



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 01:11 PM GMT

PDB ID : 3T6G
Title : Structure of the complex between NSP3 (SHEP1) and p130Cas
Authors : Mace, P.D.; Robinson, H.; Riedl, S.J.
Deposited on : 2011-07-28
Resolution : 2.50 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 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

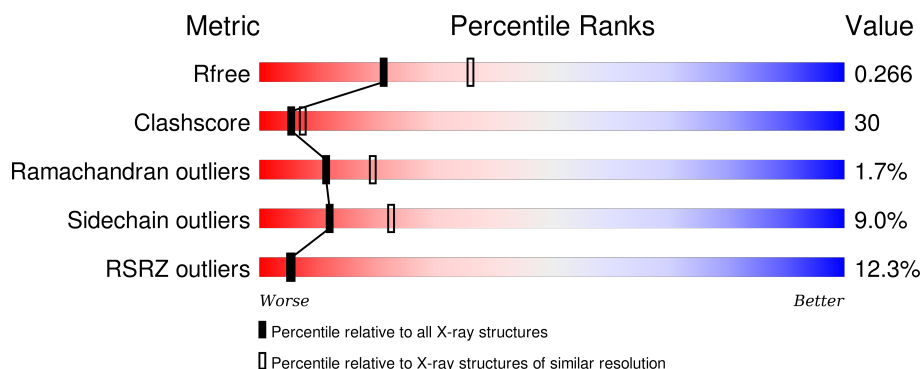
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	3553 (2.50-2.50)
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (2.50-2.50)

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	331	<div> <div>6%</div> <div>58%</div> <div>27%</div> <div>5%</div> <div>10%</div> </div>
1	C	331	<div> <div>18%</div> <div>36%</div> <div>41%</div> <div>5%</div> <div>18%</div> </div>
2	B	229	<div> <div>%</div> <div>41%</div> <div>14%</div> <div>•</div> <div>41%</div> </div>
2	D	229	<div> <div>10%</div> <div>28%</div> <div>26%</div> <div>•</div> <div>43%</div> </div>

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

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	ACT	C	1	-	-	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6598 atoms, of which 3 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 SH2 domain-containing protein 3C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	299	Total	C	N	O	S	1	1	0
			2348	1495	418	423	12			
1	C	273	Total	C	N	O	S	1	0	0
			2139	1361	383	384	11			

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	381	MET	-	INITIATING METHIONINE	UNP Q8N5H7
A	497	SER	CYS	ENGINEERED MUTATION	UNP Q8N5H7
A	598	SER	CYS	ENGINEERED MUTATION	UNP Q8N5H7
A	704	LEU	-	EXPRESSION TAG	UNP Q8N5H7
A	705	GLU	-	EXPRESSION TAG	UNP Q8N5H7
A	706	HIS	-	EXPRESSION TAG	UNP Q8N5H7
A	707	HIS	-	EXPRESSION TAG	UNP Q8N5H7
A	708	HIS	-	EXPRESSION TAG	UNP Q8N5H7
A	709	HIS	-	EXPRESSION TAG	UNP Q8N5H7
A	710	HIS	-	EXPRESSION TAG	UNP Q8N5H7
A	711	HIS	-	EXPRESSION TAG	UNP Q8N5H7
C	381	MET	-	INITIATING METHIONINE	UNP Q8N5H7
C	497	SER	CYS	ENGINEERED MUTATION	UNP Q8N5H7
C	598	SER	CYS	ENGINEERED MUTATION	UNP Q8N5H7
C	704	LEU	-	EXPRESSION TAG	UNP Q8N5H7
C	705	GLU	-	EXPRESSION TAG	UNP Q8N5H7
C	706	HIS	-	EXPRESSION TAG	UNP Q8N5H7
C	707	HIS	-	EXPRESSION TAG	UNP Q8N5H7
C	708	HIS	-	EXPRESSION TAG	UNP Q8N5H7
C	709	HIS	-	EXPRESSION TAG	UNP Q8N5H7
C	710	HIS	-	EXPRESSION TAG	UNP Q8N5H7
C	711	HIS	-	EXPRESSION TAG	UNP Q8N5H7

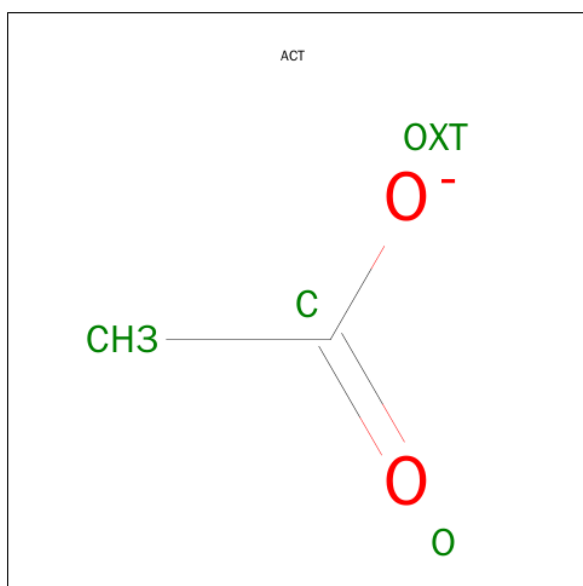
- Molecule 2 is a protein called Breast cancer anti-estrogen resistance protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	134	Total	C	N	O	S	0	0	0
			1035	657	183	192	3			
2	D	131	Total	C	N	O	S	0	0	0
			1010	644	177	186	3			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	644	MET	-	INITIATING METHIONINE	UNP P56945
B	871	LEU	-	EXPRESSION TAG	UNP P56945
B	872	GLU	-	EXPRESSION TAG	UNP P56945
D	644	MET	-	INITIATING METHIONINE	UNP P56945
D	871	LEU	-	EXPRESSION TAG	UNP P56945
D	872	GLU	-	EXPRESSION TAG	UNP P56945

- Molecule 3 is ACETATE ION (three-letter code: ACT) (formula: C₂H₃O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	C	1	Total	C	H	O	0	0
			7	2	3	2		

