Full wwPDB X-ray Structure Validation Report (i)

Jan 31, 2016 – 07:48 PM GMT

PDB ID	:	1HCI
Title	:	CRYSTAL STRUCTURE OF THE ROD DOMAIN OF ALPHA-ACTININ
Authors	:	Ylanne, J.; Scheffzek, K.; Young, P.; Saraste, M.
Deposited on	:	2001-05-04
Resolution	:	2.80 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

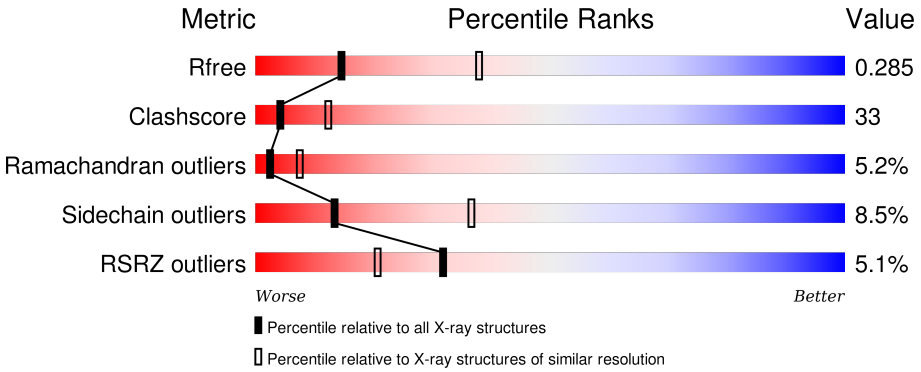
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.80 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	2393 (2.80-2.80)
Clashscore	102246	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)
RSRZ outliers	91569	2404 (2.80-2.80)

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.

Mol	Chain	Length	Quality of chain
1	A	476	5% 48% 43% 8%
1	B	476	5% 48% 42% 9%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 7900 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 ALPHA-ACTININ 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	475	Total	C	N	O	S	0	0	0
			3942	2453	714	758	17			
1	B	475	Total	C	N	O	S	0	0	0
			3942	2453	714	758	17			

- Molecule 2 is water.

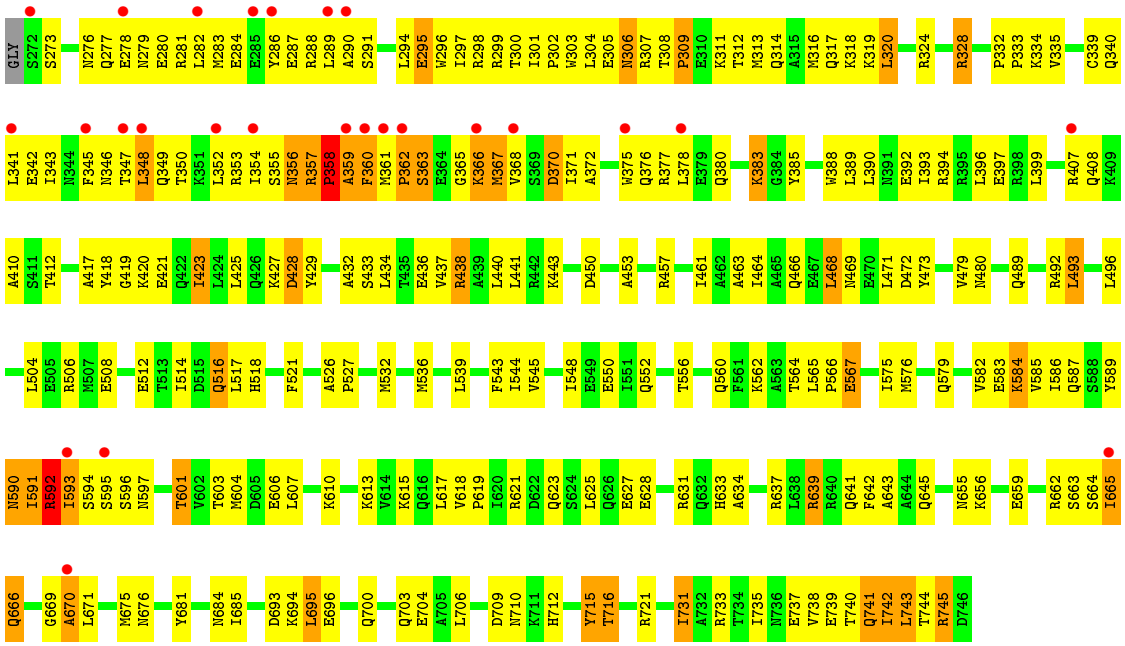
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	7	Total	O	0	0
			7	7		
2	B	9	Total	O	0	0
			9	9		

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.

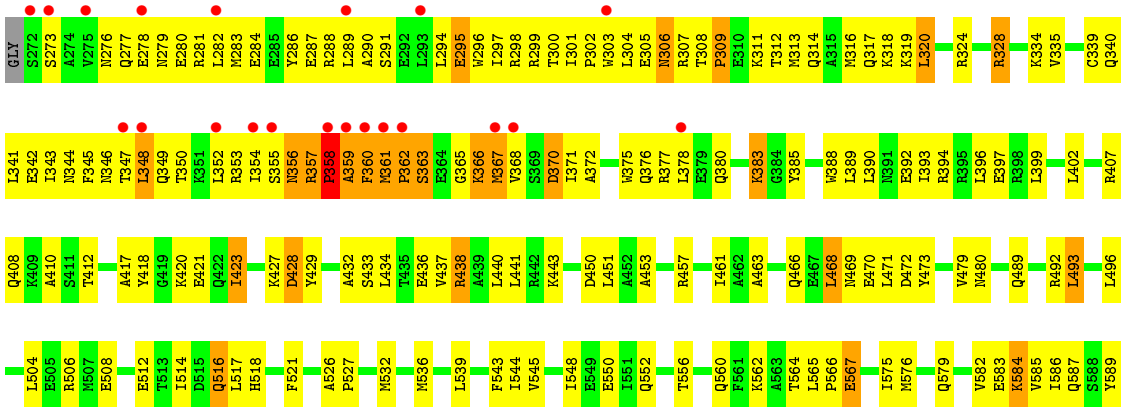
- Molecule 1: ALPHA-ACTININ 2

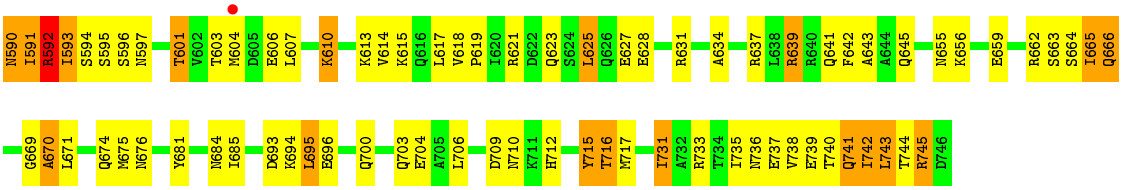
Chain A:



- Molecule 1: ALPHA-ACTININ 2

Chain B:




N590
I591
R592
I593
S594
S595
S596
N597
T601
V602
T603
M604
D605
E606
L607
K610
K613
V614
K615
Q616
L617
V618
P619
I620
R621
D622
Q623
S624
L625
Q626
E627
E628
R631
A634
R637
L638
R639
R640
Q641
F642
A643
A644
Q645
N655
K656
E659
R662
S663
S664
I665
Q666
G669
A670
L671
Q674
M675
N676
Y681
N684
I685
D693
K694
L695
E696
Q700
Q703
E704
A705
L706
D709
N710
K711
H712
Y715
T716
M717
I731
A732
R733
T734
I735
N736
E737
V738
E739
T740
Q741
I742
L743
T744
R745
D746

