



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 06:31 PM GMT

PDB ID : 1B70
Title : PHENYLALANYL TRNA SYNTHETASE COMPLEXED WITH PHENYLALANINE
Authors : Reshetnikova, L.; Moor, N.; Lavrik, O.; Vassilyev, D.G.
Deposited on : 1999-01-26
Resolution : 2.70 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

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

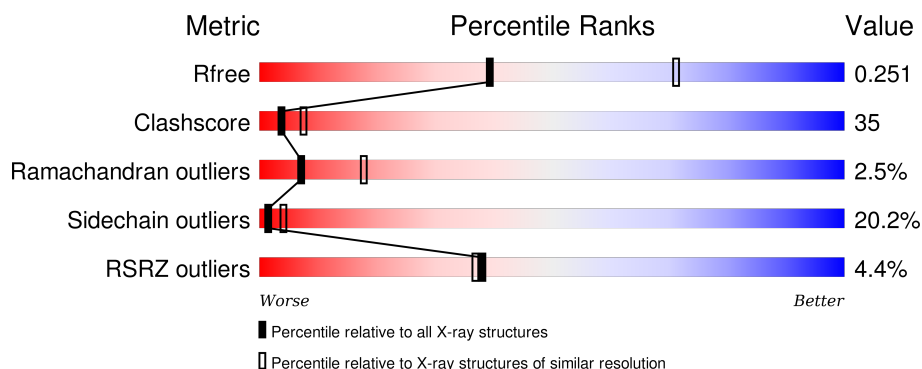
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	2103 (2.70-2.70)
Clashscore	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (2.70-2.70)
RSRZ outliers	91569	2107 (2.70-2.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	350	
2	B	785	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	PHE	A	352	-	-	-	X

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 8313 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 PHENYLALANYL-TRNA SYNTHETASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	265	Total	C	N	O	S	0	0	0
			2112	1382	359	364	7			

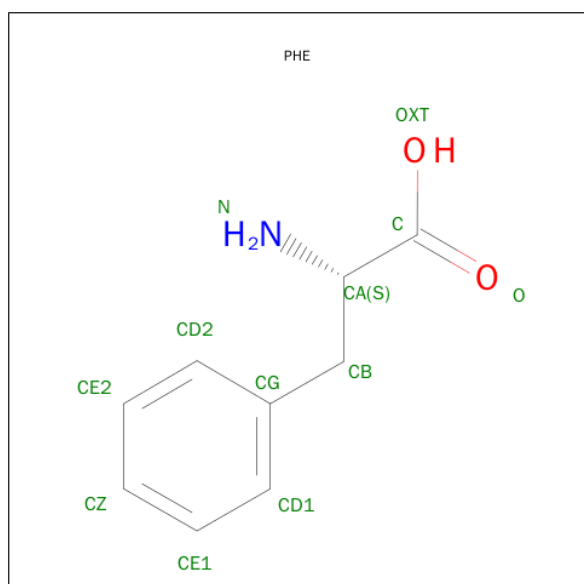
- Molecule 2 is a protein called PHENYLALANYL-TRNA SYNTHETASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	775	Total	C	N	O	S	0	0	0
			6054	3879	1078	1087	10			

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Mg	0	0
			1	1		

- Molecule 4 is PHENYLALANINE (three-letter code: PHE) (formula: C₉H₁₁NO₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			12	9	1	2		

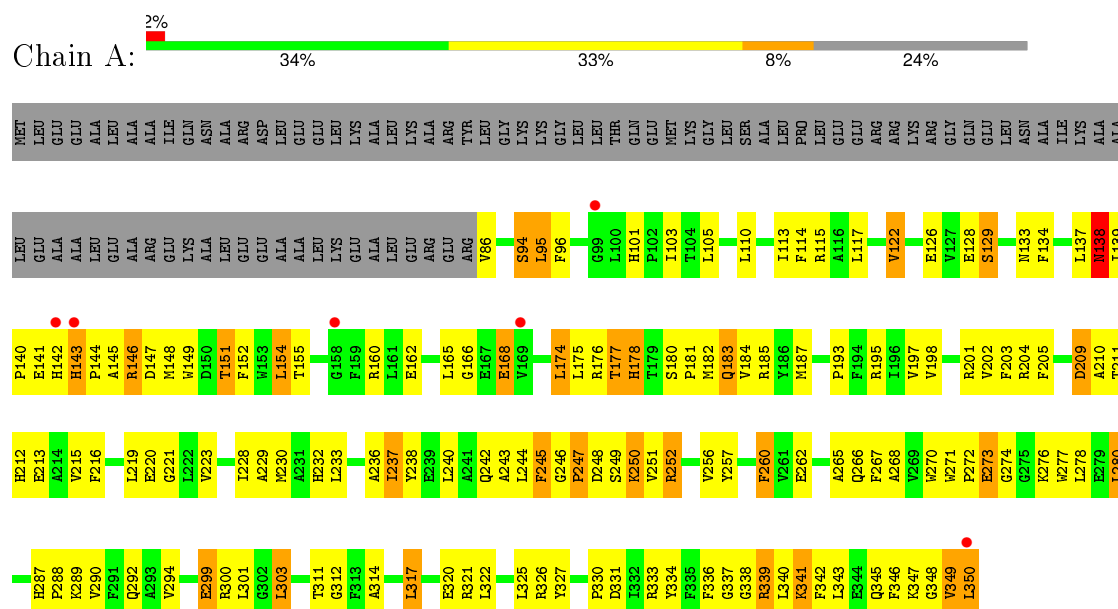
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	28	Total	O	0	0
			28	28		
5	B	106	Total	O	0	0
			106	106		

