Full wwPDB X-ray Structure Validation Report (i)

Jan 31, 2016 – 08:20 PM GMT

PDB ID	:	1JVA
Title	:	CRYSTAL STRUCTURE OF THE VMA1-DERIVED ENDONUCLEASE BEARING THE N AND C EXTEIN PROPEPTIDES
Authors	:	Mizutani, R.; Satow, Y.
Deposited on	:	2001-08-29
Resolution	:	2.10 Å(reported)

The following versions of software and data (see references (i)) 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 (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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.
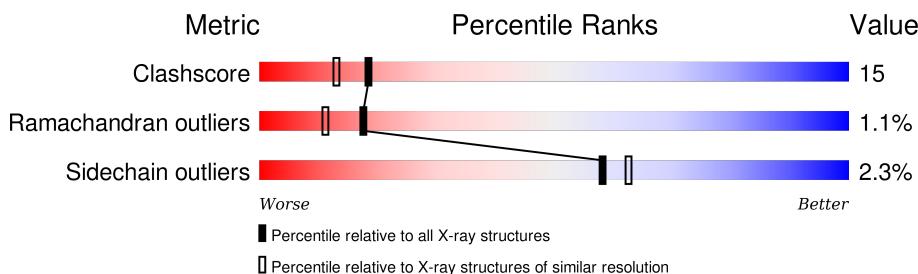
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	102246	4460 (2.10-2.10)
Ramachandran outliers	100387	4413 (2.10-2.10)
Sidechain outliers	100360	4414 (2.10-2.10)

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 <=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	475	
1	B	475	
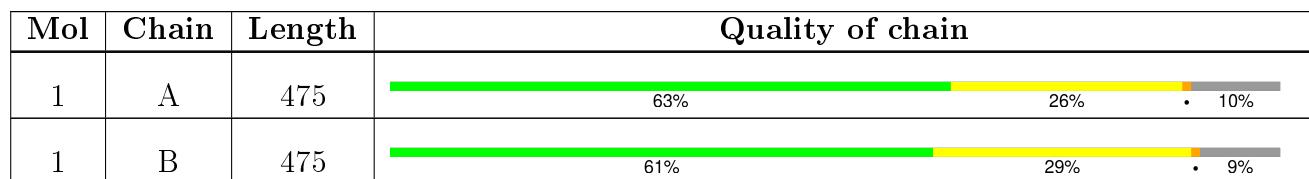
2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 6960 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 VMA1-DERIVED HOMING ENDONUCLEASE X10SSS.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	427	Total 3363	C 2132	N 574	O 645	S 12	0	0	0
1	B	430	Total 3392	C 2152	N 579	O 649	S 12	0	0	0

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	273	MET	-	INITIATING MET	UNP P17255
A	284	SER	CYS	ENGINEERED	UNP P17255
A	362	ASN	HIS	ENGINEERED	UNP P17255
A	737	SER	ASN	ENGINEERED	UNP P17255
A	738	SER	CYS	ENGINEERED	UNP P17255
B	273	MET	-	INITIATING MET	UNP P17255
B	284	SER	CYS	ENGINEERED	UNP P17255
B	362	ASN	HIS	ENGINEERED	UNP P17255
B	737	SER	ASN	ENGINEERED	UNP P17255
B	738	SER	CYS	ENGINEERED	UNP P17255

- Molecule 2 is water.

| Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	93	Total 93	O 93	0	0
2	B	112	Total 112	O 112	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.

Note EDS was not executed.

