



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 10:39 PM GMT

PDB ID : 1UM2
Title : Crystal Structure of the Vma1-Derived Endonuclease with the Ligated Extein Segment
Authors : Mizutani, R.; Anraku, Y.; Satow, Y.
Deposited on : 2003-09-22
Resolution : 2.90 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) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

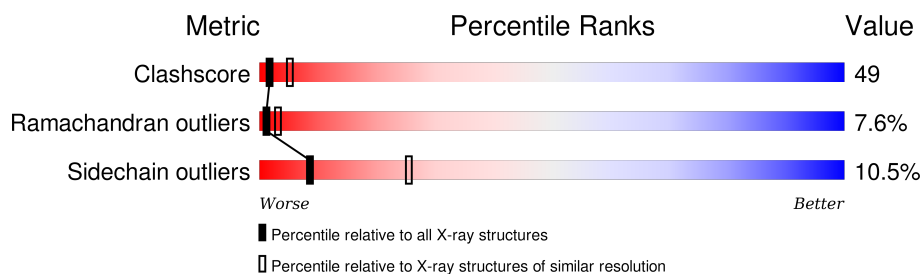
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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))
Clashscore	102246	1668 (2.90-2.90)
Ramachandran outliers	100387	1630 (2.90-2.90)
Sidechain outliers	100360	1632 (2.90-2.90)

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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	454	
1	B	454	
2	C	21	
2	D	21	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6865 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 ENDONUCLEASE PI-SCEI.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	417	Total	C	N	O	S	0	0	0
			3293	2089	561	631	12			
1	B	419	Total	C	N	O	S	0	0	0
			3313	2101	566	634	12			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	284	SER	CYS	ENGINEERED	UNP P17255
A	362	ASN	HIS	ENGINEERED	UNP P17255
B	284	SER	CYS	ENGINEERED	UNP P17255
B	362	ASN	HIS	ENGINEERED	UNP P17255

- Molecule 2 is a protein called 21-mer from Vacuolar ATP synthase catalytic subunit A.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	7	Total	C	N	O	0	0	0
			53	32	10	11			
2	D	7	Total	C	N	O	0	0	0
			53	32	10	11			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	273	MET	-	INITIATING MET	UNP P17255
C	738	SER	CYS	ENGINEERED	UNP P17255
D	273	MET	-	INITIATING MET	UNP P17255
D	738	SER	CYS	ENGINEERED	UNP P17255

- Molecule 3 is water.

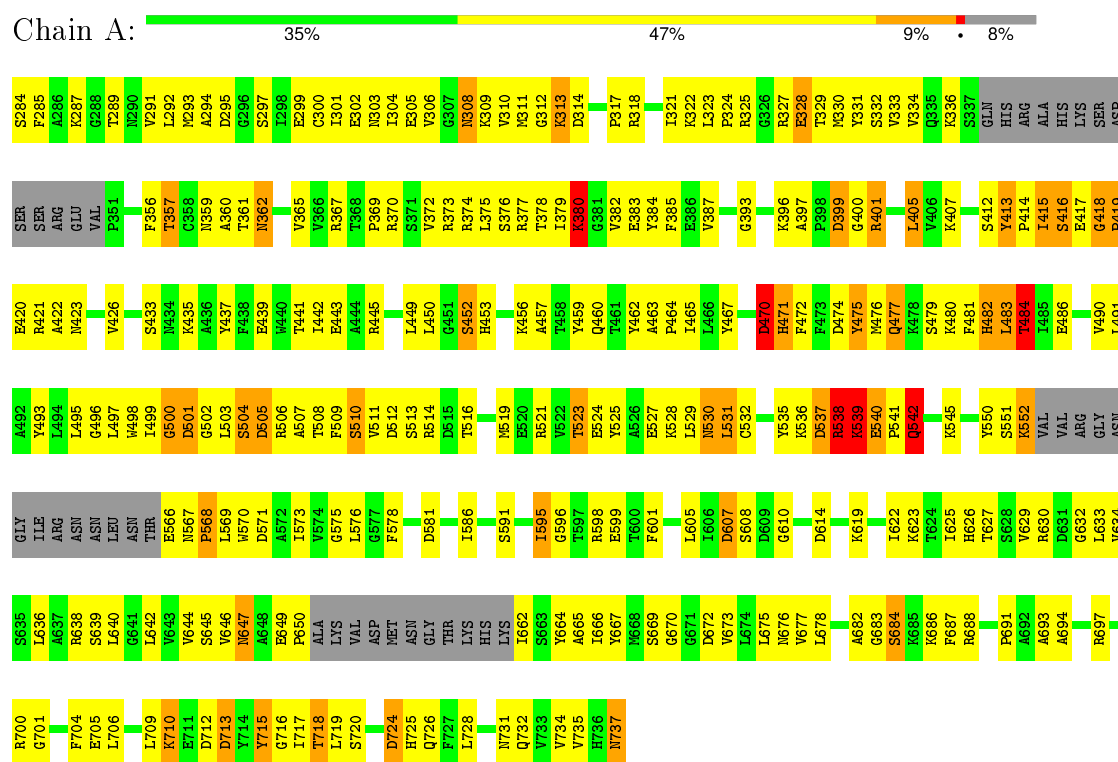
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	74	Total 74	O 74	0	0
3	B	79	Total 79	O 79	0	0

3 Residue-property plots

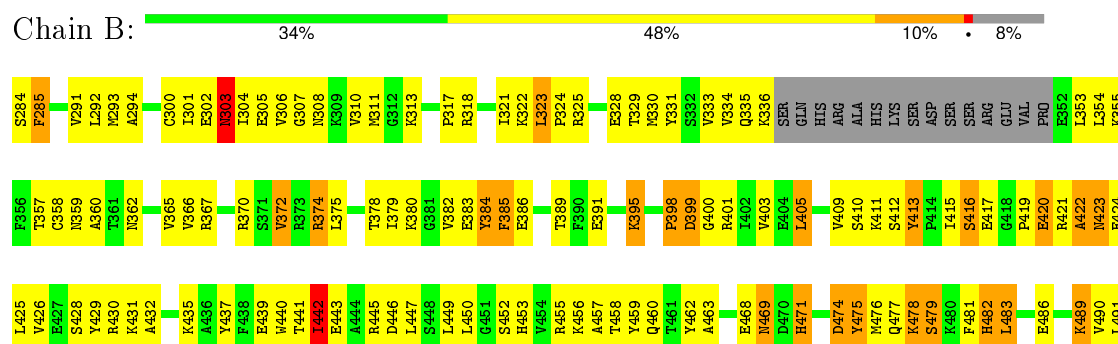
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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.

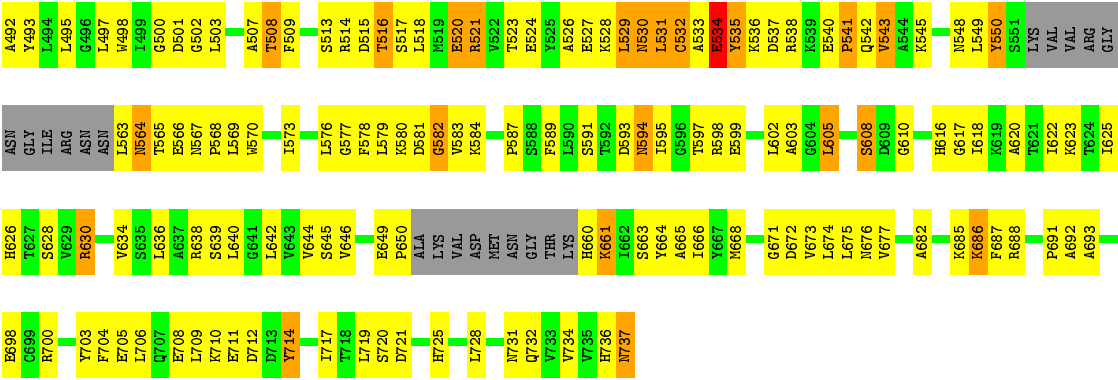
Note EDS was not executed.

• Molecule 1: ENDONUCLEASE PI-SCEI



• Molecule 1: ENDONUCLEASE PI-SCEI





4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	66.40 Å 70.40 Å 58.00 Å 100.40° 98.70° 78.90°	Depositor
Resolution (Å)	30.00 – 2.90	Depositor
% Data completeness (in resolution range)	(Not available) (30.00-2.90)	Depositor
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.214 , 0.283	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6865	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

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	0.56	0/3353	0.80	0/4523
1	B	0.62	1/3373 (0.0%)	0.81	0/4551
2	C	1.11	0/53	1.15	1/69 (1.4%)
2	D	0.92	0/53	1.09	1/69 (1.4%)
All	All	0.60	1/6832 (0.0%)	0.81	2/9212 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	534	GLU	CB-CG	5.27	1.62	1.52

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	C	739	GLY	N-CA-C	-5.71	98.84	113.10
2	D	739	GLY	N-CA-C	-5.19	100.12	113.10

There are no chirality outliers.