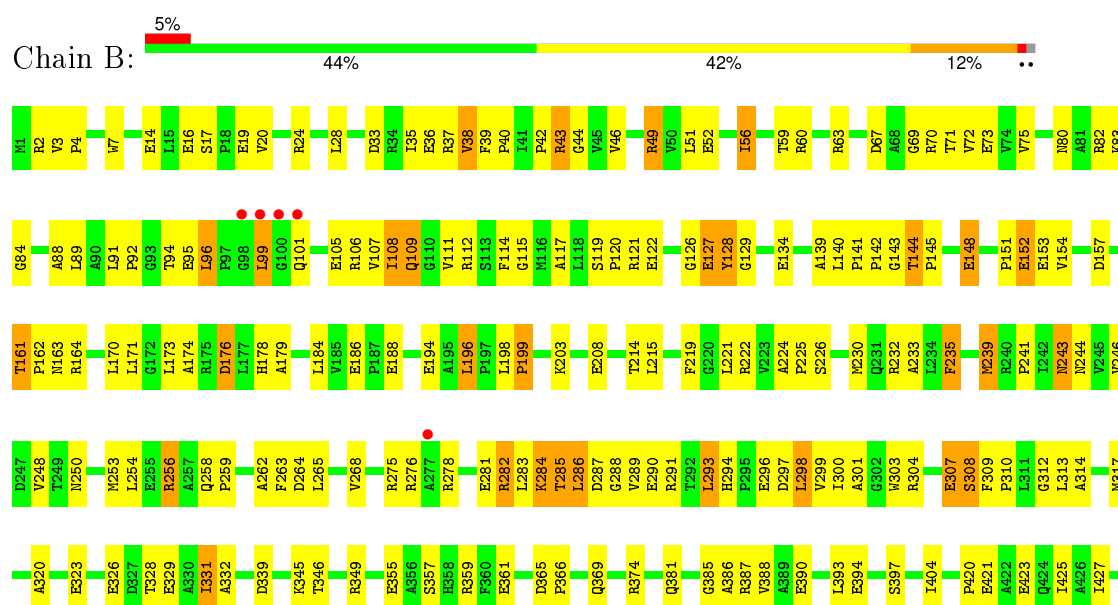
3 Residue-property plots

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.

• Molecule 1: PHENYLALANYL-TRNA SYNTHETASE



• Molecule 2: PHENYLALANYL-TRNA SYNTHETASE



LEU	G719	H656	T583	N516	R430
ARG	F720	P657	H584	D517	
GLY	Y721	B658	L585	P518	V435
LEU	L722	B659	A586	E519	E438
ASP	E723	A660	G587	D520	
THR	S724	Q661	L588	R523	T441
PRO	L725	B662	L589	F524	Y442
	A726	L663	F590	R525	R443
	L727	B664	G591	F524	
	F728	L665	E592	L526	P446
	D729	P666	G593	D527	P447
	L730	P667	V594	P528	S448
	Y731	B668	G595	P529	H449
	Q732	B669	L596	R530	R450
	G733	L670	P597	L531	L451
	F734	B671	W598	L532	D452
	L735	B672	A599	L533	L453
	F736	L673	R600	L534	R454
	L737	B674	B601	N535	
	F737	L675	R602	P536	
	E738	L676	L603	L537	
	G739	P676	S604	K541	D458
	H740		G605	A542	Y460
	K741	K680		E461	E462
	S742	P681	L608	R545	
	L743	L682	L609	L548	R465
	A744	A683	R610	F549	L466
	F745	F684	L613	P550	
	H746	Q685	E614	Y469	
	L747			G551	
	R748	S688	F617	F479	
	F749	R689	L622	A482	
	R750	A692	A623	N485	
	H751	G693	F624	R486	
	P752	F694	Q629	G487	
	R753	B695	A630	Y488	
	R754	P696	F633	A490	
	T755	L697	H634	P491	
	L756	B698	P635	K494	
	R757	L699	B636	R497	
	D758	A698	G637	L498	
	E759	V699	V638	R499	
	E760	V700	S639	E500	
	V761	V701	V642	V501	
	E762	P702	L643	L505	
	E763	A703	B645	E509	
	A764	P704	G646	V510	
	V765	T705	B647	V511	
	S766	P706	V649	T512	
	R767	Y707	G650	Y513	
	V768	G708	F651	S514	
	A769	E709	L652	F515	
	E770	V710	G653		
	A771	E711			
	L772	A712			
	R773	L713			
	A774	V714			
	R775	R715			
	GLY	E716			
	PHE	A717			
	GLY	A718			

4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	174.00Å 174.00Å 140.40Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.00 – 2.70 47.29 – 2.70	Depositor EDS
% Data completeness (in resolution range)	89.4 (50.00-2.70) 88.8 (47.29-2.70)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3001.55 (at 2.69Å)	Xtriage
Refinement program	X-PLOR 3.851	Depositor
R, R_{free}	0.224 , 0.256 0.223 , 0.251	Depositor DCC
R_{free} test set	3018 reflections (5.04%)	DCC
Wilson B-factor (Å ²)	51.3	Xtriage
Anisotropy	0.418	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 81.7	EDS
Estimated twinning fraction	0.045 for -h,-k,l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.26$	Xtriage
Outliers	0 of 59935 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	8313	wwPDB-VP
Average B, all atoms (Å ²)	70.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.76% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MG

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	0.53	0/2180	0.71	0/2957
2	B	0.50	0/6205	0.73	3/8436 (0.0%)
All	All	0.50	0/8385	0.73	3/11393 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	115	GLY	N-CA-C	-5.72	98.80	113.10
2	B	69	GLY	N-CA-C	-5.39	99.64	113.10
2	B	38	VAL	N-CA-C	5.37	125.50	111.00

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	2112	0	2062	143	0
2	B	6054	0	6109	455	0
3	A	1	0	0	0	0
4	A	12	0	8	0	0
5	A	28	0	0	0	0
5	B	106	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	8313	0	8179	576	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 35.