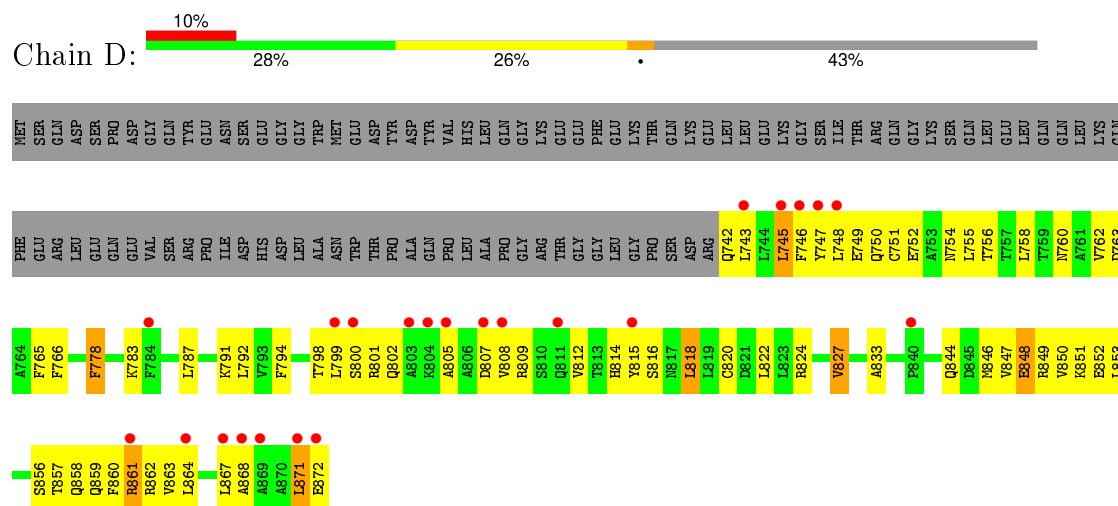
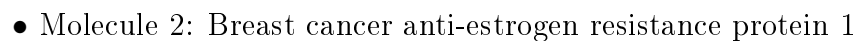
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	41	Total	O	0	0
			41	41		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	14	Total	O	0	0
			14	14		
4	C	4	Total	O	0	0
			4	4		



4 Data and refinement statistics

Property	Value	Source
Space group	I 41	Depositor
Cell constants a, b, c, α , β , γ	171.88Å 171.88Å 78.27Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.55 – 2.50 29.55 – 2.50	Depositor EDS
% Data completeness (in resolution range)	94.1 (29.55-2.50) 99.9 (29.55-2.50)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.38 (at 2.51Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6.4 _486)	Depositor
R, R_{free}	0.197 , 0.266 0.199 , 0.266	Depositor DCC
R_{free} test set	1985 reflections (5.28%)	DCC
Wilson B-factor (Å ²)	63.5	Xtriage
Anisotropy	0.626	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 71.4	EDS
Estimated twinning fraction	0.019 for -k,-h,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 39578 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6598	wwPDB-VP
Average B, all atoms (Å ²)	100.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.12% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: ACT

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.47	0/2393	0.64	1/3235 (0.0%)
1	C	0.30	0/2176	0.45	0/2936
2	B	0.45	0/1052	0.62	0/1428
2	D	0.32	0/1027	0.47	0/1395
All	All	0.39	0/6648	0.56	1/8994 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	437	VAL	CB-CA-C	-5.20	101.53	111.40

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	2348	0	2427	96	0
1	C	2139	0	2212	194	0
2	B	1035	0	1054	39	0
2	D	1010	0	1032	83	0
3	C	4	3	3	1	0
4	A	41	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	14	0	0	1	0
4	C	4	0	0	2	0
All	All	6595	3	6728	397	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 30.