There are no planarity outliers.

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	3293	0	3291	308	0
1	B	3313	0	3309	337	0
2	C	53	0	47	23	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	53	0	47	11	0
3	A	74	0	0	11	0
3	B	79	0	0	13	0
All	All	6865	0	6694	653	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 49.

All (653) 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:493:TYR:HE2	1:B:497:LEU:HD12	1.13	1.13
1:A:595:ILE:HG13	1:A:598:ARG:HH21	1.13	1.11
1:A:507:ALA:HB1	1:A:569:LEU:HD23	1.40	1.04
1:B:493:TYR:CE2	1:B:497:LEU:HD12	1.92	1.04
1:B:284:SER:HB2	1:B:359:ASN:ND2	1.75	1.01
1:A:480:LYS:HG3	1:A:483:LEU:HD23	1.41	1.00
1:A:716:GLY:O	1:A:717:ILE:HD12	1.61	0.98
2:C:282:VAL:HG22	2:C:283:GLY:H	1.26	0.97
1:B:514:ARG:HH21	1:B:543:VAL:HG11	1.32	0.95
1:B:527:GLU:OE1	1:B:532:CYS:SG	2.25	0.95
1:A:284:SER:N	2:C:738:SER:HB2	1.82	0.94
1:A:610:GLY:O	1:A:686:LYS:HE2	1.68	0.94
1:A:465:ILE:HG13	1:A:732:GLN:NE2	1.83	0.94
1:B:318:ARG:HB3	1:B:719:LEU:HD13	1.46	0.93
1:B:483:LEU:H	1:B:483:LEU:HD23	1.31	0.92
1:A:336:LYS:HE2	1:A:705:GLU:OE2	1.68	0.91
1:A:669:SER:HG	1:B:616:HIS:HD1	1.11	0.90
1:A:595:ILE:HG13	1:A:598:ARG:NH2	1.86	0.90
1:A:300:CYS:O	1:A:304:ILE:HG13	1.70	0.90
1:B:284:SER:HB2	1:B:359:ASN:HD22	1.37	0.89
1:B:285:PHE:HB3	1:B:357:THR:O	1.73	0.88
1:B:421:ARG:O	1:B:424:GLU:HG2	1.74	0.87
1:A:737:ASN:O	2:C:738:SER:HB3	1.74	0.87
1:B:292:LEU:HD23	1:B:311:MET:HG2	1.57	0.86
1:A:598:ARG:HG2	1:A:636:LEU:HD11	1.56	0.85
1:B:507:ALA:HB2	1:B:570:TRP:HB2	1.57	0.84
1:A:456:LYS:HE3	1:B:685:LYS:HZ2	1.41	0.84
1:B:478:LYS:H	1:B:478:LYS:HD3	1.43	0.83
1:B:481:PHE:CE1	1:B:568:PRO:HB2	2.14	0.82
1:A:378:THR:HA	1:A:383:GLU:HA	1.62	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:502:GLY:HA2	1:B:509:PHE:HB3	1.60	0.82
1:B:302:GLU:HG2	1:B:303:ASN:H	1.43	0.81
1:B:330:MET:O	1:B:709:LEU:HB2	1.79	0.81
1:B:526:ALA:CB	1:B:533:ALA:HB2	2.12	0.80
1:B:372:VAL:HG11	1:B:430:ARG:HE	1.45	0.80
1:B:474:ASP:O	1:B:476:MET:N	2.14	0.80
1:B:513:SER:HB3	1:B:545:LYS:HG3	1.65	0.79
1:B:481:PHE:HE1	1:B:568:PRO:HB2	1.48	0.78
1:A:291:VAL:HG12	1:A:292:LEU:H	1.48	0.78
1:A:649:GLU:HB3	1:A:650:PRO:CD	2.14	0.78
1:B:731:ASN:O	1:B:732:GLN:HB2	1.83	0.78
1:B:489:LYS:N	1:B:489:LYS:HE3	1.99	0.78
1:B:317:PRO:HG2	3:B:38:HOH:O	1.84	0.77
1:A:725:HIS:HB3	1:A:737:ASN:ND2	1.99	0.77
1:A:595:ILE:HG22	1:A:596:GLY:N	1.99	0.77
1:A:605:LEU:O	1:A:605:LEU:HD12	1.84	0.76
1:A:586:ILE:HB	1:A:632:GLY:HA3	1.65	0.76
1:A:605:LEU:HG	1:A:622:ILE:HD13	1.67	0.76
1:A:506:ARG:HG3	1:A:508:THR:HB	1.66	0.76
1:A:359:ASN:ND2	2:C:283:GLY:HA2	2.01	0.76
1:B:302:GLU:HG2	1:B:303:ASN:ND2	2.01	0.76
1:A:530:ASN:C	1:A:531:LEU:HD12	2.07	0.76
1:B:421:ARG:HA	1:B:424:GLU:OE1	1.85	0.75
1:B:302:GLU:O	1:B:304:ILE:N	2.20	0.75
1:B:383:GLU:O	1:B:415:ILE:HG12	1.87	0.74
1:B:317:PRO:HD3	3:B:107:HOH:O	1.87	0.74
1:B:334:VAL:HG22	1:B:355:LYS:HB3	1.70	0.74
1:B:737:ASN:N	1:B:737:ASN:HD22	1.83	0.73
1:B:605:LEU:HD22	1:B:622:ILE:HD13	1.69	0.73
1:A:465:ILE:HG13	1:A:732:GLN:HE21	1.50	0.73
1:B:378:THR:HG22	1:B:383:GLU:HA	1.69	0.73
1:A:356:PHE:HZ	1:A:460:GLN:HE22	1.37	0.73
2:D:282:VAL:HB	2:D:740:GLU:HB3	1.71	0.73
1:B:514:ARG:NH2	1:B:543:VAL:HG11	2.03	0.73
1:A:630:ARG:HD3	1:A:664:TYR:CD1	2.23	0.73
1:A:598:ARG:HG2	1:A:636:LEU:CD1	2.18	0.72
1:B:306:VAL:HG12	1:B:307:GLY:N	2.04	0.72
1:B:564:ASN:O	1:B:567:ASN:HB3	1.89	0.72
1:B:642:LEU:HD13	1:B:668:MET:HB3	1.72	0.72
1:A:383:GLU:O	1:A:415:ILE:HG12	1.90	0.72
1:A:301:ILE:CD1	1:A:717:ILE:HD13	2.20	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:531:LEU:HD12	1:B:549:LEU:HB3	1.72	0.71
1:B:285:PHE:CD1	1:B:285:PHE:N	2.57	0.71
1:B:570:TRP:HA	1:B:573:ILE:HD12	1.70	0.71
1:B:292:LEU:HD23	1:B:311:MET:CG	2.21	0.71
1:B:531:LEU:CD1	1:B:549:LEU:HB3	2.20	0.71
1:A:626:HIS:HB2	1:A:629:VAL:HG23	1.73	0.71
1:B:725:HIS:HB3	1:B:737:ASN:HD21	1.55	0.70
1:A:323:LEU:HB3	1:A:325:ARG:HH12	1.55	0.70
1:B:334:VAL:HG22	1:B:355:LYS:CB	2.21	0.70
1:B:424:GLU:O	1:B:428:SER:HB2	1.90	0.70
1:A:687:PHE:O	1:A:688:ARG:HG2	1.92	0.70
1:B:531:LEU:HB2	1:B:550:TYR:O	1.92	0.69
1:A:284:SER:N	1:A:359:ASN:OD1	2.26	0.69
1:B:333:VAL:HG22	1:B:706:LEU:CD1	2.22	0.69
1:B:630:ARG:HD3	1:B:664:TYR:CD2	2.28	0.69
1:B:437:TYR:HE1	1:B:439:GLU:HG3	1.57	0.69
1:A:310:VAL:HG23	1:A:318:ARG:HB2	1.74	0.69
2:C:282:VAL:HG22	2:C:283:GLY:N	2.06	0.69
1:A:506:ARG:HG3	1:A:508:THR:CB	2.21	0.69
1:A:717:ILE:O	1:A:717:ILE:CG2	2.41	0.68
1:A:484:THR:HG22	1:B:378:THR:HG21	1.75	0.68
1:A:688:ARG:HH11	1:A:688:ARG:HG2	1.57	0.68
1:A:568:PRO:HA	1:A:571:ASP:HB2	1.74	0.68
1:B:412:SER:O	1:B:413:TYR:HB3	1.94	0.68
1:B:460:GLN:HG3	1:B:704:PHE:CE1	2.29	0.68
1:B:502:GLY:HA2	1:B:509:PHE:CB	2.24	0.68
1:A:595:ILE:O	1:A:598:ARG:N	2.27	0.68
1:A:463:ALA:O	1:A:732:GLN:NE2	2.26	0.68
1:A:301:ILE:HD11	1:A:717:ILE:HD13	1.74	0.68
1:A:362:ASN:O	1:A:443:GLU:HA	1.94	0.68
1:B:293:MET:HE3	1:B:310:VAL:HA	1.75	0.68
1:B:518:LEU:O	1:B:521:ARG:HB3	1.94	0.68
1:A:480:LYS:CG	1:A:483:LEU:HD23	2.20	0.67
1:B:336:LYS:HG3	1:B:705:GLU:HG3	1.75	0.67
1:B:367:ARG:HB2	1:B:459:TYR:CE2	2.30	0.67
1:B:306:VAL:HG13	1:B:321:ILE:HA	1.75	0.67
1:B:644:VAL:HG12	1:B:645:SER:N	2.09	0.67
1:B:577:GLY:C	1:B:579:LEU:H	1.98	0.67
1:B:483:LEU:N	1:B:483:LEU:HD23	2.08	0.66
1:B:334:VAL:HG12	3:B:126:HOH:O	1.95	0.66
1:B:565:THR:C	1:B:567:ASN:H	1.98	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:415:ILE:O	1:A:417:GLU:N	2.30	0.65
1:A:724:ASP:OD2	1:A:726:GLN:HB2	1.96	0.65
1:B:503:LEU:CD1	1:B:509:PHE:HA	2.26	0.65
1:B:563:LEU:HD23	1:B:563:LEU:O	1.95	0.65
1:A:295:ASP:O	1:A:467:TYR:HE2	1.79	0.65
1:B:399:ASP:OD1	1:B:401:ARG:HG3	1.96	0.65
1:A:291:VAL:HG12	1:A:292:LEU:N	2.10	0.65
1:B:514:ARG:HH21	1:B:543:VAL:CG1	2.09	0.65
1:B:323:LEU:HB3	1:B:325:ARG:HH12	1.62	0.65
1:B:293:MET:HE3	1:B:293:MET:HA	1.79	0.65
1:B:284:SER:N	2:D:283:GLY:O	2.30	0.64