All (576) 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:165:LEU:HD12	1:A:301:LEU:HD13	1.35	1.08
2:B:285:THR:HG21	2:B:291:ARG:HE	1.25	0.99
2:B:614:GLU:HG2	2:B:624:PHE:HE1	1.24	0.97
2:B:75:VAL:HG11	2:B:108:ILE:HG21	1.45	0.97
2:B:707:TYR:HE1	2:B:711:GLU:HB2	1.30	0.93
2:B:600:LYS:HG2	2:B:601:GLU:H	1.30	0.93
2:B:294:HIS:CD2	2:B:296:GLU:H	1.86	0.93
2:B:294:HIS:HD2	2:B:296:GLU:H	0.95	0.92
2:B:121:ARG:HD3	2:B:127:GLU:O	1.71	0.89
2:B:516:MET:HE3	2:B:545:ARG:HA	1.56	0.88
1:A:101:HIS:HB2	2:B:509:GLU:HG2	1.55	0.88
2:B:198:LEU:HD12	2:B:393:LEU:HD13	1.55	0.87
2:B:701:VAL:HG22	2:B:702:PRO:HD2	1.57	0.87
1:A:143:HIS:ND1	1:A:144:PRO:HD2	1.89	0.86
2:B:707:TYR:CE1	2:B:711:GLU:HB2	2.10	0.86
2:B:764:ALA:HA	2:B:767:ARG:HG2	1.55	0.86
1:A:246:GLY:HA2	1:A:248:ASP:N	1.91	0.85
2:B:286:LEU:HD11	2:B:323:GLU:CD	1.98	0.84
2:B:710:VAL:O	2:B:714:VAL:HG23	1.77	0.84
2:B:593:GLY:HA3	2:B:604:SER:HB3	1.59	0.84
2:B:761:VAL:HG23	2:B:762:GLU:H	1.44	0.83
1:A:331:ASP:HB3	1:A:334:TYR:CD2	2.14	0.83
1:A:113:ILE:HD13	1:A:243:ALA:HB1	1.61	0.82
2:B:512:THR:HG22	2:B:545:ARG:HH21	1.44	0.81
2:B:194:GLU:OE2	2:B:387:ARG:HG2	1.80	0.81
1:A:229:ALA:H	1:A:232:HIS:HD2	1.24	0.81
2:B:219:PHE:HE2	2:B:387:ARG:HE	1.26	0.81
2:B:563:ASP:O	2:B:565:PRO:HD3	1.80	0.81
2:B:490:ALA:HB3	2:B:491:PRO:HD3	1.61	0.81
2:B:589:LEU:HB3	2:B:609:LEU:HD12	1.64	0.79
1:A:287:HIS:HD2	1:A:289:LYS:H	1.26	0.79
1:A:257:TYR:HB3	2:B:161:THR:HG21	1.65	0.79
1:A:250:LYS:H	1:A:270:TRP:HB3	1.48	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:101:HIS:HD2	1:A:103:ILE:H	1.31	0.78
1:A:311:THR:HG22	1:A:312:GLY:H	1.50	0.77
1:A:311:THR:HG22	1:A:312:GLY:N	1.97	0.77
2:B:757:ARG:HG3	2:B:759:GLU:HB2	1.66	0.77
2:B:729:ASP:N	2:B:744:ALA:HB3	2.00	0.77
2:B:596:LEU:HB2	2:B:599:ALA:HB3	1.68	0.76
2:B:673:LEU:HD22	2:B:673:LEU:N	2.00	0.76
1:A:299:GLU:HG3	1:A:300:ARG:N	2.01	0.76
1:A:246:GLY:HA2	1:A:248:ASP:H	1.47	0.75
1:A:278:LEU:HD13	1:A:325:LEU:HD13	1.68	0.75
2:B:583:THR:HG22	2:B:675:LEU:HD12	1.69	0.74
2:B:730:LEU:HB2	2:B:742:SER:O	1.87	0.74
2:B:761:VAL:HG23	2:B:762:GLU:N	2.02	0.74
2:B:722:LEU:HD11	2:B:724:SER:O	1.87	0.74
2:B:549:PHE:O	2:B:553:VAL:HG23	1.85	0.74
1:A:113:ILE:HD13	1:A:243:ALA:CB	2.18	0.74
2:B:614:GLU:HG2	2:B:624:PHE:CE1	2.16	0.73
2:B:757:ARG:HD3	2:B:759:GLU:H	1.52	0.73
2:B:702:PRO:C	2:B:704:PRO:HD2	2.09	0.73
2:B:497:ARG:O	2:B:501:VAL:HG23	1.88	0.73
2:B:287:ASP:N	2:B:317:MET:HE2	2.04	0.73
1:A:249:SER:HB2	1:A:270:TRP:O	1.89	0.72
2:B:243:ASN:HD21	2:B:246:VAL:HG23	1.54	0.72
2:B:770:GLU:CG	2:B:771:ALA:N	2.50	0.72
2:B:99:LEU:HD22	2:B:101:GLN:NE2	2.05	0.72
2:B:600:LYS:HG2	2:B:601:GLU:N	2.02	0.72
2:B:697:LEU:HD23	2:B:698:ALA:N	2.04	0.72
2:B:176:ASP:OD2	2:B:465:ARG:NH2	2.23	0.72