- Molecule 1: VMA1-DERIVED HOMING ENDONUCLEASE X10SSS
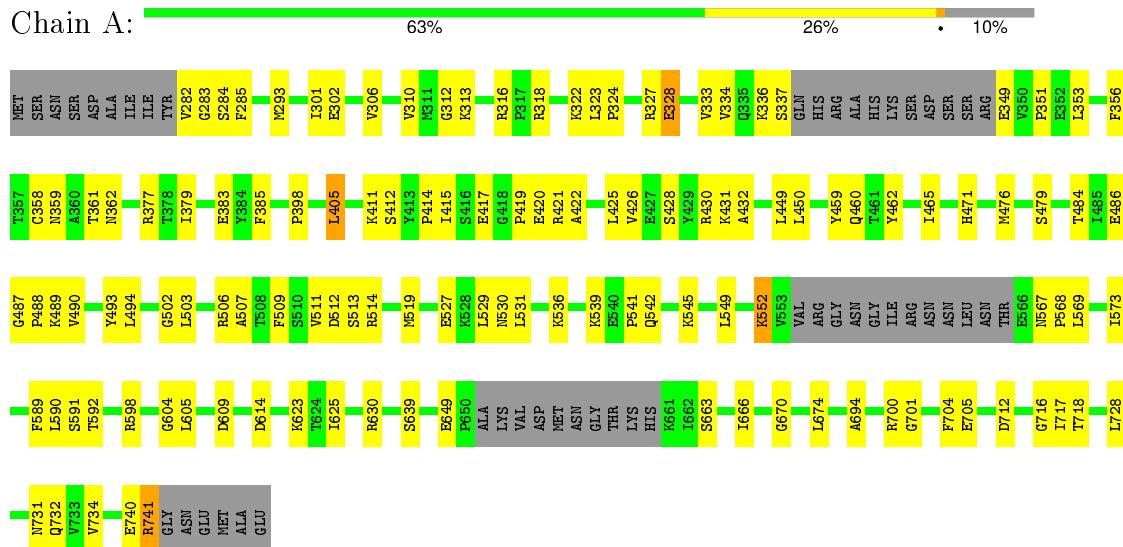
- Molecule 1: VMA1-DERIVED HOMING ENDONUCLEASE X10SSS
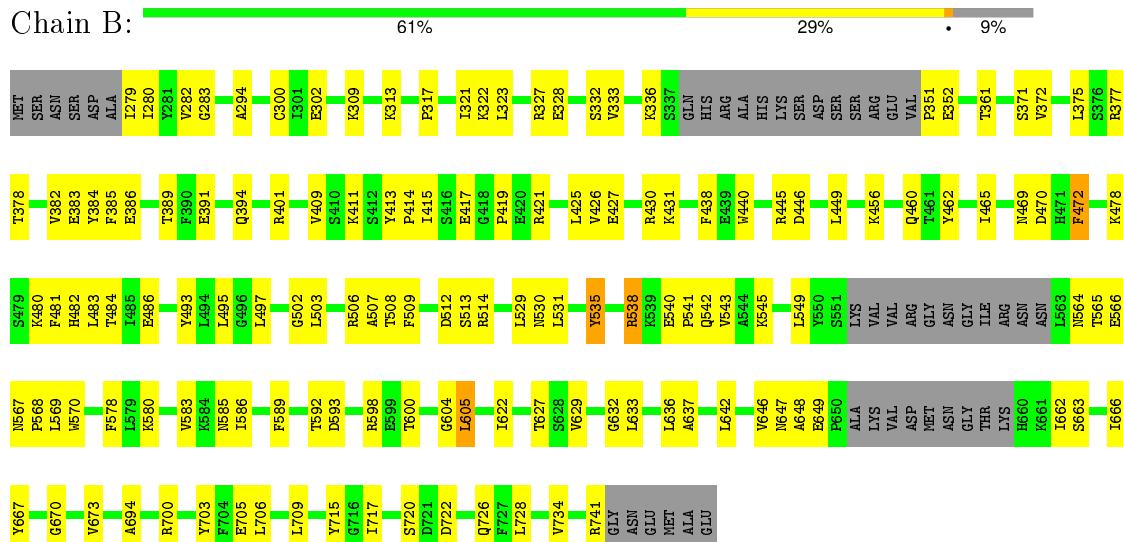
4 Data and refinement statistics (i)

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	66.18Å 68.85Å 58.52Å 103.10° 98.79° 78.98°	Depositor
Resolution (Å)	30.00 – 2.10	Depositor
% Data completeness (in resolution range)	89.4 (30.00-2.10)	Depositor
R_{merge}	0.03	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.198 , 0.240	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6960	wwPDB-VP
Average B, all atoms (Å^2)	25.0	wwPDB-VP

5 Model quality (i)

5.1 Standard geometry (i)

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	0.35	0/3423	0.57	0/4618
1	B	0.37	0/3454	0.60	0/4661
All	All	0.36	0/6877	0.59	0/9279

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3363	0	3365	98	0
1	B	3392	0	3391	117	0
2	A	93	0	0	1	0
2	B	112	0	0	2	0
All	All	6960	0	6756	209	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 15.

