



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 01:33 PM GMT

PDB ID : 3U1K
Title : Crystal structure of human PNPase
Authors : Lin, C.L.; Yuan, H.S.
Deposited on : 2011-09-30
Resolution : 2.13 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

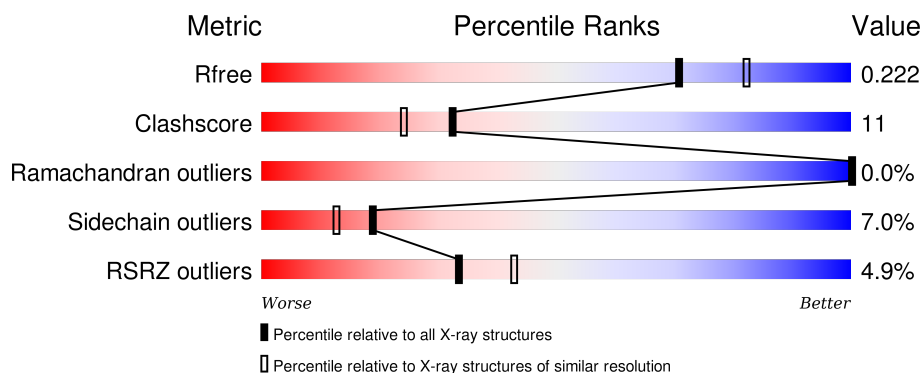
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.13 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	1693 (2.16-2.12)
Clashscore	102246	1824 (2.16-2.12)
Ramachandran outliers	100387	1798 (2.16-2.12)
Sidechain outliers	100360	1798 (2.16-2.12)
RSRZ outliers	91569	1699 (2.16-2.12)

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	630	<div> <div>5%</div> <div>79%</div> <div>17%</div> <div>• •</div> </div>
1	B	630	<div> <div>4%</div> <div>80%</div> <div>14%</div> <div>• •</div> </div>
1	C	630	<div> <div>4%</div> <div>78%</div> <div>18%</div> <div>• •</div> </div>
1	D	630	<div> <div>7%</div> <div>72%</div> <div>22%</div> <div>• •</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 criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	CIT	C	670	-	-	X	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 20205 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 Polyribonucleotide nucleotidyltransferase 1, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	619	Total	C	N	O	S	0	0	0
			4741	2997	805	919	20			
1	C	623	Total	C	N	O	S	0	0	0
			4765	3009	813	922	21			
1	B	617	Total	C	N	O	S	0	0	0
			4718	2984	801	912	21			
1	D	614	Total	C	N	O	S	0	0	0
			4705	2977	799	908	21			

There are 28 discrepancies between the modelled and reference sequences:

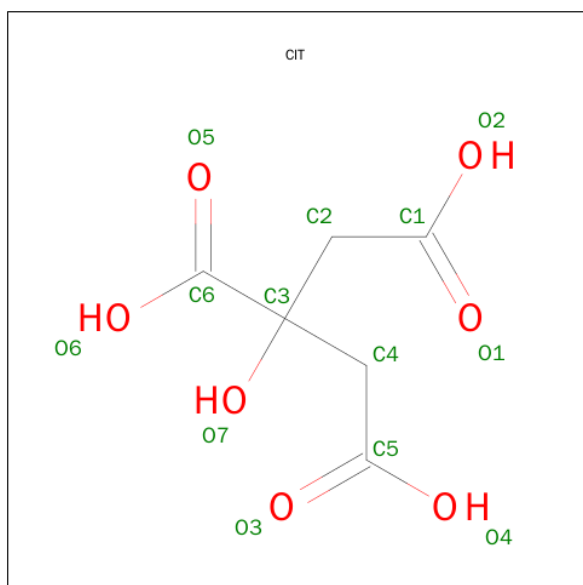
Chain	Residue	Modelled	Actual	Comment	Reference
A	40	GLY	-	EXPRESSION TAG	UNP Q8TCS8
A	41	SER	-	EXPRESSION TAG	UNP Q8TCS8
A	42	HIS	-	EXPRESSION TAG	UNP Q8TCS8
A	43	MET	-	EXPRESSION TAG	UNP Q8TCS8
A	44	ALA	-	EXPRESSION TAG	UNP Q8TCS8
A	45	SER	-	EXPRESSION TAG	UNP Q8TCS8
A	121	VAL	ILE	SEE REMARK 999	UNP Q8TCS8
C	40	GLY	-	EXPRESSION TAG	UNP Q8TCS8
C	41	SER	-	EXPRESSION TAG	UNP Q8TCS8
C	42	HIS	-	EXPRESSION TAG	UNP Q8TCS8
C	43	MET	-	EXPRESSION TAG	UNP Q8TCS8
C	44	ALA	-	EXPRESSION TAG	UNP Q8TCS8
C	45	SER	-	EXPRESSION TAG	UNP Q8TCS8
C	121	VAL	ILE	SEE REMARK 999	UNP Q8TCS8
B	40	GLY	-	EXPRESSION TAG	UNP Q8TCS8
B	41	SER	-	EXPRESSION TAG	UNP Q8TCS8
B	42	HIS	-	EXPRESSION TAG	UNP Q8TCS8
B	43	MET	-	EXPRESSION TAG	UNP Q8TCS8
B	44	ALA	-	EXPRESSION TAG	UNP Q8TCS8
B	45	SER	-	EXPRESSION TAG	UNP Q8TCS8
B	121	VAL	ILE	SEE REMARK 999	UNP Q8TCS8

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Chain	Residue	Modelled	Actual	Comment	Reference
D	40	GLY	-	EXPRESSION TAG	UNP Q8TCS8
D	41	SER	-	EXPRESSION TAG	UNP Q8TCS8
D	42	HIS	-	EXPRESSION TAG	UNP Q8TCS8
D	43	MET	-	EXPRESSION TAG	UNP Q8TCS8
D	44	ALA	-	EXPRESSION TAG	UNP Q8TCS8
D	45	SER	-	EXPRESSION TAG	UNP Q8TCS8
D	121	VAL	ILE	SEE REMARK 999	UNP Q8TCS8

- Molecule 2 is CITRIC ACID (three-letter code: CIT) (formula: $C_6H_8O_7$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			13	6	7		
2	A	1	Total	C	O	0	0
			13	6	7		
2	C	1	Total	C	O	0	0
			13	6	7		
2	C	1	Total	C	O	0	0
			13	6	7		
2	B	1	Total	C	O	0	0
			13	6	7		
2	B	1	Total	C	O	0	0
			13	6	7		
2	D	1	Total	C	O	0	0
			13	6	7		
2	D	1	Total	C	O	0	0
			13	6	7		

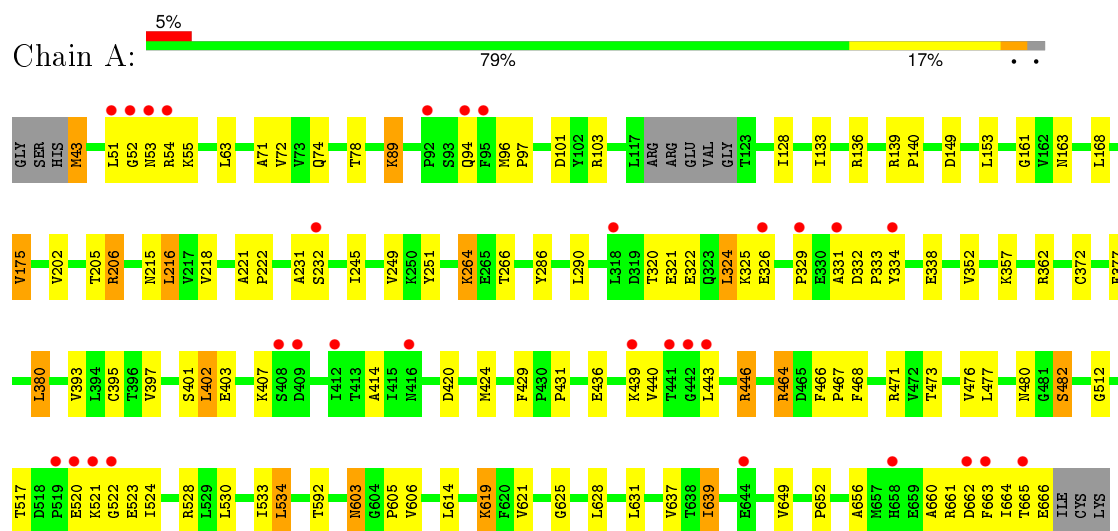
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	327	Total 327	O 327	0	0
3	C	287	Total 287	O 287	0	0
3	B	358	Total 358	O 358	0	0
3	D	200	Total 200	O 200	0	0