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, α, β, γ	103.28Å 103.28Å 218.64Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	82.78 – 2.80 82.78 – 2.70	Depositor EDS
% Data completeness (in resolution range)	98.7 (82.78-2.80) 98.7 (82.78-2.70)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.89 (at 2.69Å)	Xtriage
Refinement program	CNS 0.9	Depositor
R, R_{free}	0.270 , 0.295 0.261 , 0.285	Depositor DCC
R_{free} test set	6335 reflections (9.99%)	DCC
Wilson B-factor (Å^2)	61.4	Xtriage
Anisotropy	0.614	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 58.0	EDS
Estimated twinning fraction	0.017 for -h,-k,l 0.450 for h,-h-k,-l 0.018 for -k,-h,-l	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.34$	Xtriage
Outliers	0 of 70769 reflections	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	7900	wwPDB-VP
Average B, all atoms (Å^2)	73.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.80% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\| > 5$	RMSZ	$\#\|Z\| > 5$
1	A	0.41	0/4008	0.63	1/5401 (0.0%)
1	B	0.42	0/4008	0.63	1/5401 (0.0%)
All	All	0.42	0/8016	0.63	2/10802 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	715	TYR	N-CA-C	5.05	124.63	111.00
1	A	715	TYR	N-CA-C	5.02	124.56	111.00

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	3942	0	3889	268	0
1	B	3942	0	3889	273	0
2	A	7	0	0	0	0
2	B	9	0	0	0	0
All	All	7900	0	7778	523	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 33.