All (397) 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:454:MET:HA	1:C:457:LEU:HD12	1.21	1.17
1:A:545:GLN:O	1:A:549:THR:HG22	1.46	1.15
2:D:748:LEU:HD13	2:D:864:LEU:HD23	1.31	1.09
1:A:387:VAL:HB	1:A:388:PRO:HD3	1.09	1.09
1:C:489:MET:HE2	1:C:662:GLN:HG2	1.24	1.08
2:D:745:LEU:HD12	2:D:745:LEU:H	1.16	1.03
1:C:435:ARG:HA	1:C:522:MET:HE1	1.40	1.02
1:C:452:LYS:HE3	1:C:452:LYS:HA	1.40	1.02
1:C:414:GLU:HB2	1:C:417:LEU:HD13	1.43	1.01
1:C:450:VAL:HB	1:C:455:GLN:HE21	1.23	1.00
1:A:387:VAL:CB	1:A:388:PRO:HD3	1.92	0.96
2:D:814:HIS:O	2:D:818:LEU:HD13	1.66	0.96
1:A:387:VAL:HB	1:A:388:PRO:CD	1.98	0.94
2:D:799:LEU:HD12	2:D:812:VAL:HG11	1.49	0.92
1:C:489:MET:CE	1:C:662:GLN:HG2	2.00	0.91
2:D:743:LEU:HG	2:D:746:PHE:HE2	1.31	0.90
2:D:859:GLN:HG3	2:D:862:ARG:HH11	1.35	0.90
1:C:669:SER:O	1:C:670:GLN:HB3	1.69	0.90
2:D:743:LEU:HG	2:D:746:PHE:CE2	2.07	0.89
2:D:799:LEU:HD12	2:D:812:VAL:CG1	2.02	0.88
2:D:745:LEU:H	2:D:745:LEU:CD1	1.87	0.87
1:C:428:VAL:HG22	1:C:429:ASP:H	1.39	0.87
1:C:587:PRO:HG3	1:C:636:TYR:CE2	2.10	0.87
1:C:458:MET:HB2	1:C:460:VAL:HG13	1.58	0.86
1:C:489:MET:HE2	1:C:662:GLN:CG	2.06	0.85
2:D:745:LEU:HD12	2:D:745:LEU:N	1.91	0.84
2:B:870:ALA:C	2:B:871:LEU:HD23	1.98	0.84
1:C:678:ARG:O	1:C:682:LYS:HG2	1.77	0.84
2:D:861:ARG:HB2	2:D:861:ARG:NH1	1.92	0.84
2:D:799:LEU:CD1	2:D:812:VAL:HG11	2.08	0.83
1:C:424:LEU:HD22	1:C:653:LEU:HG	1.61	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:525:MET:CE	1:C:579:PRO:HG3	2.10	0.82
1:C:659:THR:O	1:C:663:MET:HG3	1.79	0.81
1:C:615:GLY:O	1:C:619:VAL:HG23	1.82	0.80
2:D:743:LEU:CG	2:D:746:PHE:HE2	1.94	0.80
2:B:748:LEU:HD13	2:B:864:LEU:HB3	1.65	0.79
1:C:527:SER:O	1:C:531:VAL:HG23	1.83	0.79
1:C:440:VAL:HG23	1:C:482:ARG:NH2	1.99	0.78
1:A:539:GLN:HE21	1:A:688:THR:HG23	1.46	0.78
1:C:681:GLU:HB3	1:C:685:LYS:HZ1	1.48	0.78
2:D:748:LEU:CD1	2:D:864:LEU:HD23	2.11	0.78
1:C:642:VAL:O	1:C:645:GLN:HG2	1.84	0.78
1:C:437:VAL:HG12	1:C:657:PHE:CD1	2.21	0.76
1:A:581:LEU:HD21	1:A:632:HIS:CE1	2.20	0.76
2:D:792:LEU:HD23	2:D:860:PHE:CD2	2.21	0.76
1:A:406:ILE:HG22	1:A:406:ILE:O	1.86	0.75
1:A:545:GLN:O	1:A:549:THR:CG2	2.31	0.75
1:C:579:PRO:HB2	1:C:580:PRO:HD2	1.68	0.75
1:C:437:VAL:HG12	1:C:657:PHE:CG	2.21	0.75
1:C:683:PHE:HA	1:C:686:VAL:HG23	1.69	0.74
1:C:591:PRO:O	1:C:595:LEU:HD13	1.87	0.74
1:A:498:THR:HG22	1:A:694:LEU:HD11	1.69	0.74
2:D:800:SER:O	2:D:809:ARG:HD2	1.88	0.74
1:C:462:TRP:CE2	1:C:634:GLY:HA2	2.23	0.73
1:A:677:ALA:O	1:A:681:GLU:HG3	1.87	0.73
2:D:861:ARG:HB2	2:D:861:ARG:HH11	1.50	0.73
1:C:525:MET:HE2	1:C:579:PRO:HG3	1.70	0.73
1:C:414:GLU:HG3	1:C:417:LEU:HD22	1.71	0.72
2:D:853:LEU:O	2:D:857:THR:HG23	1.88	0.72
1:C:483:PHE:CZ	1:C:590:LEU:HD22	2.24	0.72
1:C:424:LEU:CD2	1:C:653:LEU:HG	2.19	0.72
1:C:454:MET:HA	1:C:457:LEU:CD1	2.11	0.72
1:C:678:ARG:HD2	1:C:682:LYS:HE2	1.72	0.71
1:A:539:GLN:NE2	1:A:688:THR:HG23	2.03	0.71
2:D:760:ASN:HA	2:D:763:ASP:HB3	1.70	0.71
2:D:863:VAL:O	2:D:867:LEU:HD13	1.91	0.71
1:C:683:PHE:HA	1:C:686:VAL:CG2	2.20	0.71
1:C:675:SER:O	1:C:679:ARG:HG3	1.90	0.71
1:C:489:MET:HG3	1:C:490:LEU:N	2.07	0.70
1:C:541:SER:HB2	3:C:1:ACT:H3	1.74	0.69
1:C:452:LYS:HE3	1:C:452:LYS:CA	2.19	0.69
1:A:476:ARG:HG2	1:A:593:ILE:HG22	1.75	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:453:GLU:O	1:C:457:LEU:HG	1.92	0.69
1:A:539:GLN:HG3	1:A:688:THR:HG22	1.75	0.68
2:B:871:LEU:N	2:B:871:LEU:HD23	2.02	0.68
1:C:440:VAL:CG2	1:C:482:ARG:NH2	2.56	0.68
1:C:655:GLU:O	1:C:661:PHE:CD2	2.46	0.68
1:C:468:THR:HG21	1:C:630:ALA:HB2	1.76	0.68
2:D:844:GLN:O	2:D:848:GLU:HG2	1.92	0.68