1:A:475:TYR:HB2	1:A:576:LEU:HD21	1.79	0.64
1:A:716:GLY:HA3	2:C:738:SER:HA	1.79	0.64
1:A:378:THR:OG1	1:A:383:GLU:HG2	1.96	0.64
1:A:537:ASP:OD2	1:A:538:ARG:HD2	1.96	0.64
1:B:737:ASN:H	1:B:737:ASN:HD22	1.45	0.64
1:A:462:TYR:CE2	1:A:700:ARG:HB2	2.33	0.64
1:B:579:LEU:HD11	1:B:582:GLY:O	1.98	0.64
1:A:642:LEU:HD23	1:A:673:VAL:HG12	1.78	0.64
1:B:325:ARG:HH11	1:B:325:ARG:HG2	1.63	0.64
1:B:478:LYS:H	1:B:478:LYS:CD	2.11	0.63
1:A:328:GLU:HG2	1:A:329:THR:H	1.63	0.63
1:A:523:THR:HG22	1:A:524:GLU:N	2.13	0.63
1:A:375:LEU:HD12	1:A:376:SER:N	2.13	0.63
1:A:531:LEU:HB3	1:A:550:TYR:O	1.98	0.63
1:A:328:GLU:CG	1:A:329:THR:H	2.10	0.63
1:A:712:ASP:CG	1:A:713:ASP:N	2.51	0.63
1:B:501:ASP:O	1:B:509:PHE:HB2	1.98	0.63
1:B:293:MET:CE	1:B:310:VAL:HG12	2.28	0.63
1:B:292:LEU:HD23	1:B:311:MET:CB	2.28	0.63
1:A:625:ILE:HG23	1:A:662:ILE:O	1.99	0.63
1:A:414:PRO:HD2	1:A:417:GLU:OE1	1.99	0.62
1:A:303:ASN:N	1:A:303:ASN:HD22	1.98	0.62
1:A:649:GLU:HB3	1:A:650:PRO:HD2	1.81	0.62
1:B:500:GLY:HA3	1:B:608:SER:HB3	1.82	0.62
1:B:483:LEU:H	1:B:483:LEU:CD2	2.07	0.62
1:A:373:ARG:HD3	3:A:80:HOH:O	1.99	0.62
2:D:282:VAL:HG23	2:D:739:GLY:O	1.99	0.62
1:A:640:LEU:O	1:A:697:ARG:NH1	2.33	0.62
1:B:500:GLY:HA3	1:B:608:SER:CB	2.29	0.61
1:B:322:LYS:O	1:B:324:PRO:HD3	2.00	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:284:SER:N	2:D:738:SER:HB2	2.15	0.61
1:B:620:ALA:HB3	1:B:668:MET:HE3	1.81	0.61
1:B:401:ARG:NH1	1:B:445:ARG:NH2	2.47	0.61
1:A:513:SER:HB3	1:A:545:LYS:HD2	1.83	0.61
1:A:322:LYS:HB2	1:A:718:THR:HB	1.82	0.61
1:A:638:ARG:HB3	1:A:732:GLN:OE1	1.99	0.61
1:A:693:ALA:HA	1:B:430:ARG:HD2	1.82	0.61
1:B:610:GLY:O	1:B:686:LYS:HE2	2.01	0.61
1:A:405:LEU:HD22	1:A:450:LEU:HD23	1.82	0.60
1:B:550:TYR:CE1	1:B:563:LEU:HB2	2.37	0.60
1:A:334:VAL:HG13	1:A:705:GLU:HB2	1.83	0.60
1:A:302:GLU:HG2	1:A:303:ASN:ND2	2.17	0.60
1:B:285:PHE:HA	1:B:358:CYS:HA	1.83	0.60
2:C:283:GLY:O	2:C:738:SER:HB2	2.00	0.60
1:A:737:ASN:CG	1:A:737:ASN:OXT	2.40	0.60
1:B:503:LEU:HD13	1:B:508:THR:CG2	2.32	0.60
1:A:306:VAL:HG13	1:A:321:ILE:HA	1.82	0.60
1:B:413:TYR:CZ	1:B:421:ARG:HB3	2.36	0.60
1:A:506:ARG:C	1:A:508:THR:H	2.05	0.60
1:A:642:LEU:CD2	1:A:673:VAL:HG12	2.31	0.60
1:B:660:HIS:CG	1:B:661:LYS:H	2.18	0.60
1:A:327:ARG:O	1:A:328:GLU:HB2	2.01	0.60
1:B:503:LEU:HD13	1:B:508:THR:HG23	1.83	0.59
1:B:386:GLU:HA	1:B:411:LYS:O	2.01	0.59
1:A:619:LYS:HE3	3:A:123:HOH:O	2.02	0.59
1:B:533:ALA:O	1:B:534:GLU:C	2.41	0.59
1:B:476:MET:O	1:B:477:GLN:NE2	2.24	0.59
1:A:490:VAL:HG11	1:A:528:LYS:HB2	1.82	0.59
1:A:627:THR:HB	1:A:630:ARG:HH21	1.66	0.59
1:A:566:GLU:HG3	1:A:567:ASN:H	1.67	0.59
1:A:715:TYR:CD1	1:A:715:TYR:N	2.70	0.59
1:B:550:TYR:HA	1:B:567:ASN:ND2	2.17	0.59
1:A:464:PRO:HG3	1:A:697:ARG:O	2.02	0.59
1:A:595:ILE:CG1	1:A:598:ARG:HH21	2.03	0.59
1:A:374:ARG:HG3	1:A:387:VAL:HG22	1.85	0.59
1:B:479:SER:HB2	1:B:481:PHE:CD2	2.37	0.59
1:A:367:ARG:HD3	1:A:437:TYR:CE1	2.37	0.59
1:A:724:ASP:HB3	3:A:66:HOH:O	2.02	0.59
1:B:301:ILE:HA	1:B:304:ILE:HD12	1.83	0.59
1:B:372:VAL:HG13	1:B:372:VAL:O	2.03	0.59
1:B:372:VAL:HG23	1:B:389:THR:HG22	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:712:ASP:CG	1:A:713:ASP:H	2.06	0.59
1:B:526:ALA:HB1	1:B:533:ALA:HB2	1.83	0.59
1:B:431:LYS:O	1:B:431:LYS:HG2	2.02	0.58
1:B:521:ARG:HH11	1:B:521:ARG:HG2	1.67	0.58
1:A:511:VAL:CG1	1:A:519:MET:HE3	2.33	0.58
1:B:292:LEU:CD2	1:B:311:MET:HG2	2.31	0.58
1:B:660:HIS:ND1	1:B:661:LYS:N	2.51	0.58
1:A:619:LYS:HD2	3:A:26:HOH:O	2.03	0.58
1:A:330:MET:O	1:A:709:LEU:HB2	2.03	0.58
1:A:709:LEU:O	1:A:710:LYS:O	2.20	0.58
1:B:317:PRO:CG	3:B:38:HOH:O	2.48	0.58
1:B:618:ILE:HG23	1:B:674:LEU:HD23	1.84	0.58
1:B:334:VAL:CG1	3:B:126:HOH:O	2.50	0.58
1:B:294:ALA:CB	1:B:317:PRO:HB3	2.34	0.58
1:A:529:LEU:HB2	1:A:531:LEU:CD1	2.32	0.58
1:B:644:VAL:CG1	1:B:645:SER:N	2.66	0.58
1:B:593:ASP:CG	1:B:594:ASN:H	2.07	0.58
1:A:474:ASP:O	1:A:476:MET:N	2.36	0.58
1:A:323:LEU:HB3	1:A:325:ARG:NH1	2.18	0.58
1:B:526:ALA:O	1:B:531:LEU:HG	2.03	0.58
1:B:328:GLU:O	1:B:711:GLU:HA	2.04	0.57
1:B:521:ARG:NH1	1:B:521:ARG:HG2	2.19	0.57
1:A:538:ARG:HH12	1:A:545:LYS:HZ1	1.52	0.57
1:A:324:PRO:HB3	2:C:282:VAL:HG21	1.86	0.57
2:C:282:VAL:HG23	2:C:740:GLU:HB3	1.85	0.57
1:A:305:GLU:O	1:A:308:ASN:HB2	2.04	0.57
2:D:282:VAL:CG2	2:D:738:SER:H	2.17	0.57
1:A:538:ARG:H	1:A:538:ARG:HH11	1.52	0.57
1:A:284:SER:O	1:A:359:ASN:OD1	2.22	0.57
1:A:384:TYR:HA	1:A:413:TYR:O	2.03	0.57
1:A:502:GLY:HA2	1:A:509:PHE:CB	2.33	0.57
1:A:399:ASP:CG	1:A:401:ARG:HE	2.06	0.57
1:B:306:VAL:CG1	1:B:307:GLY:N	2.68	0.57
1:A:524:GLU:O	1:A:528:LYS:HG2	2.05	0.57
1:A:493:TYR:CE2	1:A:521:ARG:HG3	2.40	0.57
1:A:318:ARG:CZ	3:A:66:HOH:O	2.53	0.57
1:B:503:LEU:N	1:B:503:LEU:HD12	2.20	0.56
1:B:365:VAL:HA	1:B:441:THR:HG22	1.87	0.56
1:A:377:ARG:O	1:A:384:TYR:N	2.36	0.56
1:B:459:TYR:HB3	1:B:703:TYR:CD1	2.41	0.56
1:A:294:ALA:CB	1:A:317:PRO:HB3	2.36	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:524:GLU:HG2	1:A:524:GLU:O	2.05	0.56
1:A:456:LYS:HE3	1:B:685:LYS:NZ	2.16	0.56
1:A:536:LYS:HG2	1:A:540:GLU:CD	2.25	0.56
1:A:439:GLU:HG3	3:A:63:HOH:O	2.05	0.56
1:A:605:LEU:O	1:A:608:SER:OG	2.22	0.56
1:B:318:ARG:CB	1:B:719:LEU:HD13	2.28	0.56
1:B:302:GLU:C	1:B:304:ILE:H	2.06	0.56
1:A:365:VAL:O	1:A:460:GLN:HG2	2.06	0.56
1:B:521:ARG:HG2	1:B:682:ALA:HB2	1.87	0.56
1:B:306:VAL:HG12	1:B:307:GLY:H	1.68	0.56
1:A:293:MET:HG2	1:A:297:SER:O	2.06	0.56
1:A:538:ARG:HH12	1:A:545:LYS:NZ	2.04	0.56
1:A:367:ARG:HD3	1:A:437:TYR:CD1	2.40	0.55
1:B:323:LEU:CB	1:B:325:ARG:HH12	2.19	0.55
1:B:333:VAL:HG22	1:B:706:LEU:HD11	1.87	0.55
1:A:666:ILE:N	1:A:666:ILE:HD12	2.20	0.55
1:B:728:LEU:HD23	1:B:734:VAL:HG22	1.89	0.55
1:B:302:GLU:HG2	1:B:303:ASN:N	2.17	0.55
1:B:426:VAL:O	1:B:429:TYR:HB3	2.07	0.55
1:A:622:ILE:HG22	1:A:623:LYS:N	2.22	0.55
1:A:476:MET:SD	1:A:491:LEU:HD23	2.47	0.55