All (523) 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:A:526:ALA:HB3	1:A:527:PRO:HD3	1.41	1.02
1:B:526:ALA:HB3	1:B:527:PRO:HD3	1.39	1.02
1:B:469:ASN:HD21	1:B:480:ASN:HD21	1.15	0.95
1:A:469:ASN:HD21	1:A:480:ASN:HD21	1.17	0.92
1:B:665:ILE:CD1	1:B:666:GLN:H	1.83	0.91
1:A:350:THR:HG23	1:A:353:ARG:HH12	1.35	0.91
1:A:665:ILE:CD1	1:A:666:GLN:H	1.82	0.91
1:B:350:THR:HG23	1:B:353:ARG:HH12	1.36	0.90
1:B:342:GLU:HA	1:B:345:PHE:HB3	1.54	0.88
1:A:342:GLU:HA	1:A:345:PHE:HB3	1.54	0.87
1:A:665:ILE:HD13	1:A:666:GLN:H	1.41	0.84
1:B:665:ILE:HD13	1:B:666:GLN:H	1.42	0.83
1:A:576:MET:HG2	1:A:604:MET:SD	2.19	0.83
1:A:740:THR:HG23	1:B:350:THR:HG21	1.61	0.82
1:B:576:MET:HG2	1:B:604:MET:SD	2.20	0.81
1:A:350:THR:HG21	1:B:740:THR:HG23	1.62	0.81
1:B:367:MET:HB2	1:B:370:ASP:HB2	1.63	0.79
1:A:350:THR:HG23	1:A:353:ARG:NH1	1.98	0.78
1:A:367:MET:HB2	1:A:370:ASP:HB2	1.63	0.78
1:B:576:MET:HA	1:B:604:MET:HE1	1.66	0.76
1:B:350:THR:HG23	1:B:353:ARG:NH1	1.99	0.76
1:B:700:GLN:O	1:B:704:GLU:HG3	1.85	0.76
1:B:357:ARG:HG3	1:B:357:ARG:O	1.85	0.75
1:B:279:ASN:HD21	1:B:352:LEU:HD21	1.51	0.75
1:A:357:ARG:O	1:A:357:ARG:HG3	1.85	0.75
1:A:279:ASN:HD21	1:A:352:LEU:HD21	1.51	0.75
1:B:349:GLN:HE22	1:B:359:ALA:HB1	1.51	0.74
1:A:349:GLN:HE22	1:A:359:ALA:HB1	1.51	0.74
1:B:603:THR:HG23	1:B:606:GLU:H	1.53	0.73
1:B:273:SER:HA	1:B:276:ASN:HD22	1.52	0.72
1:A:603:THR:HG23	1:A:606:GLU:H	1.54	0.72
1:A:278:GLU:HA	1:A:281:ARG:HG2	1.72	0.72
1:A:273:SER:HA	1:A:276:ASN:HD22	1.52	0.72
1:A:681:TYR:O	1:A:685:ILE:HG12	1.89	0.71
1:A:576:MET:HA	1:A:604:MET:HE1	1.72	0.71
1:B:681:TYR:O	1:B:685:ILE:HG12	1.91	0.71
1:B:278:GLU:HA	1:B:281:ARG:HG2	1.71	0.71
1:A:694:LYS:NZ	1:A:694:LYS:HB2	2.06	0.71
1:B:671:LEU:H	1:B:671:LEU:HD23	1.56	0.70
1:B:694:LYS:HB2	1:B:694:LYS:NZ	2.05	0.70
1:A:671:LEU:HD23	1:A:671:LEU:H	1.55	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:665:ILE:CD1	1:A:666:GLN:N	2.54	0.70
1:A:589:TYR:HB2	1:A:591:ILE:HG22	1.73	0.69
1:A:696:GLU:CG	1:B:328:ARG:HG3	2.23	0.69
1:A:700:GLN:O	1:A:704:GLU:HG3	1.91	0.69
1:B:565:LEU:N	1:B:566:PRO:HD2	2.08	0.69
1:B:665:ILE:CD1	1:B:666:GLN:N	2.55	0.69
1:B:282:LEU:O	1:B:348:LEU:HG	1.93	0.69
1:A:671:LEU:HD23	1:A:671:LEU:N	2.08	0.69
1:A:696:GLU:HG2	1:B:328:ARG:HG3	1.74	0.69
1:A:313:MET:CE	1:A:397:GLU:HA	2.23	0.69
1:B:313:MET:CE	1:B:397:GLU:HA	2.23	0.69
1:A:306:ASN:ND2	1:A:308:THR:H	1.90	0.69
1:B:589:TYR:HB2	1:B:591:ILE:HG22	1.73	0.69
1:A:576:MET:HA	1:A:604:MET:CE	2.23	0.68
1:B:365:GLY:O	1:B:366:LYS:HG3	1.93	0.68
1:A:742:ILE:O	1:A:742:ILE:HG12	1.94	0.68
1:B:301:ILE:HD13	1:B:377:ARG:HG2	1.75	0.68
1:B:306:ASN:ND2	1:B:308:THR:H	1.91	0.68
1:A:282:LEU:O	1:A:348:LEU:HG	1.94	0.68
1:B:742:ILE:HG12	1:B:742:ILE:O	1.94	0.68
1:A:291:SER:OG	1:A:366:LYS:HD2	1.93	0.68
1:B:421:GLU:HG2	1:B:493:LEU:HD13	1.75	0.68
1:A:365:GLY:O	1:A:366:LYS:HG3	1.94	0.67
1:B:671:LEU:HD23	1:B:671:LEU:N	2.09	0.67
1:A:301:ILE:HD13	1:A:377:ARG:HG2	1.76	0.67
1:B:526:ALA:HB3	1:B:527:PRO:CD	2.21	0.67
1:B:576:MET:HA	1:B:604:MET:CE	2.24	0.67
1:A:328:ARG:HG3	1:B:696:GLU:CG	2.23	0.67
1:B:291:SER:OG	1:B:366:LYS:HD2	1.95	0.67
1:A:603:THR:HG22	1:A:606:GLU:OE1	1.94	0.67
1:B:492:ARG:HH11	1:B:492:ARG:HB2	1.60	0.67
1:A:341:LEU:O	1:A:342:GLU:HG2	1.95	0.67
1:B:603:THR:HG22	1:B:606:GLU:OE1	1.94	0.67
1:A:645:GLN:HE22	1:A:694:LYS:HG2	1.60	0.66
1:A:394:ARG:O	1:A:397:GLU:HB3	1.96	0.66
1:A:421:GLU:HG2	1:A:493:LEU:HD13	1.76	0.66
1:B:307:ARG:HH11	1:B:385:TYR:HD1	1.42	0.66
1:A:300:THR:C	1:A:302:PRO:HD2	2.15	0.66
1:B:341:LEU:O	1:B:342:GLU:HG2	1.95	0.66
1:B:389:LEU:O	1:B:393:ILE:HG12	1.95	0.66
1:A:434:LEU:HD21	1:A:438:ARG:NH2	2.09	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:349:GLN:NE2	1:A:359:ALA:HB1	2.11	0.66
1:A:517:LEU:HB3	1:A:582:VAL:HG22	1.78	0.66
1:B:360:PHE:CD2	1:B:362:PRO:HD3	2.30	0.66
1:A:441:LEU:HD13	1:A:504:LEU:HB3	1.77	0.66
1:A:469:ASN:ND2	1:A:480:ASN:HD21	1.91	0.66
1:A:360:PHE:CD2	1:A:362:PRO:HD3	2.30	0.66
1:A:389:LEU:O	1:A:393:ILE:HG12	1.96	0.65
1:B:394:ARG:O	1:B:397:GLU:HB3	1.96	0.65
1:B:300:THR:C	1:B:302:PRO:HD2	2.16	0.65
1:A:685:ILE:HG13	1:A:731:ILE:HD13	1.78	0.65
1:A:565:LEU:N	1:A:566:PRO:HD2	2.11	0.65
1:A:328:ARG:HG3	1:B:696:GLU:HG2	1.77	0.65
1:B:349:GLN:NE2	1:B:359:ALA:HB1	2.11	0.65
1:B:685:ILE:HG13	1:B:731:ILE:HD13	1.79	0.65
1:A:307:ARG:HH11	1:A:385:TYR:HD1	1.43	0.65
1:B:376:GLN:HA	1:B:376:GLN:HE21	1.61	0.65
1:B:645:GLN:HE22	1:B:694:LYS:HG2	1.62	0.65
1:A:436:GLU:O	1:A:440:LEU:HG	1.96	0.65
1:B:434:LEU:HD21	1:B:438:ARG:NH2	2.11	0.65
1:A:685:ILE:HG13	1:A:731:ILE:CD1	2.27	0.64
1:B:469:ASN:ND2	1:B:480:ASN:HD21	1.90	0.64
1:B:685:ILE:HG13	1:B:731:ILE:CD1	2.28	0.64
1:A:301:ILE:N	1:A:302:PRO:HD2	2.13	0.64
1:B:575:ILE:HG22	1:B:604:MET:CE	2.28	0.64
1:B:441:LEU:HD13	1:B:504:LEU:HB3	1.78	0.64
1:A:376:GLN:HA	1:A:376:GLN:HE21	1.62	0.63
1:B:517:LEU:HB3	1:B:582:VAL:HG22	1.80	0.63
1:A:526:ALA:HB3	1:A:527:PRO:CD	2.23	0.63
1:A:575:ILE:HG22	1:A:604:MET:CE	2.29	0.63
1:B:279:ASN:ND2	1:B:352:LEU:HD21	2.14	0.63
1:A:320:LEU:HA	1:A:389:LEU:HD13	1.81	0.63
1:B:394:ARG:HG3	1:B:394:ARG:HH11	1.63	0.63
1:A:492:ARG:HH11	1:A:492:ARG:HB2	1.63	0.62
1:A:706:LEU:HD11	1:B:317:GLN:HE22	1.64	0.62
1:B:286:TYR:OH	1:B:368:VAL:HG22	1.99	0.62
1:B:345:PHE:CG	1:B:345:PHE:O	2.52	0.62
1:A:317:GLN:HE22	1:B:706:LEU:HD11	1.65	0.62
1:A:305:GLU:HA	1:A:307:ARG:NH2	2.15	0.62
1:B:320:LEU:HA	1:B:389:LEU:HD13	1.81	0.62
1:B:297:ILE:O	1:B:301:ILE:HG13	2.00	0.62
1:B:301:ILE:N	1:B:302:PRO:HD2	2.14	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:319:LYS:HG2	1:A:389:LEU:HD21	1.82	0.62
1:A:564:THR:C	1:A:566:PRO:HD2	2.21	0.61
1:A:592:ARG:HH11	1:A:592:ARG:HG2	1.65	0.61
1:A:469:ASN:HD21	1:A:480:ASN:ND2	1.96	0.61
1:A:394:ARG:HG3	1:A:394:ARG:HH11	1.65	0.61
1:A:279:ASN:ND2	1:A:352:LEU:HD21	2.14	0.61