1:C:539:GLN:HG2	1:C:687:LEU:HB3	1.75	0.68
1:C:681:GLU:HB3	1:C:685:LYS:NZ	2.08	0.68
1:A:538:ALA:O	1:A:542:ARG:HG2	1.94	0.68
1:C:638:THR:O	1:C:642:VAL:HG23	1.93	0.68
1:A:429:ASP:OD1	1:A:432:THR:HG23	1.94	0.68
1:C:417:LEU:O	1:C:421:VAL:HG23	1.94	0.67
1:C:436:HIS:CE1	1:C:649:ALA:HB1	2.30	0.66
1:A:542:ARG:NH1	1:A:692:HIS:CE1	2.63	0.66
1:C:469:LEU:HD21	2:D:798:THR:OG1	1.95	0.66
2:D:749:GLU:HA	2:D:752:GLU:OE1	1.94	0.66
1:C:542:ARG:NH2	1:C:695:GLU:O	2.29	0.66
1:C:576:LYS:HB2	1:C:576:LYS:NZ	2.11	0.65
1:C:466:LEU:HD11	1:C:472:GLY:HA2	1.79	0.65
1:A:624:GLU:HG2	4:B:69:HOH:O	1.97	0.65
1:A:685:LYS:HD2	1:A:685:LYS:C	2.18	0.65
1:C:435:ARG:HA	1:C:522:MET:CE	2.23	0.64
1:A:387:VAL:HG21	2:B:742:GLN:HB3	1.80	0.64
1:C:681:GLU:O	1:C:685:LYS:HD2	1.98	0.64
2:D:805:ALA:HB3	2:D:808:VAL:CG2	2.28	0.64
2:D:747:TYR:OH	2:D:798:THR:HG21	1.98	0.64
1:A:452:LYS:N	1:A:452:LYS:HD2	2.12	0.64
1:A:597:GLU:O	1:A:598:SER:HB3	1.95	0.64
2:B:742:GLN:HA	2:B:742:GLN:HE21	1.64	0.63
1:C:617:GLU:HG2	2:D:827:VAL:HG21	1.81	0.63
1:C:417:LEU:HD12	1:C:417:LEU:N	2.14	0.63
1:C:525:MET:HE3	1:C:579:PRO:HG3	1.81	0.62
1:C:419:ARG:O	1:C:423:GLU:HG3	1.98	0.62
1:C:439:LYS:HE2	1:C:443:LEU:HD11	1.81	0.62
2:D:860:PHE:O	2:D:864:LEU:HB2	1.98	0.62
1:A:406:ILE:HD13	1:A:661:PHE:CD1	2.33	0.62
1:C:689:ALA:O	1:C:693:LYS:HG3	1.99	0.62
1:C:424:LEU:HD22	1:C:653:LEU:CG	2.28	0.62
1:C:539:GLN:HG2	1:C:687:LEU:CB	2.29	0.62
1:A:572:LEU:HB3	1:A:588:HIS:CD2	2.35	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:464:MET:HA	1:C:464:MET:HE2	1.80	0.62
2:D:766:PHE:CZ	2:D:850:VAL:HG12	2.34	0.61
2:D:859:GLN:CG	2:D:862:ARG:HH11	2.11	0.61
2:D:814:HIS:NE2	2:D:818:LEU:HD21	2.14	0.61
1:C:580:PRO:HG2	1:C:583:ASN:HB3	1.80	0.61
2:D:859:GLN:HG3	2:D:862:ARG:NH1	2.12	0.61
1:C:424:LEU:HD22	1:C:653:LEU:CD2	2.31	0.61
1:C:453:GLU:CD	1:C:453:GLU:H	2.03	0.61
1:A:577:GLU:OE1	1:A:577:GLU:HA	1.98	0.61
1:A:669:SER:O	1:A:670:GLN:HB2	2.01	0.61
1:A:678:ARG:O	1:A:682:LYS:HG2	2.00	0.60
1:C:514:LEU:O	1:C:514:LEU:HD12	2.01	0.60
2:D:867:LEU:CD1	2:D:867:LEU:H	2.14	0.60
2:B:824:ARG:HA	2:B:827:VAL:HG12	1.84	0.60
1:C:454:MET:O	1:C:458:MET:HG3	2.02	0.60
1:A:614:HIS:HB3	1:A:618:VAL:CG2	2.31	0.60
1:A:455:GLN:HG2	1:A:461:ARG:HA	1.83	0.60
1:C:414:GLU:H	1:C:414:GLU:CD	2.04	0.60
1:A:678:ARG:HG3	1:A:682:LYS:NZ	2.16	0.60
1:C:473:ARG:HG3	1:C:597:GLU:OE2	2.02	0.60
1:C:451:THR:HB	1:C:453:GLU:OE1	2.02	0.60
2:D:746:PHE:CE1	2:D:747:TYR:CD1	2.90	0.60
2:D:814:HIS:CE1	2:D:818:LEU:CD2	2.85	0.59
1:A:482:ARG:HG3	1:A:659:THR:OG1	2.02	0.59
1:C:545:GLN:O	1:C:549:THR:HG23	2.02	0.59
2:D:814:HIS:CE1	2:D:818:LEU:HD21	2.37	0.59
1:C:436:HIS:HB3	1:C:657:PHE:CD2	2.37	0.59
2:B:739:SER:HB2	2:B:742:GLN:CG	2.33	0.59
1:C:458:MET:CB	1:C:460:VAL:HG13	2.30	0.59
2:B:848:GLU:O	2:B:852:GLU:HG3	2.03	0.58
2:B:870:ALA:O	2:B:871:LEU:HD23	2.03	0.58
1:C:464:MET:HE2	1:C:467:LEU:HD21	1.83	0.58
2:D:762:VAL:HG13	2:D:766:PHE:CE2	2.38	0.58
1:A:476:ARG:HG2	1:A:593:ILE:CG2	2.33	0.58
1:C:644:LEU:HD22	1:C:647:PHE:CG	2.38	0.57
1:A:616:VAL:HG23	2:B:783:LYS:HG2	1.85	0.57
1:C:468:THR:HB	2:D:794:PHE:CD1	2.40	0.57
2:D:746:PHE:CE1	2:D:747:TYR:CE1	2.93	0.57
1:C:473:ARG:HA	1:C:476:ARG:CZ	2.35	0.57
2:D:853:LEU:HD13	2:D:853:LEU:C	2.26	0.56
1:A:669:SER:O	1:A:670:GLN:CB	2.54	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:466:LEU:HD11	1:C:472:GLY:CA	2.36	0.56
1:C:579:PRO:CB	1:C:580:PRO:HD2	2.35	0.56
2:D:791:LYS:HA	2:D:794:PHE:HD2	1.71	0.55
1:A:497:SER:O	1:A:504:ARG:HG3	2.05	0.55
2:D:833:ALA:CB	2:D:846:MET:HE2	2.36	0.55