1:B:725:HIS:HB3	1:B:737:ASN:ND2	2.21	0.55
1:B:385:PHE:O	1:B:412:SER:HA	2.07	0.55
1:B:421:ARG:O	1:B:422:ALA:O	2.24	0.55
1:A:539:LYS:O	1:A:540:GLU:CB	2.55	0.55
1:A:665:ALA:C	1:A:666:ILE:HD12	2.27	0.55
1:A:379:ILE:C	1:A:380:LYS:HG3	2.28	0.55
1:B:323:LEU:HD23	1:B:323:LEU:N	2.22	0.55
1:B:515:ASP:HB3	1:B:518:LEU:HB3	1.89	0.55
1:A:496:GLY:HA2	1:A:601:PHE:CE1	2.41	0.55
1:A:418:GLY:C	1:A:420:GLU:H	2.11	0.55
1:A:511:VAL:CG1	1:A:512:ASP:N	2.70	0.54
1:B:593:ASP:CG	1:B:594:ASN:N	2.61	0.54
1:B:323:LEU:O	1:B:325:ARG:NH1	2.40	0.54
1:A:328:GLU:CG	1:A:329:THR:N	2.70	0.54
1:A:385:PHE:CD2	1:A:419:PRO:HB3	2.41	0.54
1:B:517:SER:HA	1:B:520:GLU:OE1	2.07	0.54
1:A:595:ILE:O	1:A:598:ARG:HB2	2.08	0.54
1:B:508:THR:OG1	1:B:548:ASN:ND2	2.39	0.54
1:A:475:TYR:CE1	1:A:575:GLY:HA3	2.41	0.54
1:B:686:LYS:HD3	3:B:146:HOH:O	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:282:VAL:CG2	2:C:283:GLY:H	2.06	0.54
1:A:633:LEU:HD23	1:A:666:ILE:HG12	1.89	0.54
1:B:303:ASN:ND2	1:B:303:ASN:H	2.05	0.54
1:A:511:VAL:HG12	1:A:512:ASP:N	2.22	0.54
1:A:385:PHE:CE2	1:A:419:PRO:HB3	2.42	0.54
1:A:636:LEU:O	1:A:639:SER:OG	2.26	0.54
1:B:563:LEU:HD23	1:B:563:LEU:C	2.28	0.54
1:B:495:LEU:O	1:B:498:TRP:HB3	2.08	0.54
1:B:440:TRP:HH2	1:B:450:LEU:HD21	1.72	0.54
1:A:312:GLY:O	1:A:314:ASP:N	2.38	0.54
1:B:313:LYS:HG2	3:B:36:HOH:O	2.07	0.54
1:A:303:ASN:N	1:A:303:ASN:ND2	2.54	0.53
1:A:382:VAL:HB	3:A:130:HOH:O	2.09	0.53
1:A:289:THR:O	1:A:291:VAL:HG23	2.08	0.53
1:B:665:ALA:C	1:B:666:ILE:HD12	2.28	0.53
1:A:501:ASP:O	1:A:509:PHE:HB2	2.08	0.53
1:B:536:LYS:HG2	1:B:537:ASP:H	1.72	0.53
1:B:737:ASN:C	2:D:738:SER:HB3	2.28	0.53
1:B:503:LEU:HD12	1:B:509:PHE:HA	1.89	0.53
1:A:470:ASP:C	1:A:472:PHE:N	2.59	0.53
1:A:735:VAL:HA	3:A:5:HOH:O	2.08	0.53
1:B:737:ASN:H	1:B:737:ASN:ND2	2.07	0.53
1:B:737:ASN:N	1:B:737:ASN:ND2	2.54	0.53
1:B:331:TYR:CD1	1:B:708:GLU:HA	2.44	0.53
1:A:567:ASN:O	1:A:569:LEU:N	2.41	0.53
1:B:536:LYS:HG2	1:B:537:ASP:N	2.24	0.53
1:B:548:ASN:C	1:B:549:LEU:HD12	2.29	0.53
1:A:336:LYS:H	1:A:704:PHE:HA	1.74	0.53
1:A:328:GLU:HG2	1:A:329:THR:N	2.24	0.53
1:B:595:ILE:HG23	1:B:640:LEU:CD2	2.38	0.53
1:B:475:TYR:CG	1:B:576:LEU:HD21	2.44	0.53
1:B:325:ARG:HG2	1:B:325:ARG:NH1	2.24	0.53
1:B:300:CYS:HB3	1:B:302:GLU:OE1	2.09	0.53
1:B:374:ARG:HD2	1:B:422:ALA:HB1	1.91	0.52
1:B:301:ILE:HA	1:B:304:ILE:CD1	2.39	0.52
1:A:309:LYS:HB3	1:A:317:PRO:HB2	1.91	0.52
1:A:312:GLY:C	1:A:314:ASP:H	2.11	0.52
1:B:486:GLU:OE2	1:B:528:LYS:HD3	2.09	0.52
1:A:310:VAL:CG2	1:A:318:ARG:HB2	2.40	0.52
1:B:331:TYR:CE1	1:B:708:GLU:HB2	2.44	0.52
1:A:505:ASP:N	1:A:570:TRP:CH2	2.77	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:379:ILE:N	1:A:382:VAL:O	2.42	0.52
1:B:486:GLU:O	1:B:490:VAL:HG23	2.09	0.52
1:A:495:LEU:HD13	1:A:578:PHE:CE1	2.44	0.52
1:A:495:LEU:HD13	1:A:578:PHE:CZ	2.45	0.52
1:B:329:THR:HA	1:B:711:GLU:HA	1.92	0.52
1:B:365:VAL:HG12	1:B:365:VAL:O	2.09	0.52
1:B:704:PHE:N	1:B:704:PHE:CD1	2.78	0.52
1:B:335:GLN:OE1	1:B:354:LEU:HD12	2.10	0.52
1:B:630:ARG:HG3	1:B:666:ILE:HD11	1.91	0.52
1:A:599:GLU:OE2	1:A:697:ARG:NH2	2.43	0.52
1:A:422:ALA:O	1:A:426:VAL:HG23	2.10	0.52
1:B:523:THR:O	1:B:524:GLU:C	2.48	0.52
1:A:716:GLY:C	1:A:717:ILE:HD12	2.28	0.51
1:B:362:ASN:O	1:B:443:GLU:HA	2.09	0.51
1:B:331:TYR:HE1	1:B:708:GLU:HB2	1.75	0.51
1:A:683:GLY:O	1:A:684:SER:C	2.49	0.51
1:A:331:TYR:HD1	1:A:360:ALA:HA	1.75	0.51
1:A:591:SER:O	1:A:598:ARG:NH1	2.43	0.51
1:B:666:ILE:N	1:B:666:ILE:HD12	2.25	0.51
1:A:640:LEU:HD13	3:A:88:HOH:O	2.10	0.51
1:A:332:SER:HA	1:A:357:THR:HG23	1.92	0.51
1:B:503:LEU:H	1:B:503:LEU:HD12	1.76	0.51
1:A:359:ASN:HD22	2:C:283:GLY:HA2	1.73	0.51
1:A:536:LYS:O	1:A:537:ASP:CB	2.57	0.51
1:B:688:ARG:HH11	1:B:688:ARG:HG2	1.76	0.51
1:B:566:GLU:HA	1:B:566:GLU:OE1	2.10	0.51
1:B:501:ASP:N	1:B:608:SER:OG	2.43	0.51
1:B:306:VAL:CG1	1:B:307:GLY:H	2.23	0.51
1:B:284:SER:HB2	1:B:359:ASN:HD21	1.71	0.51
1:B:303:ASN:ND2	1:B:303:ASN:N	2.59	0.51
1:B:410:SER:O	1:B:411:LYS:HG2	2.10	0.51
1:A:502:GLY:HA2	1:A:509:PHE:HB2	1.93	0.51
1:A:284:SER:N	2:C:283:GLY:O	2.44	0.51
1:A:291:VAL:CG1	1:A:292:LEU:H	2.22	0.51
1:B:734:VAL:HB	3:B:42:HOH:O	2.10	0.51
1:A:737:ASN:C	2:C:738:SER:O	2.49	0.51
1:B:531:LEU:O	1:B:532:CYS:C	2.49	0.51
1:A:470:ASP:C	1:A:472:PHE:H	2.12	0.51
1:B:474:ASP:C	1:B:476:MET:N	2.64	0.50
1:B:620:ALA:HB3	1:B:668:MET:CE	2.40	0.50
1:B:577:GLY:C	1:B:579:LEU:N	2.63	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:331:TYR:HD2	1:B:360:ALA:HA	1.76	0.50
1:B:529:LEU:O	1:B:530:ASN:CB	2.60	0.50
1:A:731:ASN:O	1:A:732:GLN:HB2	2.09	0.50
1:A:484:THR:C	1:A:486:GLU:H	2.14	0.50
1:A:359:ASN:HD21	2:C:283:GLY:CA	2.25	0.50
1:B:532:CYS:SG	1:B:534:GLU:HG3	2.51	0.50
1:A:377:ARG:HG2	1:A:378:THR:N	2.27	0.50
1:A:644:VAL:HG12	1:A:645:SER:N	2.26	0.50
1:A:724:ASP:O	1:A:725:HIS:HB2	2.12	0.50
1:A:365:VAL:HA	1:A:441:THR:HG22	1.93	0.50
1:A:634:VAL:O	1:A:634:VAL:HG12	2.11	0.50
1:A:694:ALA:HB2	1:B:430:ARG:HH12	1.76	0.50
1:B:579:LEU:HD12	1:B:583:VAL:O	2.12	0.50
1:A:370:ARG:HB2	1:B:692:ALA:HB1	1.94	0.50
1:A:287:LYS:HB2	1:A:715:TYR:OH	2.11	0.50
1:B:591:SER:O	1:B:598:ARG:CZ	2.60	0.50
1:B:516:THR:O	1:B:520:GLU:HG3	2.12	0.50
1:A:324:PRO:HD2	1:A:716:GLY:C	2.33	0.49
1:B:322:LYS:C	1:B:323:LEU:HD23	2.33	0.49
1:B:646:VAL:HG13	1:B:665:ALA:O	2.12	0.49
1:A:323:LEU:N	1:A:324:PRO:HD3	2.26	0.49
1:B:536:LYS:CG	1:B:537:ASP:H	2.23	0.49
1:B:671:GLY:O	1:B:675:LEU:HG	2.12	0.49
1:B:598:ARG:HB3	1:B:636:LEU:HD11	1.94	0.49
1:A:470:ASP:O	1:A:472:PHE:N	2.45	0.49
1:A:717:ILE:O	1:A:717:ILE:HG22	2.12	0.49
1:A:367:ARG:NH1	1:A:437:TYR:CZ	2.81	0.49
1:A:421:ARG:O	1:A:422:ALA:C	2.50	0.49
1:A:301:ILE:CG1	1:A:717:ILE:HD13	2.43	0.49
1:A:646:VAL:HA	1:A:665:ALA:O	2.12	0.49
1:B:714:TYR:C	1:B:714:TYR:CD1	2.85	0.49
1:A:301:ILE:HG13	1:A:717:ILE:HD13	1.94	0.49
1:B:630:ARG:HD3	1:B:664:TYR:CG	2.48	0.49
1:A:511:VAL:HG12	1:A:519:MET:HE3	1.94	0.49