All (209) 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:538:ARG:H	1:B:538:ARG:HE	1.20	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:283:GLY:HA2	1:B:361:THR:HG23	1.63	0.80
1:A:414:PRO:HD2	1:A:417:GLU:OE1	1.81	0.79
1:B:535:TYR:N	1:B:535:TYR:CD1	2.50	0.79
1:A:336:LYS:HG2	1:A:705:GLU:HG3	1.64	0.78
1:A:283:GLY:HA2	1:A:361:THR:HG23	1.66	0.78
1:A:625:ILE:HD12	1:A:625:ILE:H	1.50	0.76
1:A:567:ASN:HB2	1:A:568:PRO:HD2	1.65	0.76
1:A:625:ILE:HD12	1:A:625:ILE:N	2.01	0.74
1:B:481:PHE:CE1	1:B:568:PRO:HB2	2.23	0.74
1:B:648:ALA:HB1	1:B:662:ILE:HD11	1.70	0.74
1:A:694:ALA:HB2	1:B:430:ARG:HH12	1.55	0.72
1:A:486:GLU:HB2	1:A:489:LYS:HE2	1.71	0.71
1:A:623:LYS:HE3	1:A:649:GLU:HG3	1.74	0.69
1:B:538:ARG:NE	1:B:538:ARG:H	1.89	0.69
1:B:426:VAL:O	1:B:430:ARG:HG2	1.94	0.68
1:B:502:GLY:HA2	1:B:509:PHE:HA	1.78	0.65
1:A:285:PHE:HA	1:A:358:CYS:HA	1.79	0.64
1:B:336:LYS:HD3	1:B:703:TYR:HB3	1.79	0.64
1:B:300:CYS:HB3	1:B:302:GLU:OE1	1.98	0.63
1:B:472:PHE:HZ	1:B:495:LEU:HD12	1.63	0.63
1:A:411:LYS:HD2	1:A:425:LEU:HD21	1.80	0.62
1:B:513:SER:HB3	1:B:545:LYS:HD2	1.81	0.62
1:A:377:ARG:HD2	1:A:379:ILE:HD11	1.81	0.62
1:B:538:ARG:N	1:B:538:ARG:HE	1.96	0.62
1:B:465:ILE:HG21	1:B:592:THR:HG22	1.80	0.62
1:B:717:ILE:O	1:B:717:ILE:HG13	1.98	0.61
1:B:411:LYS:HG3	1:B:425:LEU:HD11	1.81	0.61
1:B:531:LEU:HD11	1:B:568:PRO:HG2	1.82	0.61
1:B:322:LYS:HG2	1:B:323:LEU:H	1.65	0.60
1:A:741:ARG:N	1:A:741:ARG:HD3	2.16	0.60
1:B:401:ARG:HD3	1:B:741:ARG:NH1	2.16	0.60
1:A:322:LYS:O	1:A:323:LEU:HD23	2.01	0.60
1:A:502:GLY:HA2	1:A:509:PHE:HA	1.84	0.60
1:B:413:TYR:HH	1:B:419:PRO:HA	1.67	0.59
1:B:507:ALA:HB2	1:B:570:TRP:HB2	1.85	0.59
1:A:310:VAL:HG23	1:A:318:ARG:HB2	1.85	0.59
1:A:428:SER:O	1:A:432:ALA:HB2	2.03	0.59
1:A:536:LYS:H	1:A:536:LYS:HD2	1.67	0.59
1:A:430:ARG:NH1	1:B:694:ALA:HB2	2.17	0.58
1:B:372:VAL:HG23	1:B:389:THR:HG22	1.85	0.58
1:B:493:TYR:HB2	1:B:600:THR:HG22	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:324:PRO:HD2	1:A:716:GLY:O	2.04	0.58
1:A:336:LYS:HG2	1:A:705:GLU:CG	2.32	0.58
1:A:649:GLU:HB2	1:A:663:SER:HB3	1.84	0.58