1:B:564:THR:C	1:B:566:PRO:HD2	2.20	0.61
1:B:319:LYS:HG2	1:B:389:LEU:HD21	1.82	0.61
1:A:286:TYR:OH	1:A:368:VAL:HG22	2.01	0.61
1:A:556:THR:O	1:A:560:GLN:HG3	2.01	0.61
1:B:290:ALA:HB3	1:B:366:LYS:NZ	2.16	0.61
1:B:665:ILE:HD12	1:B:666:GLN:N	2.16	0.60
1:A:345:PHE:O	1:A:345:PHE:CG	2.53	0.60
1:A:279:ASN:HD21	1:A:352:LEU:CD2	2.14	0.60
1:A:290:ALA:HB3	1:A:366:LYS:NZ	2.16	0.60
1:A:297:ILE:O	1:A:301:ILE:HG13	2.01	0.60
1:B:517:LEU:HB3	1:B:582:VAL:CG2	2.31	0.60
1:A:735:ILE:O	1:A:739:GLU:HG3	2.00	0.60
1:A:665:ILE:HD12	1:A:666:GLN:N	2.15	0.60
1:B:279:ASN:HD21	1:B:352:LEU:CD2	2.14	0.60
1:B:592:ARG:HH11	1:B:592:ARG:HG2	1.66	0.60
1:B:305:GLU:HA	1:B:307:ARG:NH2	2.15	0.60
1:A:639:ARG:HD3	1:A:709:ASP:O	2.01	0.60
1:A:463:ALA:O	1:A:466:GLN:HB3	2.01	0.60
1:A:517:LEU:HB3	1:A:582:VAL:CG2	2.30	0.60
1:A:694:LYS:HZ2	1:A:694:LYS:HB2	1.67	0.60
1:B:735:ILE:O	1:B:739:GLU:HG3	2.01	0.60
1:B:436:GLU:O	1:B:440:LEU:HG	2.01	0.60
1:A:317:GLN:HB3	1:A:393:ILE:HD12	1.84	0.60
1:B:556:THR:O	1:B:560:GLN:HG3	2.02	0.60
1:A:575:ILE:HG22	1:A:604:MET:HE1	1.84	0.59
1:B:339:CYS:O	1:B:341:LEU:O	2.21	0.59
1:A:376:GLN:HA	1:A:376:GLN:NE2	2.17	0.59
1:B:576:MET:CA	1:B:604:MET:HE1	2.32	0.59
1:B:317:GLN:HB3	1:B:393:ILE:HD12	1.83	0.59
1:A:341:LEU:C	1:A:343:ILE:H	2.06	0.59
1:A:283:MET:HB2	1:A:360:PHE:CZ	2.38	0.59
1:A:350:THR:HA	1:A:353:ARG:CZ	2.33	0.58
1:B:463:ALA:O	1:B:466:GLN:HB3	2.02	0.58
1:B:341:LEU:C	1:B:343:ILE:H	2.06	0.58
1:B:283:MET:HB2	1:B:360:PHE:CZ	2.38	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:516:GLN:HE21	1:A:516:GLN:CA	2.16	0.58
1:B:516:GLN:HA	1:B:516:GLN:NE2	2.18	0.58
1:B:376:GLN:NE2	1:B:376:GLN:HA	2.17	0.58
1:B:469:ASN:HD21	1:B:480:ASN:ND2	1.94	0.58
1:B:350:THR:HA	1:B:353:ARG:CZ	2.33	0.58
1:A:339:CYS:O	1:A:341:LEU:O	2.21	0.58
1:B:516:GLN:HE21	1:B:516:GLN:CA	2.16	0.58
1:B:284:GLU:O	1:B:288:ARG:HG2	2.04	0.57
1:B:273:SER:O	1:B:277:GLN:HG3	2.05	0.57
1:B:432:ALA:HB3	1:B:437:VAL:HG23	1.86	0.57
1:A:432:ALA:HB3	1:A:437:VAL:HG23	1.85	0.57
1:A:273:SER:O	1:A:277:GLN:HG3	2.05	0.57
1:A:516:GLN:HA	1:A:516:GLN:NE2	2.19	0.57
1:A:284:GLU:O	1:A:288:ARG:HG2	2.05	0.57
1:B:643:ALA:HB1	1:B:712:HIS:O	2.05	0.57
1:B:434:LEU:O	1:B:438:ARG:HB2	2.05	0.56
1:A:370:ASP:C	1:A:372:ALA:N	2.60	0.55
1:A:441:LEU:HD13	1:A:504:LEU:CB	2.35	0.55
1:A:282:LEU:HB3	1:A:348:LEU:HD23	1.89	0.55
1:B:639:ARG:HD3	1:B:709:ASP:O	2.06	0.55
1:A:370:ASP:C	1:A:372:ALA:H	2.10	0.55
1:B:441:LEU:HD13	1:B:504:LEU:CB	2.36	0.55
1:B:518:HIS:HA	1:B:597:ASN:HD21	1.72	0.55
1:B:694:LYS:HB2	1:B:694:LYS:HZ3	1.71	0.55
1:A:669:GLY:O	1:A:670:ALA:O	2.25	0.55
1:B:469:ASN:O	1:B:472:ASP:N	2.39	0.55
1:A:354:ILE:O	1:A:354:ILE:HG22	2.07	0.55
1:A:434:LEU:O	1:A:438:ARG:HB2	2.07	0.55
1:A:662:ARG:O	1:A:664:SER:N	2.38	0.55
1:A:643:ALA:HB1	1:A:712:HIS:O	2.07	0.55
1:B:539:LEU:HD23	1:B:617:LEU:CB	2.37	0.55
1:B:354:ILE:HG22	1:B:354:ILE:O	2.07	0.55
1:A:518:HIS:HA	1:A:597:ASN:HD21	1.72	0.55
1:B:662:ARG:O	1:B:664:SER:N	2.40	0.54
1:A:350:THR:HA	1:A:353:ARG:NH2	2.22	0.54
1:A:342:GLU:CA	1:A:345:PHE:HB3	2.34	0.54
1:B:282:LEU:HB3	1:B:348:LEU:HD23	1.89	0.54
1:B:410:ALA:HA	1:B:461:ILE:HD13	1.88	0.54
1:A:601:THR:HG23	1:B:443:LYS:HE2	1.89	0.54
1:A:539:LEU:HD23	1:A:617:LEU:CB	2.37	0.54
1:B:370:ASP:C	1:B:372:ALA:H	2.10	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:370:ASP:C	1:B:372:ALA:N	2.60	0.54
1:A:390:LEU:HB3	1:A:394:ARG:HH12	1.73	0.54
1:A:655:ASN:ND2	1:A:659:GLU:OE2	2.41	0.54
1:B:585:VAL:O	1:B:589:TYR:HD2	1.91	0.54
1:B:532:MET:O	1:B:536:MET:HG3	2.06	0.54
1:B:350:THR:HA	1:B:353:ARG:NH2	2.22	0.54
1:A:301:ILE:N	1:A:302:PRO:CD	2.70	0.54
1:B:744:THR:HG22	1:B:744:THR:O	2.08	0.54
1:A:438:ARG:HD2	1:A:508:GLU:OE2	2.07	0.54
1:A:443:LYS:HE2	1:B:601:THR:HG23	1.89	0.54
1:B:301:ILE:N	1:B:302:PRO:CD	2.71	0.54
1:B:575:ILE:HG22	1:B:604:MET:HE2	1.88	0.53
1:B:342:GLU:CA	1:B:345:PHE:HB3	2.34	0.53
1:B:592:ARG:O	1:B:593:ILE:HB	2.08	0.53
1:B:566:PRO:HG2	1:B:567:GLU:H	1.73	0.53
1:B:591:ILE:HG12	1:B:592:ARG:O	2.09	0.53
1:A:324:ARG:NH1	1:B:703:GLN:OE1	2.41	0.53
1:A:410:ALA:HA	1:A:461:ILE:HD13	1.90	0.53
1:A:521:PHE:HE2	1:A:604:MET:HE2	1.74	0.53
1:B:438:ARG:HD2	1:B:508:GLU:OE2	2.08	0.53
1:A:585:VAL:O	1:A:589:TYR:HD2	1.90	0.53
1:B:669:GLY:O	1:B:670:ALA:O	2.26	0.53
1:A:280:GLU:HA	1:A:283:MET:HG2	1.91	0.53
1:A:363:SER:HB2	1:A:366:LYS:HB2	1.91	0.53
1:B:312:THR:O	1:B:396:LEU:HD13	2.09	0.53
1:B:363:SER:HB2	1:B:366:LYS:HB2	1.91	0.53
1:B:468:LEU:HG	1:B:473:TYR:CD1	2.45	0.52
1:B:410:ALA:HA	1:B:461:ILE:CD1	2.38	0.52
1:A:576:MET:CA	1:A:604:MET:HE1	2.37	0.52
1:B:280:GLU:HA	1:B:283:MET:HG2	1.91	0.52
1:B:655:ASN:ND2	1:B:659:GLU:OE2	2.42	0.52
1:A:536:MET:HE3	1:A:613:LYS:HB3	1.92	0.52
1:B:390:LEU:HB3	1:B:394:ARG:HH12	1.73	0.52
1:B:304:LEU:C	1:B:306:ASN:H	2.13	0.52
1:A:566:PRO:HG2	1:A:567:GLU:H	1.74	0.52
1:A:432:ALA:CB	1:A:437:VAL:HG23	2.40	0.52
1:B:516:GLN:CA	1:B:516:GLN:NE2	2.73	0.52
1:B:575:ILE:HG22	1:B:604:MET:HE1	1.90	0.52
1:A:312:THR:O	1:A:396:LEU:HD13	2.10	0.52
1:B:316:MET:HE3	1:B:392:GLU:HG3	1.92	0.52
1:B:634:ALA:HA	1:B:637:ARG:NH2	2.25	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:469:ASN:O	1:A:472:ASP:N	2.40	0.51
1:A:584:LYS:HD2	1:A:584:LYS:C	2.31	0.51
1:A:316:MET:HE3	1:A:392:GLU:HG3	1.92	0.51
1:A:591:ILE:HG12	1:A:592:ARG:O	2.10	0.51
1:A:592:ARG:O	1:A:593:ILE:HB	2.09	0.51
1:A:304:LEU:C	1:A:306:ASN:H	2.12	0.51
1:A:367:MET:CB	1:A:370:ASP:HB2	2.38	0.51
1:A:539:LEU:HD23	1:A:617:LEU:HB2	1.91	0.51
1:B:584:LYS:C	1:B:584:LYS:HD2	2.31	0.51
1:A:703:GLN:OE1	1:B:324:ARG:NH1	2.43	0.51
1:A:532:MET:O	1:A:536:MET:HG3	2.10	0.51
1:A:516:GLN:CA	1:A:516:GLN:NE2	2.73	0.51
1:A:544:ILE:HG23	1:A:544:ILE:O	2.10	0.51
1:A:744:THR:HG22	1:A:744:THR:O	2.09	0.51
1:A:634:ALA:HA	1:A:637:ARG:NH2	2.26	0.51
1:B:282:LEU:HB3	1:B:348:LEU:CD2	2.42	0.50