2:B:610:LYS:O	2:B:614:GLU:HG3	1.90	0.72
1:A:331:ASP:O	1:A:334:TYR:HB2	1.89	0.71
2:B:730:LEU:HD12	2:B:730:LEU:C	2.11	0.71
2:B:99:LEU:HD13	2:B:101:GLN:HB2	1.72	0.71
1:A:134:PHE:HZ	1:A:151:THR:HG21	1.56	0.71
1:A:211:THR:C	1:A:212:HIS:HD1	1.93	0.71
2:B:770:GLU:O	2:B:774:ALA:HB2	1.91	0.71
2:B:702:PRO:CB	2:B:704:PRO:HD2	2.21	0.70
1:A:149:TRP:CD1	1:A:177:THR:HG23	2.26	0.70
2:B:762:GLU:O	2:B:765:VAL:HG12	1.89	0.70
2:B:656:HIS:NE2	2:B:658:GLU:HB2	2.06	0.70
2:B:519:GLU:HB3	2:B:523:ARG:HH12	1.56	0.70
1:A:165:LEU:HD12	1:A:301:LEU:CD1	2.18	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:137:LEU:O	1:A:139:ILE:N	2.25	0.70
2:B:734:PRO:HB2	2:B:735:PRO:HD3	1.74	0.70
1:A:155:THR:CG2	2:B:534:LEU:HD21	2.22	0.69
2:B:666:PRO:HB2	2:B:667:PRO:CD	2.22	0.69
2:B:258:GLN:HE22	2:B:369:GLN:NE2	1.90	0.69
2:B:751:HIS:HD2	2:B:752:PRO:HD2	1.57	0.69
2:B:278:ARG:NH2	2:B:308:SER:HB3	2.06	0.69
1:A:134:PHE:CZ	1:A:151:THR:HG21	2.28	0.69
2:B:153:GLU:HG3	2:B:154:VAL:N	2.07	0.69
2:B:287:ASP:H	2:B:317:MET:HE2	1.57	0.68
2:B:51:LEU:HD21	2:B:67:ASP:HB2	1.73	0.68
2:B:602:ARG:HG2	2:B:602:ARG:HH11	1.57	0.68
2:B:604:SER:HA	2:B:608:LEU:HD22	1.75	0.68
2:B:724:SER:HB2	2:B:748:ARG:HB2	1.76	0.68
2:B:643:LEU:HA	2:B:647:GLU:O	1.93	0.68
2:B:656:HIS:CD2	2:B:658:GLU:H	2.12	0.67
2:B:663:LEU:O	2:B:665:LEU:N	2.27	0.67
2:B:700:VAL:HA	2:B:741:LYS:O	1.93	0.67
2:B:698:ALA:HA	2:B:743:LEU:O	1.95	0.67
2:B:736:LEU:HB2	2:B:737:PRO:HD2	1.77	0.67
2:B:728:PHE:HE1	2:B:745:PHE:C	1.99	0.66
2:B:243:ASN:ND2	2:B:246:VAL:H	1.94	0.66
2:B:688:SER:HB3	2:B:752:PRO:HA	1.76	0.66
2:B:693:ALA:HB3	2:B:749:PHE:HB2	1.77	0.66
2:B:656:HIS:HB3	2:B:659:ILE:HD12	1.77	0.66
1:A:101:HIS:CD2	1:A:103:ILE:H	2.13	0.66
2:B:243:ASN:ND2	2:B:246:VAL:HG23	2.11	0.66
2:B:663:LEU:C	2:B:665:LEU:H	1.99	0.66
2:B:178:HIS:O	2:B:430:ARG:NH1	2.29	0.66
2:B:278:ARG:HH21	2:B:308:SER:HB3	1.61	0.66
2:B:767:ARG:N	2:B:767:ARG:HE	1.95	0.65
1:A:180:SER:O	1:A:183:GLN:HB2	1.95	0.65
2:B:215:LEU:HB2	2:B:393:LEU:HB2	1.78	0.65
2:B:751:HIS:HB3	2:B:754:ARG:O	1.95	0.65
2:B:438:GLU:HA	2:B:438:GLU:OE1	1.97	0.65
2:B:650:GLY:HA3	2:B:673:LEU:HD13	1.77	0.65
2:B:770:GLU:HG2	2:B:771:ALA:H	1.62	0.65
2:B:551:GLY:O	2:B:555:VAL:HG23	1.96	0.64
2:B:600:LYS:N	2:B:600:LYS:HD2	2.12	0.64
1:A:160:ARG:HG2	1:A:168:GLU:OE2	1.97	0.64
2:B:285:THR:CG2	2:B:291:ARG:HE	2.06	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:246:GLY:CA	1:A:248:ASP:H	2.09	0.64
1:A:145:ALA:O	1:A:148:MET:HG3	1.97	0.64
2:B:28:LEU:HD13	2:B:176:ASP:HB3	1.78	0.64
2:B:567:ARG:HA	2:B:591:GLY:HA3	1.79	0.64
1:A:138:ASN:HD21	1:A:289:LYS:HE2	1.62	0.64
1:A:336:PHE:HB3	2:B:513:TYR:CE1	2.32	0.64
2:B:707:TYR:HE1	2:B:711:GLU:CB	2.07	0.64
2:B:656:HIS:HD2	2:B:658:GLU:H	1.45	0.64
2:B:517:ASP:HB3	2:B:520:ASP:OD1	1.96	0.64