1:A:337:SER:OG	1:A:353:LEU:HD21	2.03	0.58
1:B:646:VAL:HG12	1:B:647:ASN:N	2.18	0.58
1:B:413:TYR:OH	1:B:419:PRO:HA	2.03	0.57
1:A:322:LYS:HB2	1:A:718:THR:HB	1.85	0.57
1:B:322:LYS:HG2	1:B:323:LEU:N	2.20	0.57
1:B:493:TYR:HB2	1:B:600:THR:CG2	2.35	0.57
1:A:716:GLY:O	1:A:717:ILE:HD12	2.05	0.57
1:B:586:ILE:HB	1:B:632:GLY:HA3	1.87	0.57
1:B:514:ARG:NH2	1:B:543:VAL:HG11	2.20	0.57
1:B:279:ILE:HG22	1:B:280:ILE:HG13	1.87	0.57
1:A:531:LEU:HD21	1:A:568:PRO:HD2	1.87	0.56
1:A:486:GLU:OE1	1:B:377:ARG:HA	2.04	0.56
1:B:478:LYS:O	1:B:478:LYS:HG2	2.06	0.56
1:A:334:VAL:HG13	1:A:705:GLU:HB2	1.88	0.56
1:B:549:LEU:HD22	1:B:569:LEU:HD22	1.86	0.56
1:A:283:GLY:CA	1:A:361:THR:HG23	2.36	0.56
1:A:282:VAL:O	1:A:282:VAL:HG13	2.05	0.56
1:A:349:GLU:O	1:A:351:PRO:HD3	2.05	0.56
1:A:507:ALA:HB1	1:A:569:LEU:HD23	1.88	0.55
1:A:431:LYS:HG3	1:A:431:LYS:O	2.06	0.55
1:B:480:LYS:HA	1:B:480:LYS:HE2	1.86	0.55
1:A:417:GLU:CD	1:A:421:ARG:HH22	2.10	0.55
1:B:351:PRO:HB2	1:B:352:GLU:OE1	2.07	0.55
1:A:383:GLU:O	1:A:415:ILE:HG12	2.06	0.55
1:A:623:LYS:CE	1:A:649:GLU:HG3	2.38	0.54
1:B:666:ILE:N	1:B:666:ILE:HD12	2.23	0.54
1:B:503:LEU:N	1:B:503:LEU:HD12	2.23	0.54
1:B:540:GLU:HG3	1:B:541:PRO:HD2	1.88	0.54
1:B:535:TYR:CD2	1:B:538:ARG:HG3	2.43	0.54
1:B:649:GLU:N	1:B:663:SER:O	2.41	0.54
1:A:283:GLY:HA3	1:A:362:ASN:HA	1.90	0.54
1:B:605:LEU:HD13	1:B:622:ILE:HD13	1.88	0.54
1:B:565:THR:O	1:B:566:GLU:HB2	2.08	0.54
1:B:637:ALA:O	1:B:642:LEU:HB2	2.09	0.53
1:B:414:PRO:O	1:B:417:GLU:HG2	2.08	0.53
1:B:531:LEU:HD11	1:B:568:PRO:CG	2.39	0.53
1:B:294:ALA:HB1	1:B:317:PRO:HB3	1.89	0.53
1:A:465:ILE:HD12	1:A:639:SER:HB2	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:536:LYS:O	1:A:539:LYS:HG2	2.09	0.53
1:B:535:TYR:HD1	1:B:535:TYR:N	2.03	0.52
1:B:462:TYR:CZ	1:B:700:ARG:HB2	2.44	0.52
1:A:324:PRO:HD2	1:A:716:GLY:C	2.29	0.52
1:B:383:GLU:O	1:B:415:ILE:HG12	2.09	0.52
1:A:327:ARG:O	1:A:328:GLU:HB2	2.10	0.52
1:A:336:LYS:NZ	1:A:705:GLU:HG2	2.25	0.51
1:A:336:LYS:HD2	1:A:704:PHE:O	2.09	0.51
1:B:647:ASN:HB2	1:B:667:TYR:HE1	1.76	0.51