1:A:642:PHE:CE1	1:A:695:LEU:HD22	2.46	0.50
1:A:399:LEU:HD13	1:A:471:LEU:HB3	1.92	0.50
1:A:548:ILE:O	1:A:552:GLN:HG3	2.11	0.50
1:A:410:ALA:HA	1:A:461:ILE:CD1	2.42	0.50
1:B:642:PHE:CE1	1:B:695:LEU:HD22	2.47	0.50
1:B:733:ARG:HG3	1:B:733:ARG:HH11	1.77	0.50
1:A:733:ARG:HG3	1:A:733:ARG:HH11	1.76	0.50
1:A:297:ILE:HD12	1:A:297:ILE:C	2.32	0.50
1:B:394:ARG:NH1	1:B:394:ARG:HG3	2.27	0.50
1:B:489:GLN:HG2	1:B:493:LEU:HD22	1.94	0.50
1:A:543:PHE:HE1	1:A:628:GLU:HG3	1.77	0.50
1:B:623:GLN:O	1:B:627:GLU:HG3	2.12	0.50
1:B:273:SER:HA	1:B:276:ASN:ND2	2.25	0.50
1:A:489:GLN:HG2	1:A:493:LEU:HD22	1.93	0.49
1:A:457:ARG:O	1:A:461:ILE:HG13	2.12	0.49
1:B:399:LEU:HD13	1:B:471:LEU:HB3	1.93	0.49
1:B:548:ILE:O	1:B:552:GLN:HG3	2.12	0.49
1:A:506:ARG:HH11	1:A:506:ARG:HG3	1.76	0.49
1:B:694:LYS:O	1:B:695:LEU:C	2.51	0.49
1:A:737:GLU:O	1:A:741:GLN:NE2	2.45	0.49
1:B:594:SER:O	1:B:596:SER:N	2.46	0.49
1:B:307:ARG:NH1	1:B:385:TYR:HB2	2.27	0.49
1:A:623:GLN:O	1:A:627:GLU:HG3	2.13	0.49
1:A:350:THR:HA	1:A:353:ARG:NH1	2.28	0.49
1:B:348:LEU:HD12	1:B:360:PHE:CE1	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:348:LEU:HD12	1:A:360:PHE:CE1	2.47	0.49
1:B:506:ARG:HG3	1:B:506:ARG:HH11	1.77	0.49
1:A:380:GLN:O	1:A:383:LYS:HB2	2.13	0.49
1:A:468:LEU:HG	1:A:473:TYR:CD1	2.48	0.49
1:A:282:LEU:HB3	1:A:348:LEU:CD2	2.41	0.49
1:B:615:LYS:O	1:B:619:PRO:HD2	2.12	0.49
1:A:615:LYS:O	1:A:619:PRO:HD2	2.12	0.49
1:B:521:PHE:HE2	1:B:604:MET:HE2	1.78	0.49
1:B:421:GLU:HG2	1:B:493:LEU:CD1	2.42	0.49
1:A:273:SER:HA	1:A:276:ASN:ND2	2.25	0.49
1:B:297:ILE:C	1:B:297:ILE:HD12	2.33	0.49
1:B:492:ARG:O	1:B:496:LEU:HB2	2.12	0.49
1:A:307:ARG:NH1	1:A:385:TYR:HB2	2.28	0.48
1:A:394:ARG:HG3	1:A:394:ARG:NH1	2.28	0.48
1:B:517:LEU:CB	1:B:582:VAL:HG22	2.43	0.48
1:B:367:MET:CB	1:B:370:ASP:HB2	2.38	0.48
1:A:352:LEU:HD12	1:A:359:ALA:HA	1.95	0.48
1:A:492:ARG:O	1:A:496:LEU:HB2	2.13	0.48
1:B:539:LEU:HD23	1:B:617:LEU:HB2	1.94	0.48
1:B:733:ARG:O	1:B:737:GLU:HG3	2.14	0.48
1:B:294:LEU:HD21	1:B:371:ILE:HG12	1.94	0.48
1:A:662:ARG:C	1:A:664:SER:H	2.17	0.48
1:B:295:GLU:O	1:B:298:ARG:HB3	2.13	0.48
1:B:350:THR:HA	1:B:353:ARG:NH1	2.28	0.48
1:B:348:LEU:HD12	1:B:360:PHE:HE1	1.77	0.48
1:B:675:MET:HE2	1:B:738:VAL:HG12	1.95	0.48
1:B:543:PHE:HE1	1:B:628:GLU:HG3	1.79	0.48
1:B:380:GLN:O	1:B:383:LYS:HB2	2.13	0.48
1:B:352:LEU:HD12	1:B:359:ALA:HA	1.95	0.48
1:A:741:GLN:C	1:A:743:LEU:H	2.17	0.48
1:A:348:LEU:HD12	1:A:360:PHE:HE1	1.78	0.48
1:A:294:LEU:HD21	1:A:371:ILE:HG12	1.95	0.48
1:B:662:ARG:C	1:B:664:SER:H	2.16	0.48
1:A:295:GLU:O	1:A:298:ARG:HB3	2.14	0.48
1:A:594:SER:O	1:A:596:SER:N	2.46	0.47
1:A:575:ILE:HG22	1:A:604:MET:HE2	1.96	0.47
1:A:675:MET:HE2	1:A:738:VAL:HG12	1.96	0.47
1:B:427:LYS:O	1:B:429:TYR:N	2.47	0.47
1:B:281:ARG:HG3	1:B:282:LEU:CD1	2.45	0.47
1:B:303:TRP:HE3	1:B:304:LEU:HD22	1.80	0.47
1:A:517:LEU:CB	1:A:582:VAL:HG22	2.42	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:427:LYS:O	1:A:429:TYR:N	2.48	0.47
1:B:432:ALA:CB	1:B:437:VAL:HG23	2.44	0.47
1:A:733:ARG:O	1:A:737:GLU:HG3	2.14	0.47
1:B:737:GLU:O	1:B:741:GLN:NE2	2.47	0.47
1:A:303:TRP:HE3	1:A:304:LEU:HD22	1.80	0.47
1:B:544:ILE:O	1:B:544:ILE:HG23	2.15	0.47
1:A:696:GLU:HG2	1:B:328:ARG:CG	2.44	0.47
1:B:589:TYR:O	1:B:590:ASN:C	2.53	0.47
1:A:715:TYR:C	1:A:716:THR:HG23	2.35	0.47
1:B:304:LEU:N	1:B:304:LEU:HD22	2.30	0.47
1:A:417:ALA:O	1:A:418:TYR:C	2.53	0.47
1:A:304:LEU:N	1:A:304:LEU:HD22	2.30	0.47
1:B:526:ALA:CB	1:B:527:PRO:HD3	2.26	0.46
1:A:281:ARG:HG3	1:A:282:LEU:CD1	2.45	0.46
1:B:585:VAL:CG2	1:B:586:ILE:N	2.78	0.46
1:B:715:TYR:O	1:B:716:THR:HG23	2.15	0.46
1:B:496:LEU:HA	1:B:496:LEU:HD12	1.74	0.46
1:B:741:GLN:C	1:B:743:LEU:H	2.18	0.46
1:A:589:TYR:O	1:A:590:ASN:C	2.53	0.46
1:A:585:VAL:CG2	1:A:586:ILE:N	2.78	0.46
1:A:318:LYS:HD2	1:A:318:LYS:O	2.15	0.46
1:A:706:LEU:HD11	1:B:317:GLN:NE2	2.30	0.46
1:A:278:GLU:CA	1:A:281:ARG:HG2	2.43	0.46
1:B:715:TYR:C	1:B:716:THR:HG23	2.36	0.46
1:B:313:MET:HE3	1:B:397:GLU:HA	1.98	0.46
1:B:417:ALA:O	1:B:418:TYR:C	2.52	0.46
1:A:464:ILE:O	1:A:468:LEU:HB2	2.16	0.45
1:A:585:VAL:HG23	1:A:586:ILE:N	2.32	0.45
1:B:304:LEU:O	1:B:306:ASN:N	2.49	0.45
1:B:346:ASN:HA	1:B:349:GLN:HB2	1.99	0.45
1:A:304:LEU:HD22	1:A:304:LEU:H	1.81	0.45
1:A:304:LEU:O	1:A:306:ASN:N	2.48	0.45
1:A:545:VAL:CG1	1:A:550:GLU:HB3	2.47	0.45
1:B:518:HIS:HA	1:B:597:ASN:ND2	2.31	0.45
1:A:340:GLN:O	1:A:343:ILE:HB	2.17	0.45
1:B:357:ARG:CG	1:B:357:ARG:O	2.60	0.45
1:B:304:LEU:H	1:B:304:LEU:HD22	1.82	0.45
1:A:565:LEU:N	1:A:566:PRO:CD	2.80	0.45
1:B:457:ARG:O	1:B:461:ILE:HG13	2.17	0.45
1:B:335:VAL:HG22	1:B:375:TRP:CZ2	2.51	0.45
1:A:421:GLU:HG2	1:A:493:LEU:CD1	2.43	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:715:TYR:O	1:A:716:THR:HG23	2.16	0.45
1:B:565:LEU:N	1:B:566:PRO:CD	2.77	0.44
1:A:548:ILE:HD13	1:A:633:HIS:CE1	2.52	0.44
1:B:545:VAL:CG1	1:B:550:GLU:HB3	2.48	0.44
1:A:335:VAL:HG22	1:A:375:TRP:CZ2	2.52	0.44
1:A:346:ASN:HA	1:A:349:GLN:HB2	1.99	0.44
1:B:278:GLU:CA	1:B:281:ARG:HG2	2.43	0.44
1:B:340:GLN:O	1:B:343:ILE:HB	2.16	0.44
1:B:576:MET:N	1:B:604:MET:HE1	2.32	0.44
1:B:402:LEU:HB3	1:B:468:LEU:HD13	2.00	0.44
1:A:296:TRP:C	1:A:298:ARG:N	2.71	0.44
1:B:296:TRP:C	1:B:298:ARG:N	2.71	0.44
1:A:576:MET:N	1:A:604:MET:HE1	2.33	0.44
1:A:518:HIS:HA	1:A:597:ASN:ND2	2.33	0.44
1:A:357:ARG:O	1:A:357:ARG:CG	2.61	0.44
1:A:639:ARG:NH1	1:A:709:ASP:OD1	2.51	0.44
1:B:639:ARG:HG2	1:B:710:ASN:CG	2.38	0.44
1:A:427:LYS:O	1:A:428:ASP:C	2.57	0.44
1:B:318:LYS:O	1:B:318:LYS:HD2	2.18	0.44
1:B:585:VAL:HG23	1:B:586:ILE:N	2.32	0.43
1:B:585:VAL:O	1:B:589:TYR:CD2	2.71	0.43
1:A:594:SER:C	1:A:596:SER:N	2.71	0.43
1:A:419:GLY:O	1:A:423:ILE:HG23	2.18	0.43
1:A:589:TYR:HB2	1:A:591:ILE:CG2	2.45	0.43
1:B:423:ILE:HD12	1:B:423:ILE:O	2.18	0.43
1:A:371:ILE:HG22	1:A:371:ILE:O	2.19	0.43