1:B:441:THR:C	1:B:442:ILE:HG22	2.33	0.49
1:A:498:TRP:CD2	1:A:573:ILE:HD13	2.47	0.49
1:A:728:LEU:CD2	1:A:734:VAL:HG22	2.42	0.49
1:A:688:ARG:NH1	1:A:688:ARG:HG2	2.25	0.49
1:B:447:LEU:HD21	1:B:455:ARG:NE	2.28	0.49
1:B:577:GLY:O	1:B:579:LEU:N	2.45	0.49
1:A:359:ASN:O	1:A:362:ASN:HB2	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:626:HIS:HB2	1:A:629:VAL:CG2	2.42	0.48
1:B:409:VAL:HG12	1:B:410:SER:N	2.28	0.48
1:A:385:PHE:HE2	1:A:419:PRO:HD3	1.77	0.48
1:B:527:GLU:CG	1:B:532:CYS:HA	2.43	0.48
1:A:586:ILE:CB	1:A:632:GLY:HA3	2.40	0.48
1:B:415:ILE:O	1:B:416:SER:C	2.52	0.48
1:A:717:ILE:O	1:A:717:ILE:HG23	2.13	0.48
1:B:331:TYR:CD2	1:B:360:ALA:HA	2.49	0.48
1:B:440:TRP:CD1	1:B:440:TRP:N	2.81	0.48
1:A:717:ILE:O	1:A:718:THR:C	2.51	0.48
1:A:484:THR:C	1:A:486:GLU:N	2.67	0.48
1:A:633:LEU:CD2	1:A:666:ILE:HG12	2.43	0.48
1:A:566:GLU:HG3	1:A:567:ASN:N	2.29	0.48
1:A:479:SER:CB	1:A:480:LYS:HZ2	2.27	0.48
1:B:565:THR:C	1:B:567:ASN:N	2.66	0.48
1:B:474:ASP:O	1:B:475:TYR:C	2.51	0.48
1:B:333:VAL:HG11	1:B:460:GLN:HE22	1.79	0.48
1:A:399:ASP:OD2	1:A:401:ARG:HG3	2.13	0.48
1:B:492:ALA:HB2	1:B:597:THR:HG23	1.96	0.48
1:A:293:MET:HE3	1:A:309:LYS:O	2.14	0.48
1:B:728:LEU:CD2	1:B:734:VAL:HG22	2.43	0.48
1:A:646:VAL:HG13	1:A:665:ALA:O	2.14	0.47
1:B:405:LEU:HD22	1:B:450:LEU:HD23	1.96	0.47
1:A:456:LYS:CE	1:B:685:LYS:HZ2	2.22	0.47
1:A:687:PHE:CG	1:A:688:ARG:N	2.82	0.47
1:B:379:ILE:HG22	1:B:380:LYS:HG2	1.96	0.47
1:B:497:LEU:O	1:B:497:LEU:HD23	2.14	0.47
1:B:359:ASN:O	1:B:359:ASN:OD1	2.31	0.47
2:D:282:VAL:HG23	2:D:738:SER:H	1.79	0.47
1:A:532:CYS:CB	1:A:552:LYS:NZ	2.76	0.47
1:B:540:GLU:O	1:B:542:GLN:N	2.47	0.47
1:B:737:ASN:OXT	2:D:738:SER:HB3	2.14	0.47
1:A:292:LEU:HD23	1:A:311:MET:HG2	1.95	0.47
1:B:447:LEU:HD22	1:B:706:LEU:HD22	1.97	0.47
1:B:660:HIS:CG	1:B:661:LYS:N	2.82	0.47
1:A:393:GLY:HA3	1:A:407:LYS:HD3	1.96	0.47
1:B:569:LEU:HG	1:B:573:ILE:HD11	1.97	0.47
1:A:302:GLU:CG	1:A:303:ASN:ND2	2.78	0.47
1:B:358:CYS:SG	1:B:362:ASN:OD1	2.72	0.47
1:B:302:GLU:N	1:B:302:GLU:OE1	2.42	0.47
1:A:623:LYS:HD2	1:A:664:TYR:O	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:437:TYR:CE1	1:B:439:GLU:HG3	2.42	0.47
1:A:462:TYR:CZ	1:A:700:ARG:HB2	2.49	0.47
1:A:512:ASP:OD1	1:A:514:ARG:N	2.48	0.47
1:B:398:PRO:C	1:B:400:GLY:H	2.17	0.47
1:A:530:ASN:N	1:A:531:LEU:HD12	2.30	0.47
1:A:532:CYS:HB3	1:A:552:LYS:NZ	2.30	0.47
1:A:359:ASN:HD21	2:C:283:GLY:C	2.17	0.47
1:B:365:VAL:CG2	1:B:736:HIS:HB2	2.44	0.47
1:A:318:ARG:HA	3:A:67:HOH:O	2.15	0.46
1:A:325:ARG:NE	1:A:715:TYR:HD2	2.13	0.46
1:A:379:ILE:HB	1:A:384:TYR:CE1	2.50	0.46
1:B:622:ILE:HG22	1:B:623:LYS:N	2.30	0.46
1:B:610:GLY:O	1:B:686:LYS:CE	2.63	0.46
1:A:291:VAL:CG1	1:A:292:LEU:N	2.79	0.46
1:B:317:PRO:CD	3:B:38:HOH:O	2.62	0.46
1:A:327:ARG:HG2	1:A:713:ASP:HA	1.97	0.46
1:B:453:HIS:HB2	3:B:101:HOH:O	2.15	0.46
1:B:584:LYS:O	1:B:628:SER:OG	2.32	0.46
1:A:529:LEU:O	1:A:530:ASN:CB	2.63	0.46
1:B:527:GLU:HG2	1:B:532:CYS:HA	1.98	0.46
1:B:321:ILE:O	1:B:322:LYS:HB2	2.15	0.46
1:B:333:VAL:HG11	1:B:460:GLN:NE2	2.31	0.46
1:A:513:SER:HB3	1:A:545:LYS:CD	2.46	0.46
1:A:539:LYS:HB2	1:A:539:LYS:NZ	2.30	0.46
1:B:599:GLU:HA	1:B:677:VAL:HG22	1.98	0.46
1:B:412:SER:O	1:B:413:TYR:CB	2.62	0.46
1:B:481:PHE:CE1	1:B:568:PRO:CB	2.93	0.46
1:B:370:ARG:NH2	1:B:429:TYR:O	2.35	0.46
1:B:468:GLU:C	1:B:469:ASN:O	2.53	0.46
1:B:646:VAL:HG22	1:B:666:ILE:HG13	1.98	0.46
1:B:580:LYS:O	1:B:581:ASP:C	2.52	0.46
1:A:511:VAL:HG11	1:A:519:MET:HE3	1.98	0.46
1:A:284:SER:OG	2:C:738:SER:N	2.48	0.46
1:A:321:ILE:CG1	1:A:322:LYS:N	2.79	0.46
1:B:422:ALA:O	1:B:424:GLU:N	2.49	0.46
1:B:521:ARG:CG	1:B:521:ARG:HH11	2.29	0.46
1:B:455:ARG:HG3	1:B:455:ARG:HH11	1.81	0.45
1:B:391:GLU:CG	1:B:409:VAL:HG21	2.46	0.45
1:A:397:ALA:HB2	1:A:449:LEU:HD11	1.97	0.45
1:B:721:ASP:HA	1:B:725:HIS:HE2	1.80	0.45
1:B:334:VAL:HG22	1:B:355:LYS:HB2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:410:SER:C	1:B:411:LYS:HG2	2.36	0.45
1:A:551:SER:O	1:A:552:LYS:C	2.55	0.45
1:B:625:ILE:HG22	1:B:663:SER:HB3	1.98	0.45
1:A:595:ILE:CG1	1:A:598:ARG:NH2	2.68	0.45
1:A:474:ASP:O	1:A:477:GLN:N	2.49	0.45
1:A:474:ASP:C	1:A:476:MET:N	2.68	0.45
1:B:710:LYS:O	1:B:711:GLU:C	2.54	0.45
1:A:737:ASN:OXT	2:C:739:GLY:HA3	2.16	0.45
1:A:333:VAL:HG11	1:A:460:GLN:OE1	2.16	0.45
1:A:598:ARG:HH11	1:A:639:SER:HB2	1.82	0.45
1:B:372:VAL:CG1	1:B:372:VAL:O	2.65	0.45
1:A:640:LEU:O	1:A:697:ARG:HD3	2.17	0.45
2:D:282:VAL:HG22	2:D:738:SER:H	1.82	0.45
1:A:313:LYS:CE	1:A:726:GLN:NE2	2.80	0.45
1:A:336:LYS:HE3	1:A:704:PHE:O	2.17	0.45
1:A:475:TYR:CB	1:A:576:LEU:HD21	2.47	0.44
1:A:331:TYR:CD1	1:A:360:ALA:HA	2.52	0.44
1:B:474:ASP:O	1:B:477:GLN:HG2	2.17	0.44
1:B:687:PHE:CD1	1:B:687:PHE:C	2.91	0.44
1:B:532:CYS:SG	1:B:534:GLU:CG	3.05	0.44
1:B:422:ALA:O	1:B:423:ASN:C	2.56	0.44
1:A:313:LYS:HE3	1:A:726:GLN:NE2	2.32	0.44
1:B:479:SER:HB2	1:B:481:PHE:HD2	1.82	0.44
1:A:539:LYS:O	1:A:540:GLU:HB3	2.17	0.44
1:A:607:ASP:OD2	1:A:682:ALA:N	2.43	0.44
1:B:591:SER:O	1:B:598:ARG:NH1	2.51	0.44
1:B:463:ALA:HB3	1:B:728:LEU:HD21	2.00	0.44
1:A:709:LEU:HA	1:A:709:LEU:HD23	1.78	0.44
1:A:308:ASN:HA	1:A:308:ASN:HD22	1.56	0.44
1:B:329:THR:O	1:B:359:ASN:HA	2.18	0.44
1:A:499:ILE:HG13	1:A:601:PHE:CZ	2.52	0.44
1:B:429:TYR:O	1:B:432:ALA:HB3	2.18	0.44
1:A:599:GLU:HB3	1:A:677:VAL:HG22	1.99	0.44
1:B:446:ASP:HB3	1:B:449:LEU:HD12	2.00	0.43
1:A:399:ASP:CG	1:A:401:ARG:NE	2.70	0.43
1:A:318:ARG:HB3	1:A:719:LEU:HD13	1.99	0.43
1:B:620:ALA:CB	1:B:668:MET:HE3	2.48	0.43
1:B:395:LYS:HG3	1:B:395:LYS:O	2.18	0.43
2:C:282:VAL:HA	2:C:740:GLU:HB3	2.00	0.43
1:B:323:LEU:O	1:B:325:ARG:HG2	2.18	0.43
1:A:540:GLU:H	1:A:541:PRO:HD3	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:301:ILE:O	1:B:304:ILE:HD12	2.17	0.43
1:A:605:LEU:CG	1:A:622:ILE:HD13	2.43	0.43
1:A:506:ARG:C	1:A:508:THR:N	2.72	0.43