1:B:564:ASN:O	1:B:567:ASN:HB3	2.10	0.51
1:A:625:ILE:N	1:A:625:ILE:CD1	2.72	0.51
1:A:284:SER:H	1:A:359:ASN:CG	2.13	0.51
1:A:312:GLY:HA3	1:A:318:ARG:NH1	2.25	0.51
1:B:375:LEU:HD23	1:B:375:LEU:N	2.26	0.51
1:B:535:TYR:CE1	1:B:538:ARG:HD3	2.46	0.50
1:A:336:LYS:HG3	1:A:704:PHE:CA	2.41	0.50
1:A:283:GLY:HA2	1:A:359:ASN:HD21	1.75	0.50
1:B:352:GLU:OE1	1:B:352:GLU:N	2.45	0.50
1:B:503:LEU:H	1:B:503:LEU:HD12	1.75	0.50
1:B:483:LEU:N	1:B:483:LEU:HD23	2.27	0.50
1:A:282:VAL:HG21	1:A:324:PRO:CG	2.42	0.50
1:A:569:LEU:O	1:A:573:ILE:HG13	2.11	0.50
1:A:731:ASN:O	1:A:732:GLN:HB2	2.12	0.50
1:B:333:VAL:HG22	1:B:706:LEU:CD1	2.42	0.50
1:B:430:ARG:HH11	1:B:430:ARG:HG3	1.75	0.49
1:A:625:ILE:H	1:A:625:ILE:CD1	2.23	0.49
1:A:313:LYS:HG2	2:A:4:HOH:O	2.11	0.49
1:B:598:ARG:HG2	1:B:636:LEU:HD11	1.94	0.49
1:B:313:LYS:HG2	2:B:40:HOH:O	2.12	0.49
1:A:694:ALA:H	1:B:430:ARG:NH1	2.11	0.49
1:B:378:THR:HG22	1:B:383:GLU:HG2	1.95	0.49
1:B:391:GLU:OE2	1:B:409:VAL:HG21	2.13	0.49
1:A:316:ARG:HH11	1:A:316:ARG:HG3	1.77	0.49
1:A:591:SER:O	1:A:598:ARG:CZ	2.61	0.49
1:A:336:LYS:HZ1	1:A:705:GLU:HG2	1.78	0.48
1:A:333:VAL:HG21	1:A:356:PHE:CZ	2.49	0.48
1:B:580:LYS:O	1:B:583:VAL:HG22	2.13	0.48
1:A:419:PRO:O	1:A:420:GLU:C	2.52	0.48
1:A:549:LEU:HD22	1:A:569:LEU:HD22	1.96	0.48
1:B:495:LEU:HD13	1:B:578:PHE:CE2	2.49	0.47
1:A:383:GLU:C	1:A:415:ILE:HG12	2.35	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:293:MET:HA	1:A:293:MET:HE3	1.96	0.47
1:A:490:VAL:O	1:A:494:LEU:HG	2.14	0.47
1:B:565:THR:C	1:B:567:ASN:H	2.17	0.47
1:A:476:MET:HG3	1:A:488:PRO:HG3	1.96	0.47
1:A:511:VAL:HG12	1:A:512:ASP:N	2.29	0.47
1:B:673:VAL:HG23	2:B:87:HOH:O	2.14	0.47
1:A:459:TYR:CD2	1:A:701:GLY:HA3	2.49	0.47
1:B:580:LYS:HE3	1:B:585:ASN:ND2	2.30	0.47
1:A:405:LEU:HD22	1:A:450:LEU:HD23	1.96	0.47
1:B:662:ILE:O	1:B:662:ILE:HG23	2.14	0.46
1:B:427:GLU:OE2	1:B:431:LYS:HD2	2.15	0.46
1:A:694:ALA:CB	1:B:430:ARG:HH12	2.27	0.46
1:A:716:GLY:C	1:A:717:ILE:HD12	2.35	0.46
1:B:378:THR:HA	1:B:382:VAL:O	2.15	0.46
1:A:513:SER:OG	1:A:545:LYS:HG2	2.16	0.46
1:B:512:ASP:OD1	1:B:514:ARG:HB2	2.15	0.46