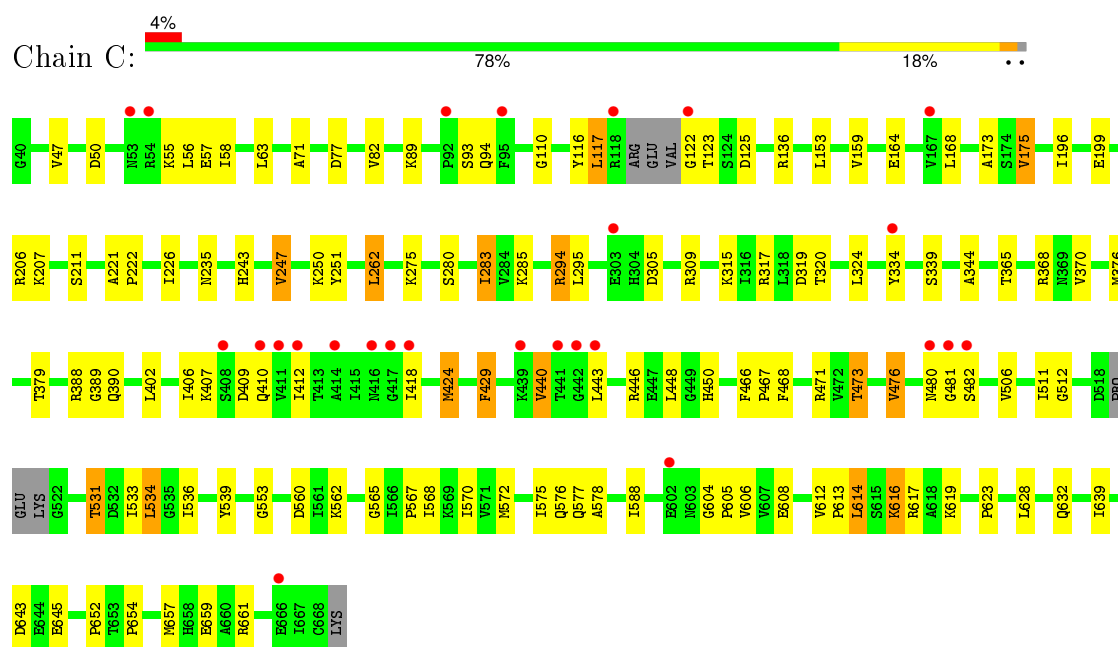
3 Residue-property plots [i](#)

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

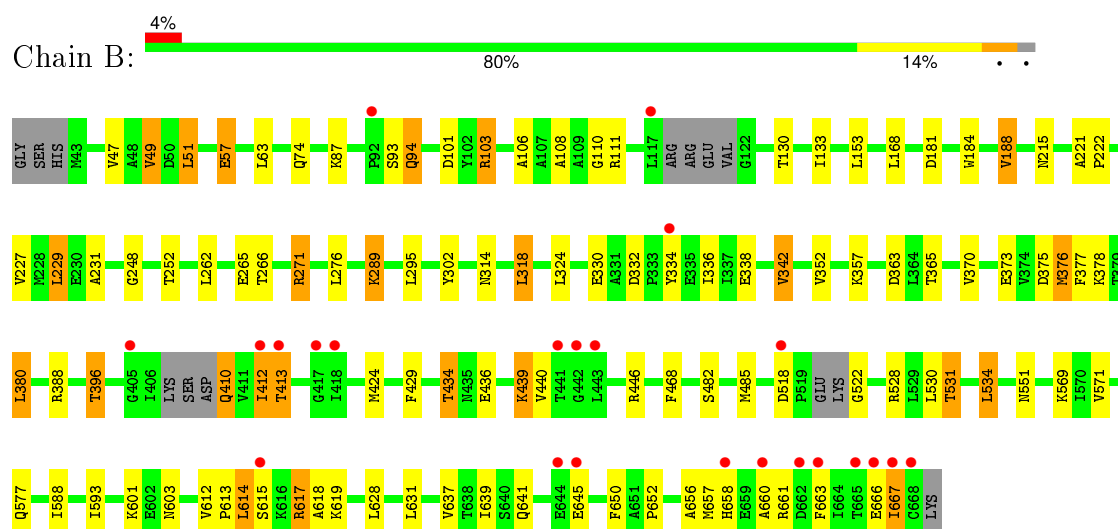
- Molecule 1: Polyrribonucleotide nucleotidyltransferase 1, mitochondrial



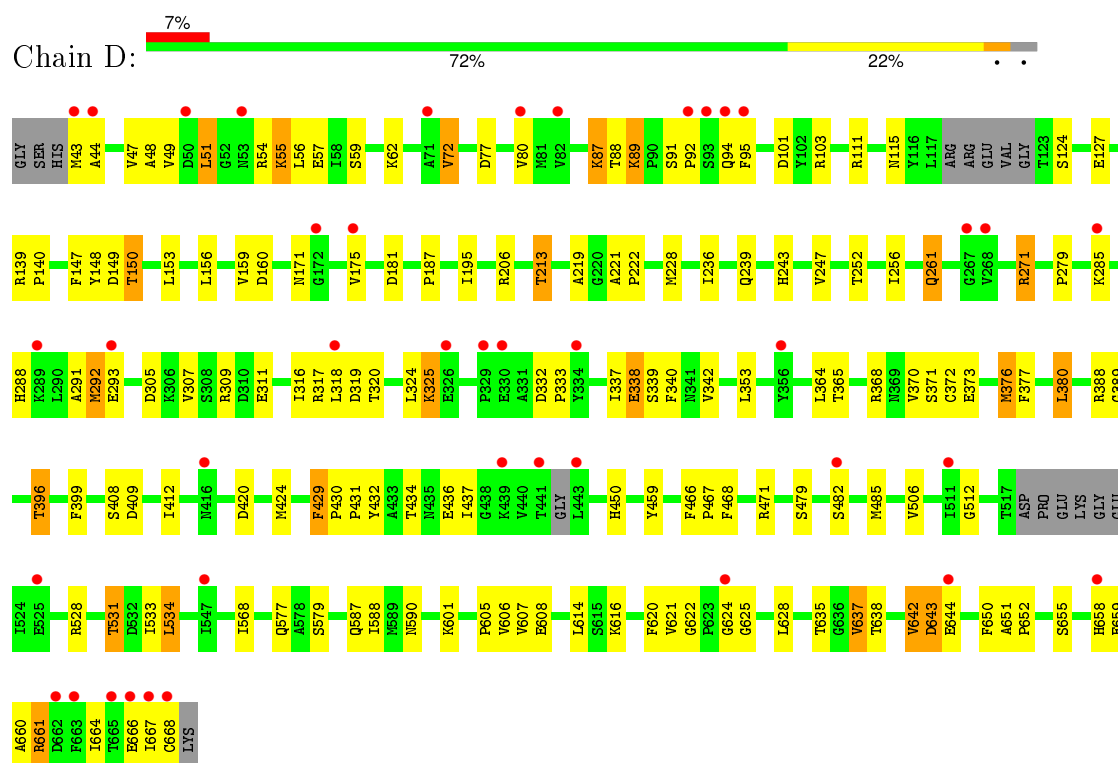
- Molecule 1: Polyrribonucleotide nucleotidyltransferase 1, mitochondrial



