C	10	ASN
1	C	16	ASN
1	C	24	SER
1	C	28	SER
1	C	33	CYS
1	C	38	VAL
1	C	63	LEU
1	C	84	ARG
1	C	88	LEU
1	C	89	ASP

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Mol	Chain	Res	Type
1	C	94	ILE
1	C	120	ASN
1	C	121	VAL
1	C	124	TYR
1	C	131	GLN
1	C	137	THR
1	C	141	ILE
1	C	153	LEU
1	C	154	LYS
1	C	161	ASP
1	C	167	PHE
1	C	170	SER
1	C	182	LEU
1	C	192	THR
1	C	204	ARG
1	C	212	GLN
1	C	220	GLN
1	C	246	LEU
1	C	254	ARG
1	C	279	LEU
1	C	288	LYS
1	C	291	LEU
1	C	293	VAL
1	C	294	LEU
1	C	297	GLU
1	C	325	LEU
1	C	326	VAL
1	C	344	VAL
1	C	347	VAL
1	C	350	ARG
1	C	359	VAL
1	C	366	LEU
1	C	373	MSE
1	C	383	GLN
1	C	385	ASP
1	C	387	LEU
1	C	390	THR
1	C	394	LEU
1	C	407	SER
1	C	425	LEU
1	C	429	THR
1	C	437	THR

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Mol	Chain	Res	Type
1	C	438	CYS
1	C	445	ARG
1	C	450	VAL
1	C	453	LYS
1	C	454	LEU
1	C	457	THR
1	C	458	VAL
1	C	461	LEU
1	C	480	LEU
1	C	489	THR
1	C	504	ASP
1	C	510	PHE
1	C	515	ARG
1	C	519	SER
1	C	531	LEU
1	C	539	ARG
1	D	2	SER
1	D	3	GLN
1	D	4	LEU
1	D	5	VAL
1	D	10	ASN
1	D	16	ASN
1	D	24	SER
1	D	33	CYS
1	D	38	VAL
1	D	63	LEU
1	D	84	ARG
1	D	88	LEU
1	D	89	ASP
1	D	90	VAL
1	D	94	ILE
1	D	120	ASN
1	D	121	VAL
1	D	124	TYR
1	D	131	GLN
1	D	137	THR
1	D	141	ILE
1	D	153	LEU
1	D	154	LYS
1	D	161	ASP
1	D	167	PHE
1	D	170	SER

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Mol	Chain	Res	Type
1	D	182	LEU
1	D	192	THR
1	D	204	ARG
1	D	212	GLN
1	D	220	GLN
1	D	225	TYR
1	D	227	GLU
1	D	246	LEU
1	D	254	ARG
1	D	279	LEU
1	D	288	LYS
1	D	289	GLU
1	D	291	LEU
1	D	294	LEU
1	D	325	LEU
1	D	326	VAL
1	D	344	VAL
1	D	347	VAL
1	D	350	ARG
1	D	359	VAL
1	D	366	LEU
1	D	373	MSE
1	D	377	MSE
1	D	383	GLN
1	D	390	THR
1	D	394	LEU
1	D	407	SER
1	D	425	LEU
1	D	429	THR
1	D	437	THR
1	D	438	CYS
1	D	445	ARG
1	D	450	VAL
1	D	453	LYS
1	D	454	LEU
1	D	457	THR
1	D	461	LEU
1	D	475	SER
1	D	480	LEU
1	D	489	THR
1	D	504	ASP
1	D	510	PHE