1:B:648:ALA:HA	1:B:663:SER:O	2.16	0.46
1:B:514:ARG:HH21	1:B:543:VAL:HG11	1.81	0.45
1:B:382:VAL:HB	1:B:384:TYR:CE1	2.50	0.45
1:A:336:LYS:HG3	1:A:704:PHE:C	2.36	0.45
1:A:694:ALA:HB2	1:B:430:ARG:NH1	2.28	0.45
1:B:282:VAL:O	1:B:282:VAL:HG13	2.15	0.45
1:B:513:SER:HB3	1:B:545:LYS:CD	2.46	0.45
1:B:430:ARG:NH1	1:B:430:ARG:HG3	2.31	0.45
1:A:460:GLN:O	1:A:701:GLY:HA2	2.17	0.45
1:B:327:ARG:O	1:B:328:GLU:HB2	2.17	0.45
1:B:371:SER:O	1:B:389:THR:HA	2.16	0.45
1:A:630:ARG:HG3	1:A:666:ILE:HD11	1.97	0.45
1:B:333:VAL:HG11	1:B:460:GLN:HE22	1.80	0.45
1:A:674:LEU:O	1:A:674:LEU:HD12	2.17	0.45
1:B:446:ASP:O	1:B:449:LEU:HB2	2.17	0.45
1:B:294:ALA:CB	1:B:317:PRO:HB3	2.47	0.44
1:B:469:ASN:C	1:B:469:ASN:OD1	2.55	0.44
1:A:740:GLU:H	1:A:740:GLU:CD	2.21	0.44
1:A:398:PRO:HD3	1:A:449:LEU:HD21	1.98	0.44
1:B:321:ILE:HG13	1:B:322:LYS:N	2.33	0.44
1:B:391:GLU:HA	1:B:438:PHE:CZ	2.52	0.44
1:B:540:GLU:HG2	1:B:542:GLN:H	1.83	0.43
1:A:333:VAL:HG11	1:A:460:GLN:OE1	2.18	0.43
1:A:493:TYR:CE1	1:A:604:GLY:HA2	2.53	0.43
1:B:440:TRP:CD1	1:B:440:TRP:N	2.86	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:715:TYR:CD1	1:B:715:TYR:N	2.86	0.43
1:B:649:GLU:HB2	1:B:663:SER:HB3	1.99	0.43
1:B:483:LEU:H	1:B:483:LEU:HD23	1.83	0.43
1:A:536:LYS:H	1:A:536:LYS:CD	2.31	0.43
1:B:586:ILE:HG12	1:B:629:VAL:HA	2.00	0.43
1:A:740:GLU:O	1:A:741:ARG:HB3	2.18	0.43
1:A:639:SER:HA	1:A:732:GLN:NE2	2.33	0.43
1:B:313:LYS:HE3	1:B:726:GLN:OE1	2.19	0.43
1:B:728:LEU:CD2	1:B:734:VAL:HG22	2.48	0.43
1:B:309:LYS:HB3	1:B:317:PRO:HB2	2.01	0.43
1:A:605:LEU:HD12	1:A:609:ASP:OD1	2.19	0.43
1:B:720:SER:OG	1:B:722:ASP:OD1	2.35	0.43
1:B:484:THR:HG22	1:B:486:GLU:OE1	2.19	0.42
1:B:646:VAL:HG12	1:B:647:ASN:H	1.84	0.42
1:B:469:ASN:OD1	1:B:593:ASP:HA	2.19	0.42
1:A:462:TYR:CE2	1:A:700:ARG:HB2	2.54	0.42
1:A:471:HIS:HB3	1:A:589:PHE:CD1	2.55	0.42
1:B:413:TYR:CD2	1:B:421:ARG:HD3	2.55	0.42
1:B:633:LEU:HG	1:B:666:ILE:HG21	2.00	0.42
1:B:361:THR:HB	1:B:445:ARG:HH22	1.84	0.42
1:A:494:LEU:HD12	1:A:529:LEU:HD12	2.00	0.42
1:A:385:PHE:O	1:A:412:SER:HA	2.20	0.42