1:C:450:VAL:CB	1:C:455:GLN:HE21	2.07	0.55
1:C:653:LEU:O	1:C:656:VAL:HB	2.06	0.55
1:A:581:LEU:HG	1:A:635:LEU:CD2	2.35	0.55
1:C:617:GLU:HG3	4:C:70:HOH:O	2.06	0.55
1:C:620:LEU:HD22	2:D:827:VAL:HG11	1.87	0.55
1:A:525:MET:HE2	1:A:525:MET:HA	1.88	0.55
1:A:570:LYS:O	1:A:574:GLU:HG3	2.07	0.55
1:A:406:ILE:CG2	1:A:406:ILE:O	2.55	0.55
2:B:824:ARG:O	2:B:827:VAL:CG1	2.54	0.55
1:A:437:VAL:HG13	1:A:657:PHE:CD1	2.42	0.55
1:C:452:LYS:CE	1:C:452:LYS:HA	2.26	0.55
2:D:815:TYR:CZ	2:D:863:VAL:HG21	2.42	0.55
2:D:743:LEU:CD2	2:D:746:PHE:HE2	2.19	0.55
1:C:429:ASP:OD1	1:C:431:ARG:HB3	2.07	0.55
1:A:678:ARG:HG3	1:A:682:LYS:HZ3	1.72	0.54
1:C:440:VAL:CG2	1:C:482:ARG:HH22	2.20	0.54
1:A:490:LEU:CD1	1:A:531:VAL:HG22	2.37	0.54
1:C:428:VAL:HG22	1:C:429:ASP:N	2.18	0.54
2:D:859:GLN:HA	2:D:862:ARG:NH1	2.22	0.54
1:C:466:LEU:CD1	1:C:472:GLY:CA	2.85	0.54
2:D:748:LEU:HD11	2:D:861:ARG:HH12	1.73	0.54
2:B:824:ARG:O	2:B:827:VAL:HG12	2.06	0.54
1:C:497:SER:HB3	1:C:504:ARG:HG2	1.90	0.54
2:D:867:LEU:CD1	2:D:867:LEU:N	2.71	0.54
1:A:685:LYS:HD2	1:A:685:LYS:O	2.08	0.54
1:A:421:VAL:HG11	1:A:489:MET:CE	2.38	0.53
1:C:422:LYS:HZ1	1:C:496:GLY:C	2.12	0.53
1:A:566:LYS:CB	1:A:567:PRO:HD3	2.38	0.53
2:D:867:LEU:H	2:D:867:LEU:HD13	1.73	0.53
1:C:642:VAL:O	1:C:645:GLN:CG	2.56	0.53
1:C:648:GLN:CD	1:C:648:GLN:N	2.61	0.53
1:C:434:ALA:O	1:C:438:THR:HB	2.08	0.53
2:D:746:PHE:HE1	2:D:747:TYR:CE1	2.27	0.53
1:C:451:THR:OG1	1:C:454:MET:HB2	2.09	0.53
1:C:437:VAL:CG1	1:C:657:PHE:CD1	2.92	0.53
1:A:678:ARG:HA	1:A:681:GLU:OE1	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:435:ARG:HB3	1:C:647:PHE:CE2	2.44	0.53
1:C:669:SER:O	1:C:670:GLN:CB	2.51	0.52
1:C:473:ARG:HB2	1:C:476:ARG:NH2	2.23	0.52
2:D:754:ASN:OD1	2:D:791:LYS:HD2	2.09	0.52
2:B:741:ARG:HD2	2:B:871:LEU:O	2.10	0.52
1:A:406:ILE:CD1	1:A:661:PHE:CD1	2.92	0.52
2:D:751:CYS:O	2:D:755:LEU:HD23	2.10	0.52
1:C:658:SER:OG	1:C:661:PHE:HB3	2.10	0.52
2:D:799:LEU:HD12	2:D:812:VAL:HG12	1.88	0.52
2:B:743:LEU:HD21	2:B:802:GLN:HB2	1.91	0.52
1:C:483:PHE:CE1	1:C:590:LEU:HD22	2.45	0.52
1:C:648:GLN:H	1:C:648:GLN:CD	2.13	0.52
1:A:387:VAL:CB	1:A:388:PRO:CD	2.70	0.52
1:C:683:PHE:CA	1:C:686:VAL:HG23	2.39	0.52
1:A:406:ILE:CD1	1:A:661:PHE:CE1	2.93	0.52
1:A:481:GLU:CD	1:A:679:ARG:HH12	2.13	0.51
1:C:427:GLU:HG2	1:C:427:GLU:O	2.10	0.51
2:D:762:VAL:CG1	2:D:766:PHE:CE2	2.94	0.51
2:D:742:GLN:OE1	2:D:742:GLN:N	2.43	0.51
1:A:387:VAL:HG21	2:B:742:GLN:CB	2.40	0.51
2:B:849:ARG:HG2	2:B:849:ARG:HH11	1.74	0.51
2:B:808:VAL:O	2:B:812:VAL:HG22	2.11	0.51
1:C:425:LEU:C	1:C:427:GLU:H	2.14	0.51
1:C:495:LEU:HA	1:C:694:LEU:CD1	2.39	0.51
1:C:576:LYS:HB2	1:C:576:LYS:HZ2	1.75	0.51
1:C:519:ARG:HB3	1:C:528:PHE:CD1	2.46	0.51
1:C:450:VAL:O	1:C:450:VAL:HG23	2.11	0.51
2:B:739:SER:HB2	2:B:742:GLN:HG3	1.92	0.51
1:C:437:VAL:HG13	1:C:657:PHE:CE2	2.46	0.51
1:A:390:VAL:HG13	1:A:471:HIS:HB2	1.92	0.51
2:B:849:ARG:HG2	2:B:849:ARG:NH1	2.26	0.50
1:A:484:HIS:HB2	4:A:28:HOH:O	2.10	0.50
2:D:778:PHE:C	2:D:778:PHE:CD1	2.84	0.50
1:C:462:TRP:NE1	1:C:634:GLY:CA	2.75	0.50
1:C:587:PRO:O	1:C:589:VAL:HG13	2.12	0.50
1:C:450:VAL:HG11	1:C:462:TRP:CE3	2.47	0.49
1:C:437:VAL:CG1	1:C:657:PHE:CE1	2.95	0.49
1:A:698:VAL:O	1:A:698:VAL:HG12	2.12	0.49
1:C:483:PHE:O	1:C:486:MET:HB3	2.12	0.49
1:C:572:LEU:HB3	1:C:588:HIS:CD2	2.46	0.49
1:C:460:VAL:CG2	1:C:461:ARG:N	2.75	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:743:LEU:HD21	2:B:802:GLN:CB	2.42	0.49
1:C:581:LEU:HD21	1:C:632:HIS:ND1	2.27	0.49
1:C:424:LEU:O	1:C:427:GLU:HB3	2.12	0.49
1:C:450:VAL:HB	1:C:455:GLN:NE2	2.08	0.49