1:A:341:LYS:H	1:A:341:LYS:HE2	1.63	0.64
2:B:758:ASP:O	2:B:761:VAL:HG22	1.98	0.64
1:A:349:VAL:O	1:A:350:LEU:HD13	1.98	0.64
2:B:600:LYS:HG2	2:B:601:GLU:HG2	1.78	0.63
2:B:644:VAL:HG22	2:B:645:GLU:H	1.63	0.63
2:B:294:HIS:HD2	2:B:296:GLU:N	1.81	0.63
2:B:609:LEU:HD23	2:B:613:LEU:CD2	2.28	0.63
1:A:287:HIS:CD2	1:A:289:LYS:H	2.14	0.63
2:B:635:HIS:ND1	2:B:636:PRO:O	2.30	0.63
2:B:767:ARG:HE	2:B:767:ARG:CA	2.11	0.63
1:A:246:GLY:CA	1:A:248:ASP:N	2.60	0.63
2:B:602:ARG:CG	2:B:602:ARG:HH11	2.11	0.63
2:B:509:GLU:HG3	2:B:510:VAL:N	2.14	0.63
1:A:155:THR:HG21	2:B:534:LEU:HD21	1.81	0.63
1:A:341:LYS:HE3	2:B:563:ASP:OD2	1.99	0.63
2:B:170:LEU:HA	2:B:173:LEU:HD12	1.81	0.63
2:B:194:GLU:O	2:B:390:GLU:HG2	1.98	0.62
2:B:609:LEU:HD22	2:B:652:LEU:CD1	2.29	0.62
2:B:548:LEU:HD13	2:B:576:VAL:CG1	2.29	0.62
1:A:349:VAL:HG12	1:A:350:LEU:HD22	1.80	0.62
2:B:285:THR:HG21	2:B:291:ARG:NE	2.08	0.62
2:B:108:ILE:O	2:B:109:GLN:HG2	1.98	0.62
2:B:355:GLU:O	2:B:359:ARG:HG3	1.99	0.61
2:B:265:LEU:HD23	2:B:268:VAL:HG21	1.81	0.61
1:A:96:PHE:CZ	2:B:567:ARG:HG3	2.34	0.61
2:B:331:ILE:HG12	2:B:332:ALA:N	2.16	0.61
2:B:645:GLU:OE2	2:B:680:LYS:HB2	2.00	0.61
2:B:773:ARG:HB2	2:B:773:ARG:NH1	2.15	0.61
2:B:286:LEU:HB3	2:B:317:MET:CE	2.30	0.61
2:B:707:TYR:HE2	2:B:727:LEU:HD22	1.66	0.61
2:B:757:ARG:CG	2:B:759:GLU:HB2	2.30	0.61
2:B:761:VAL:CG2	2:B:762:GLU:H	2.12	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:553:VAL:O	2:B:556:LEU:HB3	2.01	0.61
2:B:662:GLU:HG3	2:B:662:GLU:O	1.98	0.61
2:B:767:ARG:NE	2:B:767:ARG:HA	2.14	0.61
1:A:134:PHE:O	1:A:137:LEU:O	2.18	0.61
2:B:707:TYR:HD1	2:B:707:TYR:C	2.03	0.61
2:B:762:GLU:C	2:B:765:VAL:HG12	2.21	0.61
2:B:707:TYR:CD1	2:B:707:TYR:C	2.73	0.61
1:A:242:GLN:OE1	1:A:247:PRO:HA	2.01	0.61
2:B:108:ILE:HG22	2:B:109:GLN:N	2.17	0.60
2:B:764:ALA:HA	2:B:767:ARG:CG	2.29	0.60
1:A:290:VAL:O	1:A:294:VAL:HG23	2.00	0.60
2:B:613:LEU:O	2:B:617:PHE:HD1	1.82	0.60
2:B:643:LEU:HD13	2:B:648:GLU:HA	1.84	0.60
2:B:688:SER:CB	2:B:752:PRO:HA	2.30	0.60
2:B:303:TRP:HA	2:B:307:GLU:O	2.02	0.60
1:A:162:GLU:CG	1:A:166:GLY:HA2	2.31	0.60
2:B:671:PHE:HD1	2:B:673:LEU:HD21	1.66	0.59
2:B:697:LEU:C	2:B:697:LEU:HD23	2.22	0.59
1:A:209:ASP:OD1	1:A:210:ALA:N	2.35	0.59
2:B:751:HIS:HB2	2:B:756:LEU:CD2	2.31	0.59
2:B:732:GLN:HA	2:B:732:GLN:OE1	2.00	0.59
2:B:549:PHE:CG	2:B:550:PRO:HD3	2.38	0.59
1:A:148:MET:HE2	2:B:162:PRO:HG2	1.84	0.59
1:A:219:LEU:HB3	1:A:317:LEU:CD2	2.33	0.59
2:B:482:ALA:HB3	2:B:485:ASN:ND2	2.18	0.59
2:B:730:LEU:HD12	2:B:731:TYR:N	2.18	0.58
2:B:275:ARG:O	2:B:299:VAL:HG12	2.03	0.58
2:B:703:ALA:N	2:B:704:PRO:CD	2.66	0.58
2:B:588:LEU:HD23	2:B:588:LEU:C	2.24	0.58
1:A:143:HIS:CG	1:A:144:PRO:HD2	2.39	0.58
2:B:652:LEU:HD12	2:B:670:LEU:O	2.04	0.58