1:A:743:LEU:HD12	1:B:354:ILE:CD1	2.48	0.43
1:B:743:LEU:C	1:B:745:ARG:H	2.22	0.43
1:A:639:ARG:HG2	1:A:710:ASN:CG	2.39	0.43
1:B:468:LEU:HD12	1:B:468:LEU:HA	1.87	0.43
1:B:625:LEU:HD12	1:B:625:LEU:HA	1.90	0.43
1:B:290:ALA:HB3	1:B:366:LYS:HZ1	1.84	0.43
1:A:313:MET:HB2	1:A:396:LEU:HB3	2.01	0.43
1:A:328:ARG:CG	1:B:696:GLU:HG2	2.46	0.43
1:A:296:TRP:HA	1:A:299:ARG:HG2	2.00	0.43
1:B:427:LYS:O	1:B:428:ASP:C	2.57	0.43
1:B:357:ARG:O	1:B:358:PRO:C	2.57	0.43
1:B:514:ILE:HD13	1:B:586:ILE:HG12	2.01	0.43
1:A:357:ARG:O	1:A:358:PRO:C	2.57	0.43
1:B:408:GLN:O	1:B:412:THR:HG23	2.19	0.43
1:A:585:VAL:O	1:A:589:TYR:CD2	2.70	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:579:GLN:HG3	1:B:583:GLU:OE2	2.19	0.43
1:A:352:LEU:CD1	1:A:359:ALA:HA	2.49	0.43
1:B:613:LYS:O	1:B:614:VAL:C	2.56	0.43
1:A:521:PHE:CE2	1:A:604:MET:HE2	2.53	0.43
1:B:362:PRO:O	1:B:363:SER:C	2.57	0.43
1:A:670:ALA:HB1	1:A:671:LEU:H	1.65	0.43
1:A:514:ILE:HD13	1:A:586:ILE:HG12	2.00	0.43
1:B:313:MET:HB2	1:B:396:LEU:HB3	2.01	0.43
1:A:303:TRP:CZ3	1:A:304:LEU:HD13	2.54	0.43
1:B:303:TRP:CE3	1:B:304:LEU:HD13	2.54	0.43
1:A:743:LEU:HD12	1:B:354:ILE:HD12	2.01	0.43
1:B:309:PRO:HA	1:B:316:MET:HE1	2.01	0.43
1:B:532:MET:HE3	1:B:610:LYS:HB3	2.01	0.42
1:A:362:PRO:O	1:A:363:SER:C	2.58	0.42
1:B:433:SER:N	1:B:436:GLU:OE1	2.51	0.42
1:B:536:MET:CE	1:B:613:LYS:HB3	2.50	0.42
1:A:579:GLN:HG3	1:A:583:GLU:OE2	2.19	0.42
1:A:347:THR:HG22	1:A:347:THR:O	2.19	0.42
1:B:352:LEU:CD1	1:B:359:ALA:HA	2.49	0.42
1:B:371:ILE:O	1:B:371:ILE:HG22	2.19	0.42
1:A:286:TYR:OH	1:A:368:VAL:HG13	2.20	0.42
1:B:521:PHE:HE2	1:B:604:MET:CE	2.32	0.42
1:B:287:GLU:OE1	1:B:362:PRO:HB2	2.19	0.42
1:A:368:VAL:HG12	1:A:368:VAL:O	2.19	0.42
1:B:695:LEU:HD23	1:B:695:LEU:HA	1.84	0.42
1:B:368:VAL:HG12	1:B:368:VAL:O	2.20	0.42
1:A:743:LEU:C	1:A:745:ARG:H	2.22	0.42
1:A:715:TYR:O	1:A:716:THR:OG1	2.36	0.42
1:B:303:TRP:CZ3	1:B:304:LEU:HD13	2.54	0.42
1:B:594:SER:C	1:B:596:SER:N	2.72	0.42
1:A:298:ARG:HG2	1:A:298:ARG:HH11	1.84	0.42
1:B:603:THR:O	1:B:607:LEU:HB2	2.20	0.42
1:A:287:GLU:OE1	1:A:362:PRO:HB2	2.20	0.42
1:B:694:LYS:HB2	1:B:694:LYS:HZ2	1.85	0.42
1:A:593:ILE:HD12	1:A:593:ILE:N	2.35	0.42
1:A:493:LEU:HD12	1:A:493:LEU:HA	1.83	0.42
1:B:296:TRP:HA	1:B:299:ARG:HG2	2.00	0.42
1:B:347:THR:HG22	1:B:347:THR:O	2.20	0.42
1:B:451:LEU:HD13	1:B:451:LEU:C	2.40	0.42
1:B:450:ASP:O	1:B:453:ALA:HB3	2.20	0.42
1:A:309:PRO:HA	1:A:316:MET:HE1	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:319:LYS:CG	1:B:389:LEU:HD21	2.49	0.42
1:A:307:ARG:HG3	1:A:388:TRP:CD2	2.55	0.42
1:B:376:GLN:CA	1:B:376:GLN:NE2	2.79	0.42
1:A:423:ILE:O	1:A:423:ILE:HD12	2.20	0.42
1:A:294:LEU:O	1:A:297:ILE:HG13	2.20	0.41
1:A:303:TRP:CE3	1:A:304:LEU:HD13	2.54	0.41
1:B:286:TYR:OH	1:B:368:VAL:HG13	2.20	0.41
1:A:733:ARG:CZ	1:A:733:ARG:HB2	2.50	0.41
1:A:536:MET:CE	1:A:613:LYS:HB3	2.50	0.41
1:A:350:THR:CG2	1:A:353:ARG:HH12	2.19	0.41
1:A:317:GLN:NE2	1:B:706:LEU:HD11	2.31	0.41
1:B:526:ALA:CB	1:B:527:PRO:CD	2.91	0.41
1:B:307:ARG:HG3	1:B:388:TRP:CD2	2.56	0.41
1:B:536:MET:HE3	1:B:613:LYS:HB3	2.02	0.41
1:A:715:TYR:O	1:A:716:THR:CB	2.68	0.41
1:A:281:ARG:HG3	1:A:282:LEU:HD12	2.03	0.41
1:A:694:LYS:O	1:A:695:LEU:C	2.56	0.41
1:B:641:GLN:O	1:B:645:GLN:HG3	2.21	0.41
1:B:715:TYR:O	1:B:716:THR:CB	2.69	0.41
1:B:716:THR:O	1:B:717:MET:C	2.59	0.41
1:B:356:ASN:O	1:B:357:ARG:HB3	2.20	0.41
1:B:301:ILE:HG12	1:B:378:LEU:HA	2.03	0.41
1:A:506:ARG:NH1	1:A:506:ARG:HG3	2.34	0.41
1:B:296:TRP:CE3	1:B:334:LYS:HG2	2.56	0.41
1:A:603:THR:O	1:A:607:LEU:HB2	2.20	0.41
1:A:319:LYS:CG	1:A:389:LEU:HD21	2.49	0.41
1:B:733:ARG:O	1:B:736:ASN:HB3	2.21	0.41
1:A:508:GLU:O	1:A:512:GLU:HB2	2.21	0.41
1:A:433:SER:N	1:A:436:GLU:OE1	2.50	0.41
1:B:434:LEU:CD2	1:B:438:ARG:NH2	2.81	0.41
1:B:506:ARG:NH1	1:B:506:ARG:HG3	2.35	0.41
1:A:296:TRP:CE3	1:A:334:LYS:HG2	2.55	0.41
1:B:562:LYS:HD3	1:B:618:VAL:CG1	2.50	0.41
1:A:332:PRO:N	1:A:333:PRO:HD2	2.36	0.41
1:B:361:MET:HA	1:B:362:PRO:HD2	1.91	0.41
1:B:656:LYS:CE	1:B:684:ASN:HD22	2.34	0.41
1:A:356:ASN:O	1:A:357:ARG:HB3	2.21	0.41
1:B:671:LEU:O	1:B:674:GLN:N	2.53	0.41
1:A:390:LEU:O	1:A:393:ILE:N	2.54	0.41
1:A:300:THR:O	1:A:304:LEU:HD23	2.21	0.41
1:A:316:MET:HE2	1:A:392:GLU:HB3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:294:LEU:O	1:B:297:ILE:HG13	2.21	0.41
1:B:438:ARG:CD	1:B:508:GLU:OE2	2.69	0.41
1:A:425:LEU:HD21	1:A:496:LEU:HD11	2.02	0.41
1:A:468:LEU:HA	1:A:468:LEU:HD12	1.85	0.41
1:B:298:ARG:HG2	1:B:298:ARG:HH11	1.86	0.41
1:A:450:ASP:O	1:A:453:ALA:HB3	2.21	0.41
1:A:341:LEU:C	1:A:343:ILE:N	2.73	0.41
1:B:281:ARG:HG3	1:B:282:LEU:HD12	2.03	0.41
1:A:313:MET:HE3	1:A:397:GLU:HA	1.98	0.41
1:A:301:ILE:HG12	1:A:378:LEU:HA	2.03	0.41
1:B:589:TYR:HB2	1:B:591:ILE:CG2	2.44	0.41
1:B:302:PRO:O	1:B:304:LEU:O	2.40	0.41
1:B:303:TRP:C	1:B:304:LEU:O	2.57	0.41
1:B:619:PRO:O	1:B:623:GLN:HB2	2.21	0.41
1:A:619:PRO:O	1:A:623:GLN:HB2	2.21	0.41
1:A:408:GLN:O	1:A:412:THR:HG23	2.21	0.41
1:B:466:GLN:O	1:B:469:ASN:HB2	2.21	0.40
1:A:696:GLU:OE2	1:A:721:ARG:NH2	2.47	0.40
1:B:593:ILE:O	1:B:593:ILE:HG22	2.22	0.40
1:A:562:LYS:HD3	1:A:618:VAL:CG1	2.51	0.40
1:A:280:GLU:O	1:A:283:MET:HG2	2.21	0.40
1:A:308:THR:HA	1:A:309:PRO:HD2	1.89	0.40
1:A:434:LEU:CD2	1:A:438:ARG:NH2	2.81	0.40
1:B:508:GLU:O	1:B:512:GLU:HB2	2.21	0.40
1:A:641:GLN:O	1:A:645:GLN:HG3	2.22	0.40
1:A:438:ARG:CD	1:A:508:GLU:OE2	2.70	0.40
1:B:350:THR:CG2	1:B:353:ARG:HH12	2.19	0.40
1:B:344:ASN:C	1:B:346:ASN:H	2.25	0.40
1:B:276:ASN:O	1:B:280:GLU:HG3	2.22	0.40
1:B:300:THR:O	1:B:304:LEU:HD23	2.22	0.40
1:A:656:LYS:CE	1:A:684:ASN:HD22	2.35	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	473/476 (99%)	385 (81%)	64 (14%)	24 (5%)	2 8
1	B	473/476 (99%)	386 (82%)	62 (13%)	25 (5%)	2 7
All	All	946/952 (99%)	771 (82%)	126 (13%)	49 (5%)	2 7