- Molecule 1: Polyrribonucleotide nucleotidyltransferase 1, mitochondrial



• Molecule 1: Polyrribonucleotide nucleotidyltransferase 1, mitochondrial



4 Data and refinement statistics

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α , β , γ	289.75 Å 289.75 Å 92.78 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	28.50 – 2.13 28.37 – 2.13	Depositor EDS
% Data completeness (in resolution range)	100.0 (28.50-2.13) 100.0 (28.37-2.13)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.21 (at 2.14 Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.1_743)	Depositor
R, R_{free}	0.180 , 0.223 0.179 , 0.222	Depositor DCC
R_{free} test set	8129 reflections (5.27%)	DCC
Wilson B-factor (Å ²)	34.4	Xtriage
Anisotropy	0.321	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 48.2	EDS
Estimated twinning fraction	0.010 for h,-h-k,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 162291 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	20205	wwPDB-VP
Average B, all atoms (Å ²)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.62% 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: CIT

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	0.39	0/4818	0.56	0/6525
1	B	0.40	0/4793	0.56	1/6490 (0.0%)
1	C	0.35	0/4841	0.52	0/6553
1	D	0.33	0/4779	0.51	0/6470
All	All	0.37	0/19231	0.54	1/26038 (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	B	229	LEU	CA-CB-CG	5.77	128.58	115.30

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	4741	0	4825	100	0
1	B	4718	0	4801	85	0
1	C	4765	0	4845	103	0
1	D	4705	0	4797	128	0
2	A	26	0	10	1	0
2	B	26	0	10	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	26	0	10	7	0
2	D	26	0	10	1	0
3	A	327	0	0	11	0
3	B	358	0	0	7	0
3	C	287	0	0	16	0
3	D	200	0	0	5	0
All	All	20205	0	19308	403	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 11.