1:A:271:TRP:CZ3	1:A:274:GLY:HA3	2.39	0.58
2:B:706:PRO:O	2:B:710:VAL:HG23	2.03	0.58
1:A:311:THR:CG2	1:A:312:GLY:H	2.16	0.58
2:B:751:HIS:CD2	2:B:752:PRO:HD2	2.39	0.58
2:B:161:THR:HG22	2:B:162:PRO:HD2	1.85	0.58
2:B:671:PHE:CD1	2:B:673:LEU:HD21	2.39	0.58
1:A:210:ALA:HA	1:A:331:ASP:OD1	2.04	0.58
1:A:114:PHE:HA	1:A:117:LEU:HD13	1.84	0.58
1:A:265:ALA:HB2	2:B:469:TYR:HE2	1.69	0.58
2:B:575:ARG:HG2	2:B:581:GLU:HG2	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:757:ARG:HD2	2:B:759:GLU:HG2	1.86	0.57
2:B:770:GLU:CG	2:B:771:ALA:H	2.16	0.57
1:A:96:PHE:CE1	2:B:567:ARG:HG3	2.40	0.57
2:B:570:LEU:HD22	2:B:570:LEU:N	2.19	0.57
2:B:657:PRO:HA	2:B:660:ALA:HB3	1.86	0.57
2:B:7:TRP:CE3	2:B:233:ALA:HB1	2.39	0.57
2:B:758:ASP:HA	2:B:761:VAL:HG22	1.87	0.57
2:B:462:GLU:OE1	2:B:465:ARG:NH1	2.38	0.57
2:B:536:PRO:HB3	2:B:542:ALA:HA	1.87	0.57
1:A:311:THR:CG2	1:A:312:GLY:N	2.66	0.57
2:B:286:LEU:HB3	2:B:317:MET:HE2	1.86	0.56
2:B:728:PHE:O	2:B:729:ASP:HB2	2.05	0.56
2:B:770:GLU:HG3	2:B:771:ALA:N	2.18	0.56
2:B:359:ARG:HH11	2:B:359:ARG:HG3	1.69	0.56
2:B:20:VAL:O	2:B:24:ARG:HG2	2.06	0.56
2:B:601:GLU:O	2:B:602:ARG:HD2	2.05	0.56
1:A:210:ALA:HA	1:A:333:ARG:HD2	1.87	0.56
2:B:239:MET:HE3	2:B:355:GLU:HG3	1.88	0.56
2:B:767:ARG:NE	2:B:767:ARG:CA	2.67	0.56
1:A:349:VAL:O	1:A:350:LEU:HD22	2.06	0.56
2:B:557:LYS:HZ2	2:B:664:GLU:HG2	1.71	0.56
2:B:555:VAL:HA	2:B:558:GLU:CD	2.26	0.56
2:B:570:LEU:HD21	2:B:588:LEU:HD22	1.88	0.56
2:B:235:PHE:CZ	2:B:241:PRO:HD2	2.40	0.56
2:B:600:LYS:H	2:B:600:LYS:HD2	1.71	0.55
2:B:644:VAL:O	2:B:646:GLY:N	2.40	0.55
2:B:39:PHE:HB2	2:B:152:GLU:HA	1.88	0.55
1:A:343:LEU:HD13	2:B:509:GLU:O	2.06	0.55
2:B:516:MET:CE	2:B:545:ARG:HA	2.34	0.55
2:B:381:GLN:HE21	2:B:388:VAL:HG23	1.72	0.55
1:A:228:ILE:O	1:A:311:THR:HG21	2.06	0.55
2:B:71:THR:HG22	2:B:72:VAL:N	2.20	0.55
1:A:278:LEU:HD13	1:A:325:LEU:CD1	2.35	0.55
2:B:80:ASN:O	2:B:82:ARG:HD3	2.06	0.55
1:A:337:GLY:O	1:A:339:ARG:N	2.33	0.55
2:B:557:LYS:HA	2:B:560:LEU:HD12	1.88	0.55
2:B:520:ASP:OD2	2:B:524:PHE:HE1	1.91	0.54
1:A:195:ARG:HG2	1:A:223:VAL:HG13	1.90	0.54
2:B:589:LEU:CB	2:B:609:LEU:HD12	2.35	0.54
2:B:771:ALA:HA	2:B:774:ALA:HB3	1.89	0.54
2:B:734:PRO:CB	2:B:735:PRO:HD3	2.37	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:162:GLU:HG2	1:A:166:GLY:HA2	1.89	0.54
1:A:138:ASN:ND2	1:A:289:LYS:HE2	2.23	0.54
2:B:703:ALA:N	2:B:704:PRO:HD2	2.23	0.54
2:B:705:THR:HG23	2:B:706:PRO:HD2	1.90	0.54
2:B:587:GLY:HA3	2:B:671:PHE:CE2	2.42	0.54
1:A:113:ILE:O	1:A:117:LEU:HD12	2.08	0.54
2:B:635:HIS:HB2	2:B:656:HIS:HA	1.89	0.54
2:B:44:GLY:HA3	2:B:94:THR:OG1	2.07	0.54
2:B:609:LEU:HD21	2:B:671:PHE:HD2	1.73	0.54
2:B:661:GLN:C	2:B:663:LEU:N	2.60	0.54
1:A:229:ALA:N	1:A:232:HIS:HD2	2.00	0.54