All (49) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	355	SER
1	A	356	ASN
1	A	358	PRO
1	A	362	PRO
1	A	363	SER
1	A	383	LYS
1	A	428	ASP
1	A	665	ILE
1	A	670	ALA
1	B	355	SER
1	B	356	ASN
1	B	358	PRO
1	B	362	PRO
1	B	363	SER
1	B	383	LYS
1	B	428	ASP
1	B	665	ILE
1	B	670	ALA
1	A	309	PRO
1	A	311	LYS
1	A	359	ALA
1	A	595	SER
1	A	742	ILE
1	B	309	PRO
1	B	311	LYS
1	B	359	ALA
1	B	595	SER
1	B	742	ILE
1	A	306	ASN
1	A	367	MET
1	A	592	ARG
1	A	663	SER
1	A	666	GLN

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Mol	Chain	Res	Type
1	B	306	ASN
1	B	367	MET
1	B	592	ARG
1	B	663	SER
1	B	666	GLN
1	A	366	LYS
1	A	590	ASN
1	B	366	LYS
1	B	590	ASN
1	A	357	ARG
1	A	593	ILE
1	B	357	ARG
1	B	470	GLU
1	B	593	ILE
1	A	716	THR
1	B	716	THR

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	426/426 (100%)	390 (92%)	36 (8%)	13 36
1	B	426/426 (100%)	390 (92%)	36 (8%)	13 36
All	All	852/852 (100%)	780 (92%)	72 (8%)	13 36