All (403) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:531:THR:HG22	1:B:577:GLN:HE21	1.11	1.12
1:D:661:ARG:HH11	1:D:661:ARG:HG2	1.13	1.08
1:A:51:LEU:HD12	1:A:53:ASN:H	1.22	1.02
1:C:482:SER:HB2	3:C:676:HOH:O	1.58	1.02
1:C:294:ARG:HH11	1:C:294:ARG:HG2	1.24	0.98
1:C:613:PRO:HG2	1:C:616:LYS:HG3	1.48	0.96
1:A:51:LEU:HB2	1:A:54:ARG:O	1.68	0.94
1:A:661:ARG:HA	3:A:1034:HOH:O	1.66	0.93
1:B:378:LYS:O	1:B:603:ASN:ND2	2.01	0.92
1:B:614:LEU:HB3	1:B:617:ARG:HB3	1.52	0.92
1:D:89:LYS:H	1:D:89:LYS:HD3	1.35	0.90
1:B:614:LEU:N	1:B:615:SER:HB3	1.89	0.88
1:C:406:ILE:HG12	1:C:418:ILE:HD12	1.55	0.88
1:A:51:LEU:CB	1:A:54:ARG:H	1.87	0.87
1:C:531:THR:CG2	1:C:577:GLN:HE21	1.87	0.87
1:D:89:LYS:HD3	1:D:89:LYS:N	1.89	0.86
1:A:621:VAL:HG12	1:A:625:GLY:HA2	1.56	0.85
1:A:89:LYS:HD2	1:A:89:LYS:H	1.42	0.85
1:C:482:SER:N	2:C:670:CIT:O5	2.09	0.85
1:C:531:THR:HG22	1:C:577:GLN:HE21	1.41	0.85
1:D:353:LEU:O	1:D:528:ARG:NH2	2.10	0.84
1:B:365:THR:HA	1:B:531:THR:HG23	1.57	0.84
1:B:531:THR:HG22	1:B:577:GLN:NE2	1.93	0.84
1:A:101:ASP:HB2	1:A:153:LEU:HD23	1.65	0.79
1:C:71:ALA:HB2	1:C:175:VAL:HG22	1.64	0.79
1:A:51:LEU:HB3	1:A:54:ARG:H	1.46	0.79
1:A:51:LEU:HD21	1:A:202:VAL:HG13	1.65	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:531:THR:HG22	1:D:577:GLN:HE21	1.46	0.79
1:D:661:ARG:HG2	1:D:661:ARG:NH1	1.93	0.78
1:B:377:PHE:HB2	1:B:380:LEU:HD22	1.66	0.77
1:C:294:ARG:HG2	1:C:294:ARG:NH1	1.99	0.77
1:A:482:SER:HB2	3:A:672:HOH:O	1.83	0.77
1:C:94:GLN:HG3	1:C:334:TYR:CG	2.21	0.76
1:D:365:THR:HA	1:D:531:THR:HG23	1.67	0.76
1:D:531:THR:CG2	1:D:577:GLN:HE21	1.99	0.76
1:A:51:LEU:HD12	1:A:53:ASN:N	1.99	0.76
1:A:94:GLN:HG2	1:A:334:TYR:CD1	2.22	0.75
1:A:517:THR:HG22	1:A:524:ILE:HA	1.67	0.75
1:C:280:SER:OG	1:C:283:ILE:HG23	1.85	0.74
1:D:424:MET:SD	1:D:471:ARG:NH1	2.59	0.74
1:B:657:MET:O	1:B:661:ARG:HG2	1.87	0.74
1:D:49:VAL:CG1	1:D:56:LEU:HB3	2.17	0.74
1:A:664:ILE:HB	3:A:1034:HOH:O	1.87	0.72
1:A:94:GLN:HG3	3:A:753:HOH:O	1.88	0.72
1:C:390:GLN:HB2	1:C:480:ASN:HB2	1.72	0.71
1:B:376:MET:HB3	1:B:377:PHE:CD1	2.24	0.71
1:C:365:THR:HA	1:C:531:THR:HG23	1.70	0.71
1:C:379:THR:HG21	1:D:159:VAL:O	1.90	0.71
1:A:480:ASN:ND2	3:A:13:HOH:O	2.07	0.71
1:D:388:ARG:HG2	1:D:388:ARG:HH11	1.55	0.70
1:A:54:ARG:HH12	1:A:205:THR:HG22	1.56	0.69
1:C:511:ILE:CD1	1:C:578:ALA:HB2	2.21	0.69
1:B:531:THR:CG2	1:B:577:GLN:HE21	1.99	0.69
1:D:316:ILE:O	1:D:320:THR:HG23	1.92	0.69
1:C:481:GLY:CA	3:C:732:HOH:O	2.41	0.69
1:C:473:THR:HG21	1:D:115:ASN:HD21	1.58	0.69
1:C:94:GLN:HG3	1:C:334:TYR:CD1	2.27	0.69
1:A:628:LEU:HD22	1:A:639:ILE:HG21	1.75	0.68
1:B:613:PRO:C	1:B:615:SER:HB3	2.15	0.67
1:D:124:SER:OG	1:D:127:GLU:HG3	1.93	0.67
1:C:511:ILE:HD12	1:C:578:ALA:HB2	1.74	0.67
3:C:708:HOH:O	1:D:62:LYS:HD3	1.93	0.67
1:D:614:LEU:HD21	1:D:644:GLU:OE1	1.95	0.66
1:D:87:LYS:HG3	1:D:149:ASP:HB3	1.78	0.66
1:B:439:LYS:N	1:B:439:LYS:HE2	2.10	0.66
1:A:215:ASN:HB3	1:A:232:SER:OG	1.94	0.66
1:C:652:PRO:HG2	1:D:111:ARG:HB3	1.78	0.66
1:D:307:VAL:O	1:D:311:GLU:HG3	1.96	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:608:GLU:OE2	1:D:661:ARG:NH2	2.28	0.66
1:D:655:SER:O	1:D:658:HIS:HB3	1.96	0.66
1:C:407:LYS:HD3	1:C:412:ILE:HG22	1.78	0.66
1:B:363:ASP:OD1	3:B:770:HOH:O	2.13	0.65
1:D:620:PHE:HA	1:D:667:ILE:HD13	1.77	0.65
1:A:51:LEU:HB3	1:A:53:ASN:N	2.10	0.65
1:A:216:LEU:HD23	1:A:231:ALA:HB2	1.78	0.65
1:B:330:GLU:N	1:B:330:GLU:OE1	2.24	0.65
1:D:213:THR:HG23	1:D:236:ILE:HG21	1.79	0.65
1:D:420:ASP:OD2	1:D:459:TYR:OH	2.12	0.65
1:C:243:HIS:O	1:C:247:VAL:HG12	1.97	0.64
1:D:614:LEU:HD11	1:D:644:GLU:HG2	1.78	0.64
1:C:409:ASP:HB3	1:C:412:ILE:HB	1.79	0.64
1:A:51:LEU:HB3	1:A:52:GLY:C	2.18	0.64
1:D:620:PHE:HD1	1:D:667:ILE:HD11	1.63	0.64
1:D:667:ILE:HD12	1:D:668:CYS:N	2.13	0.64
1:C:164:GLU:OE2	1:C:206:ARG:HG2	1.98	0.64
1:D:616:LYS:HB3	1:D:668:CYS:HB2	1.80	0.63
1:A:482:SER:N	2:A:1:CIT:O5	2.26	0.63
1:B:370:VAL:HG22	1:B:588:ILE:HG21	1.81	0.63
1:A:51:LEU:CD2	1:A:202:VAL:HG13	2.28	0.62
1:C:196:ILE:O	1:C:199:GLU:HG2	1.99	0.62
1:A:128:ILE:HD11	1:A:443:LEU:HD21	1.80	0.62
1:D:373:GLU:HG3	1:D:376:MET:HE2	1.81	0.61
1:D:49:VAL:HG13	1:D:56:LEU:HB3	1.82	0.61
1:A:661:ARG:O	1:A:665:THR:HB	2.00	0.61
1:D:89:LYS:H	1:D:89:LYS:CD	2.04	0.60
1:A:51:LEU:O	1:A:251:TYR:CE2	2.55	0.60
1:B:617:ARG:HG3	1:B:618:ALA:N	2.16	0.60
1:A:332:ASP:OD2	1:A:333:PRO:HD2	2.01	0.60
1:C:406:ILE:HG12	1:C:418:ILE:CD1	2.29	0.60
1:B:434:THR:HG23	1:B:436:GLU:HG3	1.82	0.60
1:C:136:ARG:HD3	1:C:560:ASP:OD1	2.01	0.60
1:D:87:LYS:HB3	1:D:89:LYS:HE2	1.83	0.60
1:B:631:LEU:HD13	1:B:663:PHE:CD2	2.36	0.60
1:B:617:ARG:CZ	1:B:641:GLN:HE22	2.15	0.59
1:A:621:VAL:CG1	1:A:625:GLY:HA2	2.30	0.59
1:D:195:ILE:HB	1:D:213:THR:HG22	1.84	0.59
1:C:207:LYS:HG2	3:C:765:HOH:O	2.02	0.59
1:D:568:ILE:HG13	3:D:737:HOH:O	2.01	0.59
1:A:521:LYS:HG2	1:A:523:GLU:HG3	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:54:ARG:NH1	1:A:163:ASN:OD1	2.34	0.59
1:D:661:ARG:HH11	1:D:661:ARG:CG	1.99	0.59
1:C:440:VAL:HG11	1:D:103:ARG:HD2	1.85	0.59
3:B:679:HOH:O	1:D:396:THR:HG21	2.02	0.59
1:B:617:ARG:NH1	1:B:641:GLN:HE22	2.01	0.59
1:B:518:ASP:O	1:B:522:GLY:HA2	2.02	0.59
1:C:285:LYS:NZ	3:C:1009:HOH:O	2.20	0.58
1:A:43:MET:HE1	1:A:266:THR:HA	1.84	0.58
1:D:512:GLY:HA3	1:D:533:ILE:HG21	1.83	0.58
1:D:309:ARG:NH2	3:D:777:HOH:O	2.36	0.58
1:B:482:SER:OG	1:B:485:MET:HB2	2.03	0.58
1:A:331:ALA:HB1	1:A:332:ASP:HA	1.84	0.58
1:C:643:ASP:O	1:C:645:GLU:N	2.34	0.57
1:C:47:VAL:HG13	1:C:262:LEU:HD13	1.87	0.57
1:D:288:HIS:O	1:D:292:MET:HB3	2.04	0.57
1:C:317:ARG:NH1	3:C:737:HOH:O	2.26	0.57
1:B:613:PRO:HB2	1:B:615:SER:CB	2.34	0.57
1:D:332:ASP:OD1	1:D:333:PRO:HD2	2.04	0.57
1:B:373:GLU:OE1	1:B:376:MET:HE1	2.04	0.57
1:C:71:ALA:CB	1:C:175:VAL:HG22	2.34	0.56
1:B:338:GLU:O	1:B:342:VAL:HG13	2.05	0.56
1:D:148:TYR:O	1:D:150:THR:HG22	2.04	0.56
1:A:619:LYS:HD3	1:A:619:LYS:O	2.04	0.56
1:A:51:LEU:N	1:A:52:GLY:HA2	2.19	0.56
1:B:614:LEU:H	1:B:614:LEU:HD12	1.70	0.56
1:D:373:GLU:HG3	1:D:376:MET:CE	2.36	0.56
1:C:429:PHE:HA	1:C:476:VAL:HG13	1.87	0.56