1:A:392:VAL:O	1:A:392:VAL:HG13	2.12	0.49
1:C:519:ARG:HG3	1:C:520:GLY:N	2.26	0.49
1:C:471:HIS:HB3	2:D:750:GLN:OE1	2.13	0.49
1:A:539:GLN:HG2	1:A:688:THR:N	2.27	0.48
1:A:421:VAL:HG11	1:A:489:MET:HE1	1.94	0.48
2:D:822:LEU:HD13	2:D:853:LEU:HA	1.96	0.48
2:B:849:ARG:NH2	2:B:852:GLU:OE1	2.46	0.48
1:C:460:VAL:HG23	1:C:461:ARG:N	2.29	0.48
2:D:861:ARG:CB	2:D:861:ARG:HH11	2.21	0.48
1:C:568:PHE:O	1:C:571:SER:HB3	2.13	0.48
2:D:847:VAL:O	2:D:851:LYS:HB2	2.13	0.48
2:D:820:CYS:O	2:D:824:ARG:HG3	2.13	0.48
1:A:419:ARG:HG2	1:A:419:ARG:HH11	1.79	0.48
1:A:581:LEU:HG	1:A:635:LEU:HD23	1.95	0.48
2:D:858:GLN:C	2:D:860:PHE:H	2.17	0.47
1:C:583:ASN:O	1:C:643:LYS:HE2	2.14	0.47
1:A:436:HIS:CE1	1:A:647:PHE:HZ	2.32	0.47
2:D:801:ARG:O	2:D:801:ARG:HG2	2.13	0.47
1:C:560:LEU:O	1:C:564:LYS:HB2	2.15	0.47
1:C:424:LEU:HD23	1:C:427:GLU:OE1	2.14	0.47
1:C:579:PRO:HB2	1:C:580:PRO:CD	2.42	0.47
1:A:436:HIS:CE1	1:A:647:PHE:CZ	3.03	0.47
1:C:494:ILE:HA	1:C:507:LEU:HD21	1.97	0.47
2:B:751:CYS:O	2:B:755:LEU:HD13	2.14	0.47
2:D:849:ARG:HA	2:D:849:ARG:HE	1.79	0.47
2:D:859:GLN:CB	2:D:862:ARG:NH1	2.78	0.47
1:A:539:GLN:CG	1:A:688:THR:HG22	2.44	0.47
1:C:417:LEU:N	1:C:417:LEU:CD1	2.77	0.46
1:C:689:ALA:HB1	1:C:693:LYS:HE3	1.96	0.46
1:C:617:GLU:HG2	2:D:827:VAL:CG2	2.45	0.46
2:D:815:TYR:O	2:D:818:LEU:N	2.49	0.46
1:A:566:LYS:N	1:A:567:PRO:CD	2.77	0.46
1:C:462:TRP:CD1	1:C:634:GLY:N	2.84	0.46
1:C:561:TYR:HA	1:C:565:LEU:HB2	1.96	0.46
2:B:749:GLU:CD	2:B:749:GLU:C	2.74	0.46
2:B:765:PHE:HZ	2:B:846:MET:HG2	1.80	0.46
1:A:515:ALA:HB2	1:A:531:VAL:CG1	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:413:LEU:HD21	1:A:683:PHE:HZ	1.81	0.46
1:C:639:ASN:HB3	1:C:643:LYS:NZ	2.31	0.46
1:C:635:LEU:HD23	1:C:635:LEU:C	2.36	0.46
1:C:452:LYS:CA	1:C:452:LYS:CE	2.90	0.45
1:C:504:ARG:HD3	1:C:694:LEU:HD21	1.98	0.45
1:A:471:HIS:C	1:A:473:ARG:H	2.20	0.45
1:C:666:LEU:HD12	1:C:667:TRP:CH2	2.51	0.45
1:C:466:LEU:CD1	1:C:472:GLY:HA3	2.47	0.45
1:C:620:LEU:HD22	2:D:827:VAL:CG1	2.45	0.45
1:A:469:LEU:HD21	2:B:798:THR:OG1	2.17	0.45
1:A:663:MET:HA	1:A:667:TRP:CE3	2.52	0.45
1:C:424:LEU:HD11	1:C:652:GLU:HB3	1.98	0.45
1:C:537:MET:CE	1:C:687:LEU:HD13	2.45	0.45
1:A:542:ARG:HH12	1:A:692:HIS:CE1	2.33	0.45
1:C:576:LYS:HD3	1:C:576:LYS:HA	1.80	0.45
1:A:483:PHE:CZ	1:A:590:LEU:HD22	2.51	0.45
1:A:616:VAL:N	2:B:783:LYS:HD3	2.31	0.45
1:A:411:ARG:HD2	1:A:411:ARG:HA	1.57	0.45
1:C:589:VAL:O	1:C:592:LEU:N	2.49	0.44
2:D:867:LEU:HD12	2:D:867:LEU:N	2.31	0.44
1:C:436:HIS:HB3	1:C:657:PHE:CE2	2.52	0.44
1:C:412:PRO:HD3	1:C:668:GLY:HA3	1.98	0.44
1:A:581:LEU:HD21	1:A:632:HIS:ND1	2.33	0.44
1:A:507:LEU:O	1:A:507:LEU:HD12	2.18	0.44
1:A:465:GLU:O	1:A:469:LEU:HD22	2.18	0.44
1:C:440:VAL:HG23	1:C:482:ARG:CZ	2.47	0.44
1:A:525:MET:CE	1:A:525:MET:HA	2.47	0.44
1:C:644:LEU:HD23	1:C:644:LEU:HA	1.68	0.44
1:C:428:VAL:CG2	1:C:432:THR:OG1	2.65	0.44
1:A:406:ILE:HD13	1:A:661:PHE:HD1	1.79	0.44
1:C:665:LEU:HD12	1:C:665:LEU:O	2.17	0.44
1:C:484:HIS:O	1:C:488:ILE:HG13	2.18	0.44
2:D:792:LEU:HD23	2:D:860:PHE:HD2	1.76	0.44
1:C:579:PRO:HG2	1:C:584:THR:OG1	2.17	0.44
1:C:592:LEU:HD13	1:C:626:ALA:HB2	2.00	0.44
1:C:440:VAL:HG21	1:C:657:PHE:O	2.18	0.44
1:A:497:SER:HB3	1:A:504:ARG:HG2	2.00	0.44
1:C:458:MET:HB2	1:C:460:VAL:CG1	2.39	0.44
2:D:746:PHE:O	2:D:749:GLU:N	2.51	0.44
2:B:867:LEU:O	2:B:870:ALA:N	2.51	0.44
1:A:614:HIS:HB3	1:A:618:VAL:HG22	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:686:VAL:O	1:A:690:LEU:HG	2.18	0.44
1:C:656:VAL:HA	1:C:661:PHE:CE2	2.52	0.43
1:C:616:VAL:HG23	2:D:783:LYS:HG2	1.99	0.43