All (72) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	289	LEU
1	A	295	GLU
1	A	314	GLN
1	A	320	LEU
1	A	328	ARG
1	A	348	LEU
1	A	358	PRO

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Mol	Chain	Res	Type
1	A	360	PHE
1	A	361	MET
1	A	370	ASP
1	A	407	ARG
1	A	420	LYS
1	A	423	ILE
1	A	438	ARG
1	A	468	LEU
1	A	479	VAL
1	A	493	LEU
1	A	516	GLN
1	A	567	GLU
1	A	584	LYS
1	A	587	GLN
1	A	591	ILE
1	A	592	ARG
1	A	601	THR
1	A	610	LYS
1	A	621	ARG
1	A	625	LEU
1	A	631	ARG
1	A	639	ARG
1	A	676	ASN
1	A	693	ASP
1	A	695	LEU
1	A	731	ILE
1	A	741	GLN
1	A	743	LEU
1	A	745	ARG
1	B	289	LEU
1	B	295	GLU
1	B	314	GLN
1	B	320	LEU
1	B	328	ARG
1	B	348	LEU
1	B	358	PRO
1	B	360	PHE
1	B	361	MET
1	B	370	ASP
1	B	407	ARG
1	B	420	LYS
1	B	423	ILE

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Mol	Chain	Res	Type
1	B	438	ARG
1	B	468	LEU
1	B	479	VAL
1	B	493	LEU
1	B	516	GLN
1	B	567	GLU
1	B	584	LYS
1	B	587	GLN
1	B	591	ILE
1	B	592	ARG
1	B	601	THR
1	B	610	LYS
1	B	621	ARG
1	B	625	LEU
1	B	631	ARG
1	B	639	ARG
1	B	676	ASN
1	B	693	ASP
1	B	695	LEU
1	B	731	ILE
1	B	741	GLN
1	B	743	LEU
1	B	745	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (39) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	276	ASN
1	A	306	ASN
1	A	317	GLN
1	A	349	GLN
1	A	376	GLN
1	A	408	GLN
1	A	426	GLN
1	A	480	ASN
1	A	516	GLN
1	A	530	ASN
1	A	540	GLN
1	A	579	GLN
1	A	580	ASN
1	A	587	GLN
1	A	616	GLN

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Mol	Chain	Res	Type
1	A	645	GLN
1	A	684	ASN
1	A	700	GLN
1	A	736	ASN
1	A	741	GLN
1	B	276	ASN
1	B	306	ASN
1	B	317	GLN
1	B	376	GLN
1	B	408	GLN
1	B	426	GLN
1	B	480	ASN
1	B	516	GLN
1	B	530	ASN
1	B	540	GLN
1	B	579	GLN
1	B	580	ASN
1	B	587	GLN
1	B	616	GLN
1	B	645	GLN
1	B	684	ASN
1	B	700	GLN
1	B	736	ASN
1	B	741	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

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} 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	475/476 (99%)	0.52	26 (5%)	29	18	39, 64, 131, 156	0
1	B	475/476 (99%)	0.53	22 (4%)	36	25	33, 64, 132, 156	0
All	All	950/952 (99%)	0.52	48 (5%)	32	21	33, 64, 132, 156	0

All (48) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	368	VAL	7.5
1	B	282	LEU	6.7
1	A	359	ALA	6.6
1	A	368	VAL	6.4
1	A	282	LEU	4.3
1	B	359	ALA	4.0
1	A	361	MET	3.9
1	A	354	ILE	3.7
1	B	362	PRO	3.5
1	B	361	MET	3.4
1	B	348	LEU	3.4
1	B	354	ILE	3.1
1	A	352	LEU	3.1
1	B	289	LEU	3.0
1	B	293	LEU	3.0
1	B	278	GLU	3.0
1	A	595	SER	2.9
1	A	347	THR	2.9
1	A	348	LEU	2.8
1	A	378	LEU	2.8
1	A	289	LEU	2.7
1	B	367	MET	2.7
1	B	273	SER	2.6
1	B	347	THR	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	670	ALA	2.6
1	A	290	ALA	2.6
1	A	366	LYS	2.6
1	A	362	PRO	2.6
1	B	272	SER	2.5
1	A	345	PHE	2.5
1	A	360	PHE	2.5
1	A	286	TYR	2.3
1	B	352	LEU	2.3
1	A	665	ILE	2.3
1	B	378	LEU	2.3
1	A	341	LEU	2.2
1	B	604	MET	2.2
1	B	303	TRP	2.2
1	B	360	PHE	2.1
1	A	375	TRP	2.1
1	A	407	ARG	2.1
1	A	272	SER	2.1
1	B	355	SER	2.1
1	A	593	ILE	2.1
1	B	275	VAL	2.0
1	A	278	GLU	2.0
1	A	285	GLU	2.0
1	B	358	PRO	2.0

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

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

6.3 Carbohydrates (i)

There are no carbohydrates in this entry.

6.4 Ligands (i)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.