1:A:133:ILE:HG13	3:A:855:HOH:O	2.04	0.56
1:A:71:ALA:CB	1:A:175:VAL:HG22	2.35	0.56
1:D:101:ASP:HB2	1:D:153:LEU:HD23	1.87	0.56
1:C:440:VAL:HG13	1:C:440:VAL:O	2.05	0.56
1:A:94:GLN:HG2	1:A:334:TYR:HD1	1.69	0.56
1:B:101:ASP:HB2	1:B:153:LEU:HD23	1.87	0.56
1:B:101:ASP:HB2	1:B:153:LEU:CD2	2.36	0.55
1:A:446:ARG:HB3	1:A:446:ARG:HH11	1.71	0.55
1:D:388:ARG:CG	1:D:388:ARG:HH11	2.20	0.55
1:C:531:THR:HG21	3:C:754:HOH:O	2.06	0.55
1:A:521:LYS:HG3	1:A:522:GLY:N	2.22	0.55
1:B:101:ASP:HB3	1:B:103:ARG:NH1	2.22	0.55
1:B:534:LEU:HD22	3:B:949:HOH:O	2.05	0.55
1:B:57:GLU:HG2	1:B:74:GLN:O	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:377:PHE:HB2	1:A:380:LEU:HD22	1.88	0.54
1:B:619:LYS:NZ	1:B:667:ILE:O	2.41	0.54
1:D:325:LYS:NZ	1:D:325:LYS:HB3	2.23	0.54
1:C:440:VAL:CG1	1:D:103:ARG:HD2	2.37	0.54
1:C:295:LEU:HD13	1:C:344:ALA:HA	1.89	0.54
1:D:409:ASP:OD2	1:D:412:ILE:HG13	2.08	0.54
1:D:88:THR:H	1:D:89:LYS:HZ2	1.56	0.54
1:A:51:LEU:C	1:A:51:LEU:HD13	2.29	0.54
1:D:624:GLY:N	1:D:625:GLY:HA2	2.22	0.54
1:A:89:LYS:CD	1:A:89:LYS:H	2.15	0.54
1:A:639:ILE:HG13	1:A:649:VAL:HG22	1.90	0.53
1:A:331:ALA:HB1	1:A:332:ASP:CA	2.39	0.53
1:A:51:LEU:HB3	1:A:54:ARG:N	2.21	0.53
1:C:136:ARG:CD	1:C:560:ASP:OD1	2.55	0.53
1:A:320:THR:HG22	1:A:324:LEU:CD2	2.38	0.53
1:B:410:GLN:OE1	1:D:408:SER:HB2	2.09	0.53
1:C:482:SER:N	2:C:670:CIT:C6	2.71	0.53
1:A:71:ALA:HB2	1:A:175:VAL:HG22	1.89	0.53
1:D:47:VAL:HG21	1:D:261:GLN:HG2	1.91	0.53
3:C:700:HOH:O	1:B:396:THR:HG21	2.07	0.53
1:B:637:VAL:HG11	1:B:660:ALA:HB2	1.90	0.53
1:A:521:LYS:CG	1:A:523:GLU:HG3	2.38	0.53
1:A:637:VAL:HG11	1:A:660:ALA:HB2	1.91	0.53
1:D:370:VAL:HG22	1:D:588:ILE:HG21	1.90	0.53
1:A:631:LEU:HD13	1:A:663:PHE:CD2	2.44	0.52
1:C:116:TYR:CE1	1:C:117:LEU:HD13	2.43	0.52
1:A:221:ALA:HB1	1:A:222:PRO:CD	2.40	0.52
1:C:424:MET:SD	1:C:471:ARG:NH1	2.82	0.52
1:A:614:LEU:H	1:A:614:LEU:HD22	1.72	0.52
1:C:365:THR:HA	1:C:531:THR:CG2	2.39	0.52
1:D:91:SER:OG	1:D:92:PRO:HD2	2.09	0.52
1:C:58:ILE:HG22	1:C:262:LEU:HD21	1.92	0.52
1:C:623:PRO:HB3	1:D:642:VAL:HG12	1.92	0.52
1:D:616:LYS:HZ1	1:D:668:CYS:HA	1.75	0.52
1:B:612:VAL:O	1:B:645:GLU:HG2	2.09	0.51
1:C:446:ARG:NH2	2:C:670:CIT:C5	2.73	0.51
1:B:666:GLU:O	1:B:666:GLU:HG2	2.11	0.51
1:B:373:GLU:HB2	1:B:376:MET:HE1	1.92	0.51
1:B:289:LYS:HA	1:B:289:LYS:HE3	1.92	0.51
1:A:51:LEU:HA	3:A:682:HOH:O	2.11	0.51
1:C:309:ARG:HD3	3:C:674:HOH:O	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:613:PRO:HB2	1:B:615:SER:HB3	1.92	0.51
1:D:338:GLU:O	1:D:342:VAL:HG12	2.11	0.51
1:B:652:PRO:HD2	1:B:656:ALA:HB3	1.92	0.51
1:B:365:THR:HA	1:B:531:THR:CG2	2.35	0.51
1:A:322:GLU:O	1:A:326:GLU:HG2	2.11	0.51
1:A:338:GLU:OE2	3:A:753:HOH:O	2.19	0.50
1:D:466:PHE:CG	1:D:467:PRO:HD2	2.46	0.50
1:B:324:LEU:HB3	1:B:336:ILE:HD12	1.92	0.50
1:D:368:ARG:HD2	1:D:389:GLY:HA3	1.94	0.50
1:D:320:THR:O	1:D:324:LEU:HG	2.12	0.50
1:A:631:LEU:HD13	1:A:663:PHE:CG	2.47	0.50
1:B:181:ASP:O	1:B:271:ARG:HD3	2.12	0.50
1:A:424:MET:SD	1:A:471:ARG:NH1	2.84	0.50
1:C:388:ARG:HG2	1:C:388:ARG:HH11	1.77	0.50
1:C:468:PHE:CE2	1:C:605:PRO:HG2	2.47	0.50
1:C:315:LYS:HE3	1:C:319:ASP:OD2	2.12	0.50
1:B:617:ARG:NH2	1:B:641:GLN:HE22	2.10	0.49
1:D:88:THR:H	1:D:89:LYS:NZ	2.09	0.49
1:C:196:ILE:N	1:C:196:ILE:HD12	2.27	0.49
1:B:551:ASN:OD1	3:B:697:HOH:O	2.20	0.49
1:C:320:THR:O	1:C:324:LEU:HD23	2.12	0.49
1:C:531:THR:HG22	1:C:577:GLN:NE2	2.18	0.49
1:A:402:LEU:HD22	1:A:467:PRO:O	2.13	0.49
1:D:292:MET:HG3	1:D:293:GLU:N	2.27	0.49
1:A:161:GLY:O	1:A:206:ARG:HD2	2.13	0.49
1:B:658:HIS:HA	1:B:661:ARG:HD3	1.95	0.49
1:D:616:LYS:NZ	1:D:668:CYS:HA	2.27	0.49
1:B:352:VAL:HG12	1:B:528:ARG:HG3	1.95	0.49
1:A:652:PRO:HD2	1:A:656:ALA:CB	2.42	0.49
1:C:125:ASP:OD1	1:C:448:LEU:HD11	2.12	0.49
1:C:614:LEU:HD23	1:C:645:GLU:OE2	2.13	0.49
1:D:171:ASN:O	1:D:175:VAL:HG23	2.12	0.49
1:B:94:GLN:HG2	1:B:334:TYR:CD1	2.47	0.49
1:A:51:LEU:HD11	1:A:202:VAL:HG13	1.94	0.48
1:C:612:VAL:O	1:C:645:GLU:HA	2.13	0.48
1:C:481:GLY:HA2	3:C:732:HOH:O	2.10	0.48
1:C:368:ARG:HD2	1:C:389:GLY:HA3	1.95	0.48
1:C:466:PHE:CG	1:C:467:PRO:HD2	2.49	0.48
1:A:54:ARG:NH1	1:A:205:THR:HG22	2.27	0.48
1:A:101:ASP:HB2	1:A:153:LEU:CD2	2.42	0.48
1:D:51:LEU:HD12	1:D:54:ARG:O	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:148:TYR:O	1:D:150:THR:CG2	2.61	0.48
1:D:620:PHE:CD1	1:D:667:ILE:HD11	2.47	0.48
1:C:567:PRO:HD2	1:C:570:ILE:HD12	1.95	0.48
1:A:662:ASP:O	1:A:665:THR:HG22	2.14	0.48
1:A:264:LYS:HB3	1:A:264:LYS:HE2	1.39	0.48
1:C:450:HIS:HE2	2:C:1:CIT:C6	2.27	0.48
1:D:221:ALA:HB1	1:D:222:PRO:HD2	1.94	0.48
1:C:531:THR:HG23	1:C:577:GLN:HE21	1.71	0.47
1:A:466:PHE:CG	1:A:467:PRO:HD2	2.49	0.47
1:D:219:ALA:HB3	1:D:228:MET:HB3	1.96	0.47
1:B:130:THR:O	1:B:133:ILE:HG22	2.14	0.47
1:D:49:VAL:HG12	1:D:56:LEU:HB3	1.95	0.47
1:A:512:GLY:HA3	1:A:533:ILE:HG21	1.96	0.47
1:D:319:ASP:N	1:D:319:ASP:OD1	2.47	0.47
1:B:658:HIS:O	1:B:661:ARG:HG3	2.14	0.47
1:D:377:PHE:HB2	1:D:380:LEU:HD22	1.97	0.47
1:B:153:LEU:HD12	1:D:432:TYR:HD2	1.79	0.47
1:D:621:VAL:HG12	1:D:622:GLY:O	2.15	0.47
1:A:321:GLU:O	1:A:325:LYS:HG3	2.15	0.47
1:D:48:ALA:HB1	1:D:55:LYS:HD2	1.97	0.47
1:C:110:GLY:HA3	1:C:159:VAL:CG2	2.44	0.46
1:A:43:MET:HG3	1:B:593:ILE:HG13	1.96	0.46
1:C:604:GLY:O	1:C:654:PRO:HD3	2.16	0.46
1:A:51:LEU:CG	1:A:54:ARG:H	2.28	0.46
1:C:226:ILE:O	1:C:565:GLY:HA2	2.14	0.46
1:D:637:VAL:O	1:D:637:VAL:HG12	2.16	0.46
1:B:221:ALA:HB1	1:B:222:PRO:CD	2.45	0.46
1:B:652:PRO:HD2	1:B:656:ALA:CB	2.46	0.46
1:A:221:ALA:HB1	1:A:222:PRO:HD2	1.97	0.46
1:D:59:SER:OG	1:D:72:VAL:HG13	2.15	0.46
1:D:95:PHE:HA	3:D:883:HOH:O	2.15	0.46
1:D:87:LYS:HA	1:D:89:LYS:HZ3	1.81	0.46
1:A:139:ARG:N	1:A:140:PRO:CD	2.78	0.46
1:D:482:SER:OG	1:D:485:MET:HB2	2.16	0.46
1:D:80:VAL:HG22	1:D:156:LEU:HD22	1.98	0.46
1:D:89:LYS:CD	1:D:89:LYS:N	2.64	0.46
1:B:376:MET:HB3	1:B:377:PHE:CE1	2.51	0.46
1:D:434:THR:OG1	1:D:436:GLU:OE2	2.22	0.46
1:D:291:ALA:HB2	1:D:320:THR:HG21	1.97	0.45
1:B:94:GLN:HG2	1:B:334:TYR:CG	2.50	0.45
1:A:352:VAL:HG12	1:A:528:ARG:HG3	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:294:ARG:CG	1:C:294:ARG:NH1	2.74	0.45