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Mol	Chain	Res	Type
1	D	515	ARG
1	D	519	SER
1	D	531	LEU
1	D	539	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (51) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	25	GLN
1	A	29	GLN
1	A	78	HIS
1	A	82	HIS
1	A	131	GLN
1	A	202	ASN
1	A	247	HIS
1	A	261	ASN
1	A	386	HIS
1	A	428	ASN
1	A	466	GLN
1	A	481	GLN
1	A	528	GLN
1	B	25	GLN
1	B	29	GLN
1	B	78	HIS
1	B	82	HIS
1	B	131	GLN
1	B	202	ASN
1	B	247	HIS
1	B	261	ASN
1	B	386	HIS
1	B	428	ASN
1	B	466	GLN
1	B	481	GLN
1	B	528	GLN
1	C	25	GLN
1	C	29	GLN
1	C	78	HIS
1	C	82	HIS
1	C	131	GLN
1	C	202	ASN
1	C	261	ASN
1	C	386	HIS

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Mol	Chain	Res	Type
1	C	428	ASN
1	C	466	GLN
1	C	481	GLN
1	C	528	GLN
1	D	25	GLN
1	D	29	GLN
1	D	78	HIS
1	D	82	HIS
1	D	131	GLN
1	D	202	ASN
1	D	247	HIS
1	D	261	ASN
1	D	386	HIS
1	D	428	ASN
1	D	466	GLN
1	D	481	GLN
1	D	528	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	532/541 (98%)	0.13	18 (3%) 46 42	29, 53, 164, 213	0
1	B	532/541 (98%)	0.06	9 (1%) 70 66	30, 53, 158, 222	0
1	C	532/541 (98%)	0.17	21 (3%) 40 37	31, 60, 149, 194	0
1	D	532/541 (98%)	0.19	22 (4%) 38 34	33, 60, 159, 199	0
All	All	2128/2164 (98%)	0.14	70 (3%) 47 43	29, 56, 157, 222	0

All (70) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	122	PRO	8.9
1	C	166	SER	6.8
1	D	122	PRO	5.6
1	B	166	SER	4.9
1	B	121	VAL	4.9
1	A	115	LEU	4.2
1	C	149	LEU	4.2
1	A	121	VAL	4.2
1	A	147	GLU	3.9
1	D	115	LEU	3.8
1	C	121	VAL	3.8
1	A	120	ASN	3.7
1	C	174	THR	3.6
1	D	147	GLU	3.5
1	C	47	THR	3.4
1	D	99	VAL	3.3
1	A	62	ALA	3.3
1	D	149	LEU	3.1
1	D	124	TYR	3.1
1	C	153	LEU	3.1
1	D	6	GLU	3.1

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Mol	Chain	Res	Type	RSRZ
1	D	165	SER	3.1
1	C	176	THR	2.9
1	A	90	VAL	2.9
1	A	124	TYR	2.9
1	D	69	ALA	2.8
1	D	77	LYS	2.8
1	D	121	VAL	2.8
1	C	236	THR	2.8
1	D	178	ALA	2.7
1	A	178	ALA	2.7
1	D	72	LEU	2.7
1	B	428	ASN	2.6
1	A	149	LEU	2.6
1	C	428	ASN	2.6
1	A	158	TRP	2.6
1	B	47	THR	2.6
1	C	91	CYS	2.6
1	B	171	TRP	2.5
1	A	104	CYS	2.5
1	C	98	GLY	2.5
1	C	11	PHE	2.5
1	B	138	LEU	2.5
1	B	149	LEU	2.5
1	D	34	VAL	2.4
1	D	120	ASN	2.4
1	D	51	PHE	2.4
1	D	160	PRO	2.4
1	D	62	ALA	2.4
1	C	406	THR	2.4
1	A	119	LEU	2.4
1	C	138	LEU	2.3
1	C	79	LYS	2.3
1	C	93	PHE	2.3
1	A	66	ALA	2.3
1	D	157	GLU	2.2
1	C	36	LEU	2.2
1	B	178	ALA	2.2
1	A	172	GLY	2.2
1	C	125	LEU	2.2
1	D	274	PRO	2.2
1	C	10	ASN	2.2
1	B	11	PHE	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	65	ALA	2.1
1	D	90	VAL	2.1
1	D	126	TYR	2.1
1	A	34	VAL	2.1
1	A	35	LEU	2.1
1	C	171	TRP	2.1
1	C	175	VAL	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.