1:B:310:VAL:O	1:B:318:ARG:N	2.49	0.43
1:B:415:ILE:O	1:B:417:GLU:N	2.51	0.43
1:B:321:ILE:HD11	1:B:720:SER:HA	1.99	0.43
1:A:459:TYR:CD2	1:A:701:GLY:HA3	2.54	0.43
1:A:480:LYS:HG3	1:A:483:LEU:CD2	2.30	0.43
1:A:629:VAL:O	1:A:630:ARG:C	2.56	0.43
1:A:293:MET:CE	1:A:309:LYS:O	2.66	0.43
1:A:675:LEU:O	1:A:678:LEU:N	2.52	0.43
1:A:284:SER:HA	2:C:738:SER:OG	2.18	0.43
1:B:378:THR:HG22	1:B:383:GLU:CA	2.43	0.43
1:B:581:ASP:O	1:B:583:VAL:HG22	2.19	0.43
1:B:409:VAL:CG1	1:B:410:SER:N	2.82	0.43
1:B:395:LYS:HB3	1:B:405:LEU:HD11	2.01	0.43
1:B:486:GLU:CD	1:B:528:LYS:HZ2	2.22	0.43
1:B:634:VAL:O	1:B:638:ARG:HB2	2.18	0.43
1:A:399:ASP:OD1	1:A:401:ARG:N	2.52	0.43
1:A:484:THR:HB	1:A:486:GLU:H	1.84	0.43
1:B:605:LEU:HD22	1:B:622:ILE:HG21	2.01	0.43
1:B:447:LEU:CD2	1:B:455:ARG:HE	2.31	0.43
1:A:509:PHE:CD1	1:A:511:VAL:HG23	2.54	0.43
1:A:532:CYS:HB3	1:A:552:LYS:HE3	2.01	0.43
1:B:565:THR:O	1:B:567:ASN:N	2.52	0.42
1:A:474:ASP:O	1:A:475:TYR:C	2.57	0.42
1:A:501:ASP:HB2	1:A:510:SER:O	2.19	0.42
1:A:401:ARG:NH1	1:A:445:ARG:NH2	2.66	0.42
1:B:308:ASN:N	1:B:308:ASN:HD22	2.17	0.42
1:B:540:GLU:HA	1:B:541:PRO:HD2	1.90	0.42
1:B:584:LYS:HD2	1:B:626:HIS:NE2	2.34	0.42
1:A:471:HIS:O	1:A:471:HIS:HD2	2.02	0.42
1:B:672:ASP:N	3:B:78:HOH:O	2.50	0.42
1:A:647:ASN:HB2	1:A:667:TYR:HE1	1.84	0.42
1:A:325:ARG:HG2	1:A:325:ARG:HH11	1.83	0.42
1:B:360:ALA:HB1	1:B:445:ARG:HB3	2.01	0.42
1:A:538:ARG:NH1	1:A:545:LYS:HZ1	2.17	0.42
1:B:403:VAL:HG11	1:B:449:LEU:HD13	2.01	0.42
1:A:500:GLY:HA3	1:A:608:SER:HB2	1.99	0.42
1:A:503:LEU:HD12	1:A:508:THR:HG22	2.00	0.42
1:A:672:ASP:O	1:A:673:VAL:C	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:419:PRO:O	1:B:420:GLU:C	2.57	0.42
2:D:283:GLY:O	2:D:738:SER:CB	2.67	0.42
1:B:550:TYR:HE1	1:B:563:LEU:HB2	1.83	0.42
1:B:636:LEU:O	1:B:639:SER:OG	2.27	0.42
1:A:479:SER:HB3	1:A:480:LYS:HZ2	1.84	0.42
1:A:333:VAL:HG22	1:A:706:LEU:CD1	2.49	0.42
1:B:462:TYR:CZ	1:B:700:ARG:HB2	2.55	0.42
2:D:281:TYR:CD2	2:D:282:VAL:HG12	2.55	0.42
2:C:283:GLY:O	2:C:738:SER:CB	2.68	0.42
1:B:317:PRO:N	3:B:38:HOH:O	2.52	0.42
1:A:500:GLY:HA3	1:A:608:SER:CB	2.50	0.42
1:B:491:LEU:HG	1:B:495:LEU:CD1	2.50	0.42
1:A:372:VAL:CG2	1:A:426:VAL:HG13	2.49	0.42
1:A:324:PRO:HD2	1:A:716:GLY:O	2.20	0.42
1:B:565:THR:O	1:B:566:GLU:HB2	2.19	0.42
1:B:622:ILE:CG2	1:B:623:LYS:N	2.83	0.42
1:B:336:LYS:HG3	1:B:705:GLU:CG	2.48	0.42
1:A:523:THR:CG2	1:A:524:GLU:N	2.82	0.42
1:A:385:PHE:CE2	1:A:419:PRO:HD3	2.54	0.42
1:B:587:PRO:HB2	1:B:589:PHE:CD2	2.55	0.42
1:A:336:LYS:N	1:A:704:PHE:HA	2.34	0.42
1:A:302:GLU:HG2	1:A:303:ASN:N	2.35	0.42
1:A:622:ILE:CG2	1:A:623:LYS:N	2.82	0.42
1:B:399:ASP:OD2	1:B:401:ARG:NE	2.53	0.42
1:A:666:ILE:N	1:A:666:ILE:CD1	2.82	0.42
1:A:595:ILE:HA	1:A:598:ARG:HE	1.85	0.42
1:A:726:GLN:OE1	1:A:734:VAL:HG11	2.19	0.41
1:B:399:ASP:OD1	1:B:401:ARG:CG	2.65	0.41
1:A:676:ASN:HA	3:A:98:HOH:O	2.20	0.41
1:B:602:LEU:O	1:B:603:ALA:C	2.57	0.41
1:A:724:ASP:O	1:A:725:HIS:CB	2.69	0.41
1:B:293:MET:HE1	1:B:310:VAL:HG12	2.02	0.41
1:A:302:GLU:HG2	1:A:303:ASN:H	1.85	0.41
1:A:647:ASN:HD22	1:A:647:ASN:HA	1.61	0.41
1:B:382:VAL:HB	1:B:384:TYR:CE1	2.55	0.41
1:B:639:SER:HA	1:B:732:GLN:NE2	2.35	0.41
1:B:642:LEU:HD23	1:B:673:VAL:HG12	2.03	0.41
1:A:521:ARG:O	1:A:525:TYR:HB2	2.20	0.41
1:A:418:GLY:C	1:A:420:GLU:N	2.73	0.41
1:B:303:ASN:HD22	1:B:303:ASN:N	2.18	0.41
1:B:489:LYS:CA	1:B:489:LYS:HE3	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:282:VAL:HG13	2:C:283:GLY:N	2.34	0.41
1:B:291:VAL:CG1	1:B:292:LEU:N	2.83	0.41
1:B:481:PHE:HZ	1:B:568:PRO:O	2.04	0.41
1:A:295:ASP:OD1	1:A:297:SER:OG	2.22	0.41
1:A:493:TYR:O	1:A:497:LEU:HB2	2.21	0.41
1:A:421:ARG:C	1:A:423:ASN:N	2.71	0.41
1:B:457:ALA:HA	3:B:94:HOH:O	2.20	0.41
1:A:331:TYR:HE1	1:A:360:ALA:HB1	1.85	0.41
1:B:366:VAL:HB	1:B:458:THR:HG22	2.02	0.41
1:B:503:LEU:HD13	1:B:508:THR:HG22	2.03	0.41
1:A:300:CYS:HB3	1:A:302:GLU:OE1	2.21	0.41
1:B:521:ARG:HG2	1:B:682:ALA:CB	2.51	0.41
1:B:533:ALA:O	1:B:534:GLU:O	2.38	0.41
1:B:293:MET:HA	1:B:293:MET:CE	2.47	0.41
1:A:399:ASP:CG	1:A:400:GLY:N	2.74	0.41
1:A:567:ASN:HA	1:A:568:PRO:HD2	1.72	0.41
1:A:687:PHE:O	1:A:688:ARG:NH1	2.47	0.41
1:B:447:LEU:HD21	1:B:455:ARG:HE	1.85	0.41
1:A:541:PRO:O	1:A:542:GLN:HB2	2.21	0.41
1:B:617:GLY:O	1:B:618:ILE:C	2.58	0.41
1:A:369:PRO:HD2	1:A:457:ALA:O	2.20	0.41
2:C:282:VAL:HG22	2:C:738:SER:H	1.85	0.41
1:B:573:ILE:HG22	1:B:573:ILE:O	2.21	0.41
1:A:379:ILE:O	1:A:379:ILE:HG22	2.20	0.41
1:B:666:ILE:CD1	1:B:666:ILE:N	2.84	0.41
1:B:692:ALA:O	1:B:693:ALA:HB2	2.20	0.41
1:A:452:SER:O	1:A:453:HIS:C	2.59	0.41
1:A:359:ASN:ND2	2:C:283:GLY:CA	2.76	0.40
1:B:292:LEU:HD21	1:B:311:MET:HE2	2.03	0.40
1:B:426:VAL:O	1:B:430:ARG:HG2	2.20	0.40
1:B:447:LEU:HD21	1:B:455:ARG:NH2	2.36	0.40
1:A:504:SER:O	1:A:505:ASP:HB3	2.21	0.40
1:B:587:PRO:HB2	1:B:589:PHE:CE2	2.55	0.40
1:B:375:LEU:N	1:B:375:LEU:HD23	2.35	0.40
1:B:507:ALA:H	1:B:563:LEU:CD2	2.34	0.40
1:B:481:PHE:O	1:B:482:HIS:O	2.39	0.40
1:B:302:GLU:C	1:B:304:ILE:N	2.72	0.40
1:B:529:LEU:O	1:B:530:ASN:HB2	2.20	0.40
1:B:581:ASP:O	1:B:583:VAL:N	2.50	0.40
1:B:618:ILE:HA	1:B:618:ILE:HD12	1.79	0.40
1:B:649:GLU:HA	1:B:650:PRO:HD3	1.84	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:435:LYS:HE3	1:B:435:LYS:HB2	1.91	0.40
1:A:737:ASN:OXT	1:A:737:ASN:ND2	2.54	0.40
1:B:293:MET:HE3	1:B:310:VAL:HG12	2.00	0.40
1:B:520:GLU:HG3	1:B:520:GLU:H	1.52	0.40
1:B:535:TYR:CE1	1:B:538:ARG:NH2	2.90	0.40
1:B:491:LEU:HG	1:B:495:LEU:HD11	2.03	0.40
1:B:471:HIS:HB3	1:B:589:PHE:CD1	2.57	0.40
1:B:375:LEU:HD23	1:B:375:LEU:H	1.87	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	409/454 (90%)	311 (76%)	65 (16%)	33 (8%)	1	2
1	B	411/454 (90%)	326 (79%)	59 (14%)	26 (6%)	2	5
2	C	5/21 (24%)	2 (40%)	0	3 (60%)	0	0
2	D	5/21 (24%)	3 (60%)	1 (20%)	1 (20%)	0	0
All	All	830/950 (87%)	642 (77%)	125 (15%)	63 (8%)	1	3