2:D:833:ALA:HB2	2:D:846:MET:HE2	1.99	0.43
1:C:436:HIS:HB3	1:C:657:PHE:HD2	1.81	0.43
1:C:576:LYS:HG3	1:C:577:GLU:H	1.83	0.43
1:C:464:MET:CE	1:C:467:LEU:HD21	2.49	0.43
1:A:386:THR:OG1	1:A:387:VAL:N	2.48	0.43
1:A:694:LEU:HA	1:A:694:LEU:HD12	1.80	0.43
1:C:666:LEU:HD12	1:C:667:TRP:CZ3	2.53	0.43
1:C:683:PHE:HA	1:C:686:VAL:HG21	1.95	0.43
1:A:488:ILE:O	1:A:492:VAL:HG23	2.19	0.43
2:B:867:LEU:O	2:B:869:ALA:N	2.52	0.43
2:D:815:TYR:O	2:D:816:SER:C	2.57	0.43
1:C:437:VAL:HG13	1:C:657:PHE:CZ	2.54	0.43
1:C:504:ARG:O	1:C:508:LEU:HB2	2.19	0.43
1:A:397:ASN:HA	1:A:398:PRO:HD2	1.81	0.43
2:B:739:SER:HB2	2:B:742:GLN:HG2	2.01	0.43
2:D:743:LEU:CD2	2:D:746:PHE:CE2	3.02	0.43
2:B:744:LEU:HB3	2:B:868:ALA:HB2	2.01	0.43
1:C:438:THR:HB	1:C:522:MET:HE2	2.01	0.42
1:C:695:GLU:HA	1:C:696:PRO:HD2	1.89	0.42
2:B:802:GLN:O	2:B:803:ALA:C	2.57	0.42
1:C:650:ARG:HA	1:C:651:PRO:HD2	1.86	0.42
2:B:847:VAL:HG12	2:B:851:LYS:HD3	2.01	0.42
2:D:746:PHE:CD1	2:D:747:TYR:N	2.87	0.42
1:C:460:VAL:HG23	1:C:465:GLU:OE1	2.19	0.42
1:C:462:TRP:NE1	1:C:634:GLY:HA2	2.34	0.42
1:C:514:LEU:HD12	1:C:514:LEU:C	2.39	0.42
1:A:436:HIS:CD2	1:A:653:LEU:HB3	2.54	0.42
1:A:514:LEU:HD12	1:A:514:LEU:O	2.19	0.42
2:B:744:LEU:HD13	2:B:867:LEU:HB3	2.01	0.42
2:D:799:LEU:HB2	2:D:812:VAL:HG21	2.01	0.42
1:C:617:GLU:CG	4:C:70:HOH:O	2.65	0.42
1:C:461:ARG:HB3	1:C:462:TRP:NE1	2.34	0.42
2:D:859:GLN:HG3	2:D:862:ARG:HD2	2.01	0.42
1:C:581:LEU:HD11	1:C:636:TYR:HE1	1.84	0.42
1:A:698:VAL:CG1	1:A:698:VAL:O	2.68	0.42
1:C:436:HIS:CD2	1:C:653:LEU:HB3	2.55	0.42
1:C:667:TRP:CE2	1:C:679:ARG:HB3	2.55	0.41
1:C:616:VAL:HG13	1:C:617:GLU:N	2.34	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:494:ILE:HA	1:C:507:LEU:CD2	2.50	0.41
1:A:387:VAL:CG2	2:B:742:GLN:HB3	2.48	0.41
2:B:867:LEU:HD12	2:B:867:LEU:HA	1.79	0.41
1:C:564:LYS:C	1:C:567:PRO:HD2	2.41	0.41
1:C:654:LEU:C	1:C:656:VAL:H	2.22	0.41
1:A:539:GLN:CG	1:A:688:THR:CG2	2.99	0.41
1:A:650:ARG:HA	1:A:651:PRO:HD2	1.65	0.41
1:C:464:MET:HA	1:C:464:MET:CE	2.50	0.41
2:B:752:GLU:HG2	2:B:861:ARG:HD2	2.02	0.41
1:C:434:ALA:O	1:C:522:MET:HE2	2.21	0.41
2:B:765:PHE:CE2	2:B:850:VAL:HG21	2.56	0.41
1:C:473:ARG:HG2	1:C:474:GLN:N	2.35	0.41
1:A:484:HIS:O	1:A:488:ILE:HG13	2.21	0.41
2:D:765:PHE:CE2	2:D:850:VAL:HG21	2.56	0.41
1:A:566:LYS:HB3	1:A:567:PRO:HD3	2.02	0.41
1:C:461:ARG:C	1:C:462:TRP:CG	2.95	0.41
1:C:489:MET:HE3	1:C:662:GLN:HE21	1.85	0.41
2:D:859:GLN:CA	2:D:862:ARG:NH1	2.84	0.41
1:C:667:TRP:HE1	1:C:683:PHE:HB2	1.86	0.41
1:C:667:TRP:CZ2	1:C:679:ARG:HB3	2.56	0.41
1:C:595:LEU:HD11	1:C:614:HIS:ND1	2.36	0.41
1:C:450:VAL:HG11	1:C:462:TRP:CZ3	2.55	0.41
1:C:428:VAL:HG22	1:C:432:THR:OG1	2.21	0.41
1:C:564:LYS:O	1:C:567:PRO:HD2	2.21	0.41
1:A:451:THR:OG1	1:A:454[B]:MET:HG3	2.21	0.41
1:A:586:PHE:CD2	1:A:587:PRO:HD2	2.56	0.41
1:C:446:ARG:HB2	1:C:463:GLY:HA3	2.04	0.41
1:A:555:THR:O	1:A:559:ILE:HG13	2.21	0.40
1:C:428:VAL:CG2	1:C:429:ASP:H	2.20	0.40
2:B:824:ARG:HA	2:B:827:VAL:CG1	2.50	0.40
1:C:590:LEU:HG	1:C:590:LEU:O	2.19	0.40
2:D:848:GLU:O	2:D:852:GLU:HG3	2.21	0.40
2:B:824:ARG:O	2:B:827:VAL:HG13	2.21	0.40
2:D:833:ALA:CB	2:D:846:MET:CE	3.00	0.40
2:D:755:LEU:HD13	2:D:758:LEU:HD23	2.04	0.40
1:C:624:GLU:OE2	2:D:824:ARG:HD3	2.21	0.40
1:A:656:VAL:HA	1:A:661:PHE:CE2	2.56	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	296/331 (89%)	274 (93%)	19 (6%)	3 (1%)	19	34
1	C	269/331 (81%)	238 (88%)	26 (10%)	5 (2%)	10	16
2	B	132/229 (58%)	124 (94%)	5 (4%)	3 (2%)	8	12
2	D	129/229 (56%)	110 (85%)	16 (12%)	3 (2%)	8	12
All	All	826/1120 (74%)	746 (90%)	66 (8%)	14 (2%)	11	19