1:A:320:THR:O	1:A:324:LEU:HD22	2.15	0.45
1:D:531:THR:HG22	1:D:577:GLN:HG2	1.98	0.45
1:B:388:ARG:HH12	1:B:482:SER:HB3	1.82	0.45
1:C:628:LEU:O	1:C:632:GLN:HG3	2.15	0.45
1:C:613:PRO:HA	1:C:645:GLU:OE2	2.17	0.45
1:A:619:LYS:HD3	1:A:619:LYS:C	2.37	0.45
1:D:51:LEU:HD12	1:D:51:LEU:O	2.16	0.45
1:A:215:ASN:O	1:A:231:ALA:HA	2.17	0.45
1:C:511:ILE:HD11	1:C:578:ALA:HA	1.98	0.45
1:D:309:ARG:HD3	3:D:705:HOH:O	2.15	0.45
1:A:402:LEU:CD2	1:A:467:PRO:O	2.65	0.45
1:B:412:ILE:O	1:B:413:THR:HG23	2.17	0.45
1:D:655:SER:O	1:D:658:HIS:CB	2.63	0.44
2:B:670:CIT:O3	2:B:670:CIT:C6	2.65	0.44
1:A:468:PHE:CE2	1:A:605:PRO:HG2	2.53	0.44
1:D:660:ALA:O	1:D:664:ILE:HG13	2.17	0.44
1:B:184:TRP:CH2	1:B:188:VAL:HG13	2.52	0.44
1:C:283:ILE:HD11	1:C:339:SER:CB	2.47	0.44
1:B:221:ALA:HB1	1:B:222:PRO:HD2	1.99	0.44
1:A:74:GLN:HG3	1:A:78:THR:O	2.17	0.44
1:B:215:ASN:O	1:B:231:ALA:HA	2.17	0.44
1:C:473:THR:CG2	1:D:115:ASN:HD21	2.30	0.44
1:B:388:ARG:HG2	1:B:388:ARG:HH11	1.82	0.44
1:D:399:PHE:HB2	1:D:605:PRO:HG2	1.99	0.44
1:D:468:PHE:HE1	1:D:607:VAL:HG23	1.82	0.44
1:D:279:PRO:HG3	1:D:342:VAL:HG11	2.00	0.44
1:D:430:PRO:HA	1:D:431:PRO:HD3	1.88	0.44
1:B:130:THR:HA	1:B:133:ILE:HG22	2.00	0.44
1:D:661:ARG:NH1	1:D:661:ARG:CG	2.66	0.44
1:D:333:PRO:O	1:D:337:ILE:HG13	2.18	0.44
1:C:89:LYS:HA	1:C:89:LYS:HD3	1.74	0.44
1:D:471:ARG:HG2	1:D:471:ARG:HH11	1.82	0.44
1:D:651:ALA:HA	1:D:652:PRO:HD3	1.85	0.43
1:C:512:GLY:HA3	1:C:533:ILE:HG21	1.99	0.43
1:A:420:ASP:OD2	1:A:464:ARG:NH2	2.51	0.43
1:C:606:VAL:HG23	1:C:657:MET:HE3	2.01	0.43
1:C:77:ASP:OD2	1:B:378:LYS:HD3	2.18	0.43
1:C:608:GLU:OE2	1:C:661:ARG:NH2	2.43	0.43
1:A:245:ILE:O	1:A:249:VAL:HG23	2.18	0.43
1:C:482:SER:H	2:C:670:CIT:C6	2.21	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:643:ASP:CG	1:D:644:GLU:N	2.71	0.43
1:D:94:GLN:HA	1:D:147:PHE:CD2	2.53	0.43
1:B:49:VAL:CG2	1:B:51:LEU:HD13	2.47	0.43
1:C:446:ARG:NH2	2:C:670:CIT:H41	2.33	0.43
1:B:614:LEU:HD12	1:B:614:LEU:N	2.33	0.43
1:B:569:LYS:NZ	3:B:822:HOH:O	2.40	0.43
1:B:302:TYR:OH	1:B:357:LYS:HG2	2.18	0.43
1:D:364:LEU:HD11	1:D:528:ARG:HD2	2.01	0.43
1:D:450:HIS:HE2	2:D:1:CIT:C6	2.32	0.43
1:A:51:LEU:CD1	1:A:202:VAL:HG13	2.49	0.43
1:D:531:THR:HG22	1:D:577:GLN:NE2	2.25	0.43
1:C:153:LEU:HD21	1:B:440:VAL:HG21	2.00	0.43
1:C:536:ILE:HA	1:C:539:TYR:CE2	2.54	0.43
1:C:275:LYS:NZ	3:C:731:HOH:O	2.35	0.43
1:D:655:SER:O	1:D:658:HIS:N	2.52	0.42
1:D:376:MET:HG3	1:D:377:PHE:CD1	2.53	0.42
1:D:429:PHE:HZ	1:D:479:SER:HG	1.66	0.42
1:D:77:ASP:HB2	1:D:160:ASP:HB3	2.01	0.42
1:B:108:ALA:O	1:B:111:ARG:HG2	2.19	0.42
1:A:326:GLU:O	1:A:329:PRO:HD3	2.19	0.42
1:C:534:LEU:HD22	3:C:749:HOH:O	2.19	0.42
1:B:658:HIS:HA	1:B:661:ARG:CG	2.48	0.42
1:C:110:GLY:HA3	1:C:159:VAL:HG21	2.01	0.42
1:B:248:GLY:O	1:B:252:THR:HG23	2.18	0.42
1:A:362:ARG:NH2	1:A:534:LEU:HD13	2.34	0.42
1:B:87:LYS:HD3	1:D:437:ILE:HD12	2.01	0.42
1:A:603:ASN:HB2	3:A:811:HOH:O	2.18	0.42
1:C:572:MET:HE2	1:C:575:ILE:HD12	2.01	0.42
1:C:82:VAL:HG11	1:C:173:ALA:HA	2.01	0.42
1:C:370:VAL:HG22	1:C:588:ILE:HD13	2.00	0.42
1:C:643:ASP:O	1:C:643:ASP:OD2	2.37	0.42
1:C:511:ILE:HD11	1:C:578:ALA:CA	2.50	0.42
1:C:309:ARG:NH1	3:C:791:HOH:O	2.51	0.42
1:C:482:SER:CA	2:C:670:CIT:O5	2.68	0.42
1:D:635:THR:OG1	1:D:637:VAL:HB	2.20	0.42
1:A:664:ILE:O	1:A:664:ILE:CG2	2.68	0.42
1:C:481:GLY:C	3:C:732:HOH:O	2.57	0.42
1:D:243:HIS:O	1:D:247:VAL:HG12	2.20	0.42
1:D:252:THR:O	1:D:256:ILE:HG13	2.20	0.42
1:C:247:VAL:HG23	1:C:251:TYR:CE2	2.55	0.41
1:C:606:VAL:HG23	1:C:657:MET:CE	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:136:ARG:NE	3:A:704:HOH:O	2.36	0.41
1:A:521:LYS:CG	1:A:522:GLY:N	2.83	0.41
1:D:339:SER:O	1:D:342:VAL:HG13	2.20	0.41
1:C:628:LEU:HD22	1:C:639:ILE:HD13	2.02	0.41
1:B:265:GLU:OE1	3:B:793:HOH:O	2.21	0.41
1:B:262:LEU:O	1:B:266:THR:HG22	2.20	0.41
1:B:47:VAL:HG23	1:B:262:LEU:HD13	2.02	0.41
1:B:106:ALA:HB3	1:B:110:GLY:HA2	2.03	0.41
1:B:103:ARG:NH1	3:B:809:HOH:O	2.54	0.41
1:D:317:ARG:HG3	1:D:340:PHE:CD2	2.55	0.41
1:C:55:LYS:HE2	1:C:55:LYS:HB3	1.61	0.41
1:C:221:ALA:HB1	1:C:222:PRO:CD	2.50	0.41
1:B:468:PHE:CD2	1:B:650:PHE:HE1	2.37	0.41
1:B:658:HIS:HA	1:B:661:ARG:HG2	2.03	0.41
1:A:51:LEU:HB2	1:A:54:ARG:H	1.79	0.41
1:D:620:PHE:HD1	1:D:667:ILE:CD1	2.29	0.41
1:D:187:PRO:O	1:D:222:PRO:HD3	2.21	0.41
1:C:608:GLU:HG3	1:C:657:MET:HE3	2.03	0.41
1:D:601:LYS:CE	3:D:689:HOH:O	2.68	0.41
1:A:439:LYS:HD3	1:A:439:LYS:HA	1.96	0.41
1:C:370:VAL:HG22	1:C:588:ILE:HG21	2.03	0.41
1:D:181:ASP:O	1:D:271:ARG:HD3	2.20	0.41
1:A:414:ALA:O	3:A:1154:HOH:O	2.22	0.41
1:B:314:ASN:O	1:B:318:LEU:HD22	2.21	0.41
1:D:87:LYS:HD2	1:D:89:LYS:HE2	2.02	0.41
1:D:324:LEU:HA	1:D:324:LEU:HD23	1.85	0.41
1:A:521:LYS:HD2	1:A:522:GLY:H	1.86	0.41
1:D:221:ALA:HB1	1:D:222:PRO:CD	2.51	0.41
1:B:49:VAL:HG23	1:B:51:LEU:HD13	2.03	0.41
1:B:375:ASP:CG	1:B:601:LYS:NZ	2.74	0.41
1:D:650:PHE:CD2	1:D:650:PHE:C	2.94	0.41
1:A:55:LYS:HB2	1:A:55:LYS:HE3	1.77	0.41
1:C:659:GLU:OE1	1:D:206:ARG:NH2	2.53	0.41
1:A:401:SER:HB2	1:A:403:GLU:OE1	2.20	0.41
1:D:139:ARG:HB3	1:D:140:PRO:HD3	2.02	0.41
1:A:96:MET:HA	1:A:97:PRO:HD3	1.91	0.41
1:A:431:PRO:HB2	1:A:436:GLU:O	2.21	0.41
1:A:395:CYS:HA	1:A:473:THR:O	2.21	0.41
1:D:388:ARG:NH1	1:D:388:ARG:CG	2.80	0.40
1:D:376:MET:HE2	1:D:376:MET:HB3	1.76	0.40
1:D:368:ARG:HD3	1:D:534:LEU:CD1	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:54:ARG:HA	1:D:54:ARG:HD3	1.75	0.40
1:B:412:ILE:C	1:B:413:THR:HG23	2.41	0.40
1:C:309:ARG:NH2	3:C:702:HOH:O	2.43	0.40
1:A:357:LYS:HA	1:A:357:LYS:HD3	1.91	0.40
1:A:286:TYR:O	1:A:290:LEU:HD13	2.22	0.40
1:C:235:ASN:OD1	1:C:553:GLY:HA3	2.21	0.40
1:C:122:GLY:N	3:C:1135:HOH:O	2.54	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	615/630 (98%)	599 (97%)	16 (3%)	0	100	100
1	B	609/630 (97%)	592 (97%)	17 (3%)	0	100	100
1	C	617/630 (98%)	603 (98%)	14 (2%)	0	100	100
1	D	606/630 (96%)	589 (97%)	16 (3%)	1 (0%)	52	50
All	All	2447/2520 (97%)	2383 (97%)	63 (3%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	44	ALA