All (63) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	416	SER
1	A	452	SER
1	A	470	ASP
1	A	505	ASP
1	A	510	SER
1	A	530	ASN
1	A	539	LYS

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Mol	Chain	Res	Type
1	A	540	GLU
1	A	684	SER
1	A	710	LYS
1	B	303	ASN
1	B	413	TYR
1	B	422	ALA
1	B	423	ASN
1	B	452	SER
1	B	475	TYR
1	B	530	ASN
1	B	661	LYS
2	C	282	VAL
2	D	738	SER
1	A	313	LYS
1	A	401	ARG
1	A	415	ILE
1	A	418	GLY
1	A	475	TYR
1	A	484	THR
1	A	500	GLY
1	A	568	PRO
1	A	581	ASP
1	A	595	ILE
1	A	718	THR
1	A	720	SER
1	B	372	VAL
1	B	416	SER
1	B	420	GLU
1	B	474	ASP
1	B	482	HIS
1	B	534	GLU
1	B	564	ASN
1	B	578	PHE
1	B	608	SER
1	B	630	ARG
2	C	738	SER
1	A	328	GLU
1	A	542	GLN
1	B	353	LEU
1	B	469	ASN
1	B	471	HIS
2	C	283	GLY

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Mol	Chain	Res	Type
1	A	481	PHE
1	A	537	ASP
1	A	538	ARG
1	B	479	SER
1	B	541	PRO
1	A	380	LYS
1	A	471	HIS
1	B	442	ILE
1	A	477	GLN
1	A	482	HIS
1	B	399	ASP
1	B	582	GLY
1	A	670	GLY
1	A	419	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	360/392 (92%)	321 (89%)	39 (11%)	8	24
1	B	362/392 (92%)	326 (90%)	36 (10%)	10	29
2	C	5/16 (31%)	4 (80%)	1 (20%)	1	5
2	D	5/16 (31%)	4 (80%)	1 (20%)	1	5
All	All	732/816 (90%)	655 (90%)	77 (10%)	8	25