2:B:570:LEU:N	2:B:570:LEU:CD2	2.71	0.54
1:A:252:ARG:NH2	1:A:277:TRP:HB3	2.23	0.53
2:B:520:ASP:HA	2:B:523:ARG:HB2	1.90	0.53
2:B:359:ARG:HH11	2:B:359:ARG:CG	2.21	0.53
2:B:589:LEU:HD21	2:B:608:LEU:HD23	1.90	0.53
2:B:286:LEU:HD11	2:B:323:GLU:OE1	2.08	0.53
1:A:122:VAL:O	1:A:198:VAL:HG13	2.09	0.53
2:B:224:ALA:HB1	2:B:225:PRO:HD2	1.89	0.53
1:A:342:PHE:O	1:A:345:GLN:HB2	2.09	0.53
2:B:519:GLU:HB3	2:B:523:ARG:NH1	2.21	0.53
2:B:695:ARG:HB2	2:B:747:LEU:HB2	1.91	0.53
1:A:201:ARG:HD2	1:A:215:VAL:CG1	2.39	0.53
1:A:339:ARG:NH1	2:B:562:LEU:HD22	2.24	0.53
2:B:671:PHE:HD1	2:B:673:LEU:CD2	2.22	0.52
1:A:140:PRO:O	1:A:146:ARG:HB2	2.08	0.52
2:B:523:ARG:NH1	2:B:523:ARG:HG3	2.24	0.52
2:B:589:LEU:HD12	2:B:590:PHE:H	1.74	0.52
2:B:623:ALA:O	2:B:645:GLU:N	2.43	0.52
2:B:636:PRO:C	2:B:638:VAL:H	2.12	0.52
2:B:285:THR:HG23	2:B:287:ASP:OD1	2.09	0.52
2:B:684:PHE:C	2:B:685:GLN:HG2	2.28	0.52
2:B:702:PRO:HB2	2:B:704:PRO:HD2	1.90	0.52
1:A:165:LEU:HD11	1:A:303:LEU:HD21	1.92	0.52
1:A:155:THR:HG23	2:B:534:LEU:HD11	1.92	0.52
2:B:602:ARG:NH1	2:B:602:ARG:CG	2.70	0.52
1:A:126:GLU:HG3	2:B:575:ARG:HD2	1.91	0.52
2:B:557:LYS:NZ	2:B:664:GLU:HG2	2.25	0.52
2:B:174:ALA:HB1	2:B:184:LEU:CD1	2.39	0.52
2:B:214:THR:HG22	2:B:394:GLU:HG3	1.92	0.51
2:B:657:PRO:HA	2:B:660:ALA:CB	2.41	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:180:SER:N	1:A:181:PRO:HD2	2.25	0.51
1:A:348:GLY:O	1:A:350:LEU:N	2.43	0.51
2:B:282:ARG:NH2	2:B:290:GLU:HG3	2.24	0.51
2:B:284:LYS:HD3	2:B:288:GLY:HA2	1.93	0.51
2:B:262:ALA:HB1	2:B:331:ILE:HG13	1.92	0.51
2:B:299:VAL:HG22	2:B:300:ILE:N	2.26	0.51
2:B:369:GLN:CD	2:B:369:GLN:H	2.14	0.51
2:B:694:PHE:O	2:B:695:ARG:NE	2.43	0.51
2:B:728:PHE:HE1	2:B:746:HIS:N	2.09	0.51
2:B:644:VAL:O	2:B:645:GLU:C	2.50	0.51
2:B:751:HIS:HD2	2:B:752:PRO:CD	2.24	0.51
2:B:161:THR:HB	2:B:163:ASN:OD1	2.11	0.51
2:B:381:GLN:O	2:B:385:GLY:HA2	2.10	0.51
2:B:702:PRO:HA	2:B:739:GLY:O	2.12	0.50
2:B:751:HIS:HB2	2:B:756:LEU:HD21	1.92	0.50
2:B:219:PHE:CZ	2:B:387:ARG:HB3	2.47	0.50
2:B:563:ASP:C	2:B:565:PRO:HD3	2.31	0.50
2:B:294:HIS:NE2	2:B:296:GLU:HB2	2.27	0.50
2:B:509:GLU:HA	2:B:571:PHE:CE1	2.46	0.50
2:B:596:LEU:CB	2:B:599:ALA:HB3	2.39	0.50
2:B:661:GLN:HG2	2:B:662:GLU:N	2.25	0.50
2:B:707:TYR:O	2:B:707:TYR:HD1	1.95	0.50
2:B:548:LEU:HD22	2:B:584:HIS:HB3	1.93	0.50
1:A:101:HIS:CB	2:B:509:GLU:HG2	2.36	0.50
2:B:52:GLU:HA	2:B:52:GLU:OE1	2.11	0.50
2:B:198:LEU:HD12	2:B:393:LEU:CD1	2.34	0.50
2:B:164:ARG:HH12	2:B:465:ARG:NH2	2.09	0.50
1:A:211:THR:C	1:A:212:HIS:ND1	2.64	0.50
2:B:554:ARG:O	2:B:558:GLU:HG3	2.11	0.50
2:B:108:ILE:CG2	2:B:109:GLN:N	2.75	0.49
1:A:134:PHE:HZ	1:A:151:THR:CG2	2.24	0.49
2:B:49:ARG:HG3	2:B:67:ASP:HB3	1.94	0.49
2:B:609:LEU:CD2	2:B:652:LEU:HD13	2.42	0.49
1:A:287:HIS:CD2	1:A:288:PRO:HD2	2.46	0.49