5.3.2 Protein sidechains [i](#)

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	525/534 (98%)	490 (93%)	35 (7%)	20	14
1	B	522/534 (98%)	484 (93%)	38 (7%)	17	11
1	C	527/534 (99%)	492 (93%)	35 (7%)	21	14
1	D	522/534 (98%)	483 (92%)	39 (8%)	17	10
All	All	2096/2136 (98%)	1949 (93%)	147 (7%)	19	13

All (147) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	43	MET
1	A	63	LEU
1	A	72	VAL
1	A	89	LYS
1	A	103	ARG
1	A	149	ASP
1	A	168	LEU
1	A	175	VAL
1	A	206	ARG
1	A	216	LEU
1	A	218	VAL
1	A	264	LYS
1	A	324	LEU
1	A	372	CYS
1	A	380	LEU
1	A	393	VAL
1	A	397	VAL
1	A	402	LEU
1	A	407	LYS
1	A	429	PHE
1	A	440	VAL
1	A	446	ARG
1	A	464	ARG
1	A	476	VAL
1	A	477	LEU
1	A	482	SER
1	A	520	GLU
1	A	530	LEU
1	A	534	LEU
1	A	592	THR

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Mol	Chain	Res	Type
1	A	603	ASN
1	A	606	VAL
1	A	619	LYS
1	A	639	ILE
1	A	666	GLU
1	C	50	ASP
1	C	56	LEU
1	C	57	GLU
1	C	63	LEU
1	C	93	SER
1	C	117	LEU
1	C	123	THR
1	C	168	LEU
1	C	175	VAL
1	C	211	SER
1	C	247	VAL
1	C	250	LYS
1	C	262	LEU
1	C	283	ILE
1	C	294	ARG
1	C	305	ASP
1	C	376	MET
1	C	402	LEU
1	C	410	GLN
1	C	424	MET
1	C	429	PHE
1	C	440	VAL
1	C	443	LEU
1	C	473	THR
1	C	476	VAL
1	C	506	VAL
1	C	531	THR
1	C	534	LEU
1	C	562	LYS
1	C	568	ILE
1	C	576	GLN
1	C	614	LEU
1	C	616	LYS
1	C	617	ARG
1	C	619	LYS
1	B	49	VAL
1	B	51	LEU

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Mol	Chain	Res	Type
1	B	57	GLU
1	B	63	LEU
1	B	93	SER
1	B	94	GLN
1	B	103	ARG
1	B	168	LEU
1	B	188	VAL
1	B	227	VAL
1	B	229	LEU
1	B	271	ARG
1	B	276	LEU
1	B	289	LYS
1	B	295	LEU
1	B	318	LEU
1	B	332	ASP
1	B	342	VAL
1	B	376	MET
1	B	380	LEU
1	B	396	THR
1	B	410	GLN
1	B	412	ILE
1	B	413	THR
1	B	424	MET
1	B	429	PHE
1	B	434	THR
1	B	439	LYS
1	B	446	ARG
1	B	530	LEU
1	B	531	THR
1	B	534	LEU
1	B	571	VAL
1	B	614	LEU
1	B	617	ARG
1	B	628	LEU
1	B	639	ILE
1	B	667	ILE
1	D	43	MET
1	D	51	LEU
1	D	55	LYS
1	D	57	GLU
1	D	72	VAL
1	D	87	LYS