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	387	VAL
2	B	803	ALA
1	C	670	GLN
2	B	868	ALA
2	D	787	LEU
2	B	802	GLN
1	C	489	MET
1	C	668	GLY
2	D	868	ALA
2	D	871	LEU
1	A	670	GLN
1	C	428	VAL
1	C	521	THR
1	A	651	PRO

5.3.2 Protein sidechains

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	255/282 (90%)	230 (90%)	25 (10%)	10	19
1	C	229/282 (81%)	213 (93%)	16 (7%)	19	34
2	B	111/193 (58%)	101 (91%)	10 (9%)	12	22
2	D	108/193 (56%)	96 (89%)	12 (11%)	8	14
All	All	703/950 (74%)	640 (91%)	63 (9%)	12	22

All (63) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	393	THR
1	A	395	SER
1	A	405	LEU
1	A	406	ILE
1	A	411	ARG
1	A	420	LYS
1	A	428	VAL
1	A	432	THR
1	A	437	VAL
1	A	439	LYS
1	A	452	LYS
1	A	469	LEU
1	A	473	ARG
1	A	519	ARG
1	A	549	THR
1	A	585	THR
1	A	586	PHE
1	A	590	LEU
1	A	595	LEU
1	A	628	THR
1	A	653	LEU
1	A	658	SER
1	A	683	PHE
1	A	685	LYS
1	A	694	LEU
2	B	742	GLN
2	B	787	LEU
2	B	807	ASP
2	B	819	LEU
2	B	820	CYS
2	B	849	ARG
2	B	853	LEU
2	B	864	LEU

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Mol	Chain	Res	Type
2	B	867	LEU
2	B	872	GLU
1	C	424	LEU
1	C	436	HIS
1	C	452	LYS
1	C	458	MET
1	C	460	VAL
1	C	469	LEU
1	C	474	GLN
1	C	514	LEU
1	C	542	ARG
1	C	576	LYS
1	C	585	THR
1	C	586	PHE
1	C	648	GLN
1	C	661	PHE
1	C	678	ARG
1	C	694	LEU
2	D	745	LEU
2	D	756	THR
2	D	778	PHE
2	D	802	GLN
2	D	807	ASP
2	D	818	LEU
2	D	827	VAL
2	D	848	GLU
2	D	856	SER
2	D	861	ARG
2	D	871	LEU
2	D	872	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	484	HIS
2	B	742	GLN
1	C	436	HIS
1	C	455	GLN
1	C	622	HIS
1	C	631	HIS
1	C	662	GLN
2	D	802	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

1 ligand is 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	$\# Z > 2$
3	ACT	C	1	-	1,3,3	1.45	0	0,3,3	0.00	-

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	ACT	C	1	-	-	0/0/0/0	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	1	ACT	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

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	299/331 (90%)	0.15	20 (6%) 21 23	48, 69, 99, 148	1 (0%)
1	C	273/331 (82%)	0.98	58 (21%) 1 1	79, 129, 174, 210	1 (0%)
2	B	134/229 (58%)	-0.08	2 (1%) 76 79	52, 69, 103, 139	0
2	D	131/229 (57%)	0.79	23 (17%) 2 2	67, 123, 195, 223	0
All	All	837/1120 (74%)	0.48	103 (12%) 5 5	48, 89, 169, 223	2 (0%)

All (103) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	413	LEU	7.2
2	D	803	ALA	7.0
1	C	450	VAL	6.7
1	C	415	VAL	6.3
1	C	527	SER	5.6
1	C	671	GLY	5.5
2	D	743	LEU	5.2
1	A	697	ALA	5.1
1	C	580	PRO	5.1
1	C	675	SER	4.9
2	D	872	GLU	4.9
1	C	486	MET	4.7
1	A	387	VAL	4.6
2	D	867	LEU	4.6
2	D	869	ALA	4.6
1	C	678	ARG	4.4
2	D	804	LYS	4.2
1	C	416	GLY	4.2
1	C	490	LEU	4.1
1	C	453	GLU	4.1
1	C	674	SER	4.1

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Mol	Chain	Res	Type	RSRZ
1	C	452	LYS	4.0
1	C	645	GLN	4.0
2	D	811	GLN	3.9
1	C	647	PHE	3.9
1	A	490	LEU	3.8
2	D	868	ALA	3.8
2	D	746	PHE	3.8
1	C	638	THR	3.7
1	C	667	TRP	3.7
1	C	499	GLY	3.7
1	C	672	ALA	3.6
2	D	815	TYR	3.6
1	C	673	SER	3.5
1	C	581	LEU	3.5
1	C	531	VAL	3.5
1	C	670	GLN	3.5
2	D	799	LEU	3.5
1	C	489	MET	3.4
1	A	487	SER	3.4
1	C	664	ARG	3.3
2	D	784	PHE	3.3
1	C	526	PHE	3.3
2	D	745	LEU	3.3
2	B	739	SER	3.2
1	C	441	ASP	3.2
1	A	488	ILE	3.2
1	C	653	LEU	3.1
1	A	491	ALA	3.1
1	C	491	ALA	3.0
1	C	668	GLY	3.0
1	C	511	THR	3.0
1	C	514	LEU	3.0
1	C	524	ASN	2.9
1	A	670	GLN	2.9
1	A	527	SER	2.9
1	C	669	SER	2.9
2	D	747	TYR	2.8
1	A	531	VAL	2.7
1	A	559	ILE	2.7
2	D	807	ASP	2.7
1	A	648	GLN	2.7
1	C	435	ARG	2.6

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Mol	Chain	Res	Type	RSRZ
1	C	412	PRO	2.6
1	A	530	ALA	2.6
1	C	439	LYS	2.5
1	C	455	GLN	2.5
1	C	448	LEU	2.5
1	C	530	ALA	2.5
1	C	417	LEU	2.4
2	D	748	LEU	2.4
1	C	577	GLU	2.4
2	D	840	PRO	2.4
1	C	449	GLY	2.4
2	D	861	ARG	2.4
1	C	454	MET	2.4
1	C	698	VAL	2.4
1	C	648	GLN	2.4
1	C	456	THR	2.3
1	A	489	MET	2.3
1	C	437	VAL	2.3
1	A	486	MET	2.3
1	A	526	PHE	2.3
1	C	637	HIS	2.3
1	A	698	VAL	2.3
1	C	553	ARG	2.2
1	A	529	ALA	2.2
2	B	872	GLU	2.2
1	C	498	THR	2.2
1	C	571	SER	2.1
2	D	871	LEU	2.1
1	C	461	ARG	2.1
1	C	559	ILE	2.1
2	D	800	SER	2.1
2	D	808	VAL	2.1
1	A	534	ALA	2.1
2	D	805	ALA	2.1
1	A	492	VAL	2.1
1	C	568	PHE	2.1
2	D	864	LEU	2.1
1	C	574	GLU	2.0
1	C	681	GLU	2.0
1	A	468	THR	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](#)

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(\AA^2)	Q<0.9
3	ACT	C	1	4/4	0.86	0.28	5.11	105,110,126,126	0

6.5 Other polymers [i](#)

There are no such residues in this entry.