1:A:465:ILE:HG21	1:A:592:THR:HG22	2.02	0.42
1:A:422:ALA:O	1:A:426:VAL:HG23	2.20	0.41
1:A:503:LEU:HD12	1:A:506:ARG:HD2	2.02	0.41
1:A:417:GLU:HB2	1:A:421:ARG:NH2	2.34	0.41
1:B:385:PHE:CZ	1:B:415:ILE:HG23	2.56	0.41
1:B:462:TYR:CE2	1:B:700:ARG:HB2	2.55	0.41
1:B:497:LEU:HD23	1:B:604:GLY:O	2.21	0.41
1:A:530:ASN:ND2	1:A:552:LYS:O	2.54	0.41
1:A:284:SER:N	1:A:359:ASN:ND2	2.69	0.41
1:B:646:VAL:CG1	1:B:647:ASN:N	2.84	0.41
1:A:487:GLY:N	1:A:488:PRO:CD	2.84	0.41
1:B:336:LYS:HG2	1:B:705:GLU:HG3	2.02	0.41
1:B:529:LEU:O	1:B:530:ASN:HB2	2.21	0.41
1:A:377:ARG:CD	1:A:379:ILE:HD11	2.50	0.40
1:B:332:SER:HB3	1:B:709:LEU:HD11	2.03	0.40
1:B:361:THR:HB	1:B:445:ARG:NH2	2.36	0.40
1:A:301:ILE:HG23	1:A:302:GLU:N	2.36	0.40
1:A:310:VAL:HG22	1:A:318:ARG:O	2.22	0.40
1:B:375:LEU:HD23	1:B:386:GLU:O	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:506:ARG:HG3	1:B:508:THR:HB	2.03	0.40
1:A:728:LEU:CD2	1:A:734:VAL:HG22	2.52	0.40
1:B:589:PHE:C	1:B:589:PHE:CD1	2.95	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	419/475 (88%)	387 (92%)	25 (6%)	7 (2%)	11	5
1	B	422/475 (89%)	395 (94%)	25 (6%)	2 (0%)	34	30
All	All	841/950 (88%)	782 (93%)	50 (6%)	9 (1%)	17	11

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	479	SER
1	A	552	LYS
1	B	670	GLY
1	A	670	GLY
1	B	482	HIS
1	A	328	GLU
1	A	484	THR
1	A	306	VAL
1	A	541	PRO

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	368/408 (90%)	359 (98%)	9 (2%)	57	61
1	B	371/408 (91%)	363 (98%)	8 (2%)	60	64
All	All	739/816 (91%)	722 (98%)	17 (2%)	58	62

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	405	LEU
1	A	514	ARG
1	A	519	MET
1	A	527	GLU
1	A	542	GLN
1	A	590	LEU
1	A	614	ASP
1	A	712	ASP
1	A	741	ARG
1	B	394	GLN
1	B	456	LYS
1	B	470	ASP
1	B	472	PHE
1	B	535	TYR
1	B	538	ARG
1	B	605	LEU
1	B	627	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	303	ASN
1	A	308	ASN
1	A	362	ASN
1	A	530	ASN
1	A	647	ASN
1	B	303	ASN
1	B	362	ASN
1	B	460	GLN
1	B	548	ASN
1	B	647	ASN
1	B	732	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (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.