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Mol	Chain	Res	Type
1	D	89	LYS
1	D	150	THR
1	D	213	THR
1	D	239	GLN
1	D	261	GLN
1	D	271	ARG
1	D	285	LYS
1	D	292	MET
1	D	305	ASP
1	D	318	LEU
1	D	325	LYS
1	D	338	GLU
1	D	371	SER
1	D	372	CYS
1	D	376	MET
1	D	380	LEU
1	D	396	THR
1	D	429	PHE
1	D	506	VAL
1	D	531	THR
1	D	534	LEU
1	D	579	SER
1	D	587	GLN
1	D	590	ASN
1	D	606	VAL
1	D	628	LEU
1	D	637	VAL
1	D	638	THR
1	D	642	VAL
1	D	643	ASP
1	D	659	GLU
1	D	661	ARG
1	D	666	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	577	GLN
1	B	577	GLN
1	B	641	GLN
1	D	115	ASN
1	D	577	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 ⓘ

8 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	CIT	A	1	-	3,12,12	1.32	0	3,17,17	2.03	2 (66%)
2	CIT	A	670	-	3,12,12	1.09	0	3,17,17	1.22	0
2	CIT	B	1	-	3,12,12	0.75	0	3,17,17	1.42	0
2	CIT	B	670	-	3,12,12	1.05	0	3,17,17	1.23	0
2	CIT	C	1	-	3,12,12	1.26	0	3,17,17	1.18	0
2	CIT	C	670	-	3,12,12	1.26	0	3,17,17	2.20	1 (33%)
2	CIT	D	1	-	3,12,12	1.37	0	3,17,17	2.28	1 (33%)
2	CIT	D	670	-	3,12,12	1.03	0	3,17,17	0.96	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	CIT	A	1	-	-	0/6/16/16	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	CIT	A	670	-	-	0/6/16/16	0/0/0/0
2	CIT	B	1	-	-	0/6/16/16	0/0/0/0
2	CIT	B	670	-	-	0/6/16/16	0/0/0/0
2	CIT	C	1	-	-	0/6/16/16	0/0/0/0
2	CIT	C	670	-	-	0/6/16/16	0/0/0/0
2	CIT	D	1	-	-	0/6/16/16	0/0/0/0
2	CIT	D	670	-	-	0/6/16/16	0/0/0/0

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	1	CIT	C3-C4-C5	-3.76	108.94	114.96
2	C	670	CIT	C3-C4-C5	-3.32	109.66	114.96
2	A	1	CIT	C3-C4-C5	-2.47	111.01	114.96
2	A	1	CIT	C3-C2-C1	-2.35	111.21	114.96

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1	CIT	1	0
2	B	670	CIT	1	0
2	C	1	CIT	1	0
2	C	670	CIT	6	0
2	D	1	CIT	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	619/630 (98%)	-0.06	30 (4%) 34 43	22, 34, 66, 86	0
1	B	617/630 (97%)	-0.19	23 (3%) 45 55	22, 34, 67, 100	0
1	C	623/630 (98%)	-0.07	26 (4%) 40 49	24, 38, 67, 90	0
1	D	614/630 (97%)	0.14	41 (6%) 21 28	27, 45, 77, 101	0
All	All	2473/2520 (98%)	-0.05	120 (4%) 33 43	22, 38, 71, 101	0

All (120) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	95	PHE	7.6
1	B	663	PHE	6.2
1	D	334	TYR	6.1
1	C	442	GLY	5.6
1	A	51	LEU	5.5
1	D	92	PRO	5.3
1	C	53	ASN	4.6
1	A	53	ASN	4.6
1	A	52	GLY	4.6
1	C	481	GLY	4.5
1	D	443	LEU	4.4
1	D	667	ILE	4.4
1	D	93	SER	4.3
1	C	443	LEU	4.3
1	D	94	GLN	4.3
1	C	411	VAL	4.3
1	B	615	SER	4.1
1	A	442	GLY	4.1
1	A	665	THR	4.0
1	B	442	GLY	3.9
1	A	92	PRO	3.9

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Mol	Chain	Res	Type	RSRZ
1	D	663	PHE	3.8
1	A	334	TYR	3.8
1	C	482	SER	3.7
1	A	54	ARG	3.5
1	A	519	PRO	3.5
1	A	331	ALA	3.4
1	D	658	HIS	3.4
1	A	521	LYS	3.4
1	C	441	THR	3.3
1	B	662	ASP	3.3
1	D	416	ASN	3.3
1	A	412	ILE	3.2
1	C	118	ARG	3.2
1	D	175	VAL	3.2
1	B	441	THR	3.1
1	D	82	VAL	3.1
1	B	665	THR	3.1
1	A	663	PHE	3.1
1	B	666	GLU	3.1
1	D	330	GLU	3.0
1	D	668	CYS	2.9
1	A	520	GLU	2.9
1	D	43	MET	2.9
1	C	602	GLU	2.9
1	A	329	PRO	2.9
1	C	410	GLN	2.9
1	C	92	PRO	2.9
1	D	285	LYS	2.9
1	D	318	LEU	2.8
1	B	443	LEU	2.8
1	B	92	PRO	2.8
1	A	441	THR	2.8
1	C	412	ILE	2.7
1	B	667	ILE	2.7
1	D	289	LYS	2.7
1	C	122	GLY	2.7
1	A	662	ASP	2.7
1	C	334	TYR	2.7
1	D	71	ALA	2.6
1	C	439	LYS	2.6
1	C	408	SER	2.6
1	C	414	ALA	2.6

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Mol	Chain	Res	Type	RSRZ
1	D	172	GLY	2.6
1	C	95	PHE	2.6
1	D	439	LYS	2.6
1	B	334	TYR	2.5
1	B	417	GLY	2.5
1	B	117	LEU	2.5
1	D	267	GLY	2.5
1	B	413	THR	2.5
1	A	326	GLU	2.4
1	C	666	GLU	2.4
1	D	44	ALA	2.4
1	A	408	SER	2.4
1	C	418	ILE	2.4
1	B	644	GLU	2.4
1	B	660	ALA	2.4
1	D	53	ASN	2.4
1	C	416	ASN	2.4
1	D	80	VAL	2.3
1	A	658	HIS	2.3
1	D	356	TYR	2.3
1	D	293	GLU	2.3
1	D	666	GLU	2.3
1	D	326	GLU	2.3
1	A	439	LYS	2.3
1	D	665	THR	2.3
1	C	54	ARG	2.2
1	A	443	LEU	2.2
1	D	441	THR	2.2
1	C	417	GLY	2.2
1	B	658	HIS	2.2
1	B	412	ILE	2.2
1	A	416	ASN	2.2
1	C	480	ASN	2.2
1	D	525	GLU	2.2
1	D	624	GLY	2.2
1	D	268	VAL	2.2
1	A	409	ASP	2.2
1	D	662	ASP	2.2
1	A	522	GLY	2.2
1	A	318	LEU	2.1
1	D	482	SER	2.1
1	D	50	ASP	2.1

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Mol	Chain	Res	Type	RSRZ
1	C	303	GLU	2.1
1	A	232	SER	2.1
1	D	511	ILE	2.1
1	C	167	VAL	2.1
1	B	418	ILE	2.1
1	D	547	ILE	2.1
1	A	644	GLU	2.1
1	B	668	CYS	2.1
1	D	644	GLU	2.1
1	B	405	GLY	2.1
1	A	95	PHE	2.1
1	A	94	GLN	2.0
1	D	329	PRO	2.0
1	B	518	ASP	2.0
1	B	645	GLU	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(Å ²)	Q<0.9
2	CIT	C	1	13/13	0.92	0.18	1.44	37,50,58,65	0
2	CIT	D	1	13/13	0.93	0.14	0.18	39,51,64,70	0
2	CIT	A	670	13/13	0.96	0.10	-0.06	36,45,55,64	0
2	CIT	A	1	13/13	0.95	0.09	-0.28	25,28,42,46	0
2	CIT	D	670	13/13	0.94	0.10	-0.44	32,37,50,55	0
2	CIT	C	670	13/13	0.97	0.09	-0.72	29,37,53,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	CIT	B	670	13/13	0.95	0.09	-0.83	33,42,53,57	0
2	CIT	B	1	13/13	0.97	0.07	-1.07	21,29,41,42	0

6.5 Other polymers [i](#)

There are no such residues in this entry.