All (77) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	285	PHE
1	A	299	GLU
1	A	308	ASN
1	A	357	THR
1	A	361	THR
1	A	362	ASN
1	A	380	LYS

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Mol	Chain	Res	Type
1	A	396	LYS
1	A	399	ASP
1	A	405	LEU
1	A	412	SER
1	A	413	TYR
1	A	416	SER
1	A	433	SER
1	A	435	LYS
1	A	442	ILE
1	A	470	ASP
1	A	482	HIS
1	A	483	LEU
1	A	484	THR
1	A	501	ASP
1	A	504	SER
1	A	516	THR
1	A	523	THR
1	A	527	GLU
1	A	531	LEU
1	A	535	TYR
1	A	538	ARG
1	A	539	LYS
1	A	542	GLN
1	A	552	LYS
1	A	607	ASP
1	A	614	ASP
1	A	647	ASN
1	A	691	PRO
1	A	713	ASP
1	A	715	TYR
1	A	724	ASP
1	A	737	ASN
1	B	285	PHE
1	B	303	ASN
1	B	305	GLU
1	B	323	LEU
1	B	374	ARG
1	B	384	TYR
1	B	385	PHE
1	B	395	LYS
1	B	398	PRO
1	B	405	LEU

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Mol	Chain	Res	Type
1	B	425	LEU
1	B	442	ILE
1	B	456	LYS
1	B	478	LYS
1	B	483	LEU
1	B	489	LYS
1	B	508	THR
1	B	516	THR
1	B	520	GLU
1	B	521	ARG
1	B	529	LEU
1	B	531	LEU
1	B	532	CYS
1	B	535	TYR
1	B	543	VAL
1	B	550	TYR
1	B	594	ASN
1	B	605	LEU
1	B	676	ASN
1	B	686	LYS
1	B	691	PRO
1	B	698	GLU
1	B	712	ASP
1	B	714	TYR
1	B	717	ILE
1	B	737	ASN
2	C	738	SER
2	D	282	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	303	ASN
1	A	362	ASN
1	A	469	ASN
1	A	471	HIS
1	A	647	ASN
1	A	737	ASN
1	B	303	ASN
1	B	308	ASN
1	B	548	ASN
1	B	737	ASN

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 [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section will therefore be empty.

6.4 Ligands [i](#)

EDS was not executed - this section will therefore be empty.

6.5 Other polymers [i](#)

EDS was not executed - this section will therefore be empty.