2:B:520:ASP:OD2	2:B:554:ARG:NH1	2.42	0.49
2:B:299:VAL:HG23	2:B:312:GLY:O	2.13	0.49
2:B:19:GLU:CD	2:B:19:GLU:H	2.16	0.49
2:B:582:GLU:OE2	2:B:674:ARG:HD3	2.13	0.49
2:B:729:ASP:H	2:B:744:ALA:HB3	1.73	0.49
2:B:38:VAL:HG22	2:B:153:GLU:O	2.13	0.49
2:B:725:LEU:HD23	2:B:725:LEU:C	2.32	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:242:GLN:O	1:A:245:PHE:O	2.30	0.49
2:B:300:ILE:HD13	2:B:314:ALA:HA	1.93	0.49
2:B:140:LEU:HB3	2:B:141:PRO:HD2	1.94	0.49
1:A:271:TRP:CH2	1:A:274:GLY:HA3	2.48	0.49
2:B:663:LEU:C	2:B:665:LEU:N	2.65	0.49
2:B:603:LEU:C	2:B:603:LEU:HD12	2.33	0.49
1:A:209:ASP:O	1:A:333:ARG:HD2	2.13	0.48
1:A:268:ALA:HA	1:A:278:LEU:O	2.13	0.48
2:B:120:PRO:HD2	2:B:129:GLY:H	1.77	0.48
1:A:246:GLY:C	1:A:248:ASP:H	2.16	0.48
1:A:339:ARG:HH12	2:B:562:LEU:HD22	1.78	0.48
2:B:742:SER:O	2:B:743:LEU:HD23	2.14	0.48
2:B:293:LEU:HD13	2:B:293:LEU:N	2.28	0.48
2:B:644:VAL:HG13	2:B:645:GLU:N	2.28	0.48
1:A:341:LYS:HE2	1:A:341:LYS:N	2.28	0.48
2:B:139:ALA:O	2:B:140:LEU:HD12	2.12	0.48
1:A:128:GLU:HG3	1:A:129:SER:H	1.78	0.48
2:B:661:GLN:C	2:B:663:LEU:H	2.16	0.48
2:B:720:PRO:C	2:B:721:TYR:HD1	2.16	0.48
2:B:757:ARG:HB3	2:B:760:GLU:OE2	2.14	0.48
2:B:773:ARG:C	2:B:775:ARG:N	2.66	0.48
2:B:404:ILE:HD12	2:B:446:PRO:HD3	1.95	0.48
2:B:671:PHE:CD1	2:B:673:LEU:CD2	2.97	0.48
2:B:549:PHE:CD2	2:B:550:PRO:HD3	2.49	0.48
2:B:635:HIS:CE1	2:B:636:PRO:O	2.67	0.48
2:B:119:SER:OG	2:B:122:GLU:HG3	2.13	0.48
2:B:281:GLU:HG2	2:B:310:PRO:HG3	1.96	0.48
2:B:527:ASP:HB3	2:B:528:PRO:HD2	1.95	0.48
2:B:705:THR:CG2	2:B:706:PRO:HD2	2.44	0.48
2:B:721:TYR:N	2:B:721:TYR:CD1	2.81	0.48
2:B:35:ILE:O	2:B:36:GLU:HG2	2.13	0.48
2:B:42:PRO:HA	2:B:43:ARG:NH1	2.29	0.48
2:B:294:HIS:CD2	2:B:296:GLU:HB2	2.49	0.47
2:B:765:VAL:HG13	2:B:766:SER:N	2.29	0.47
1:A:277:TRP:C	1:A:278:LEU:HD23	2.34	0.47
2:B:728:PHE:N	2:B:728:PHE:CD1	2.82	0.47
2:B:600:LYS:CG	2:B:601:GLU:H	2.11	0.47
1:A:229:ALA:H	1:A:232:HIS:CD2	2.17	0.47
2:B:585:LEU:HB2	2:B:675:LEU:HD11	1.96	0.47
2:B:605:GLY:O	2:B:608:LEU:HB3	2.14	0.47
2:B:688:SER:OG	2:B:752:PRO:HA	2.13	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:224:ALA:HB1	2:B:225:PRO:CD	2.45	0.47
2:B:120:PRO:HG2	2:B:128:TYR:HB3	1.96	0.47
2:B:92:PRO:HD3	2:B:114:PHE:O	2.15	0.47
1:A:233:LEU:O	1:A:236:ALA:HB3	2.14	0.47
2:B:509:GLU:HB2	2:B:571:PHE:CZ	2.49	0.47
2:B:757:ARG:CD	2:B:759:GLU:H	2.24	0.47
1:A:219:LEU:HB3	1:A:317:LEU:HD21	1.97	0.47
2:B:759:GLU:O	2:B:763:GLU:HB2	2.15	0.47
2:B:770:GLU:O	2:B:774:ALA:CB	2.61	0.47
1:A:271:TRP:NE1	1:A:273:GLU:HB2	2.29	0.47
2:B:498:LEU:O	2:B:498:LEU:HD12	2.14	0.47
1:A:143:HIS:CB	1:A:144:PRO:HD2	2.44	0.47
2:B:221:LEU:CD2	2:B:386:ALA:HB2	2.44	0.47
2:B:63:ARG:HD2	2:B:73:GLU:OE2	2.14	0.47
2:B:91:LEU:HB3	2:B:92:PRO:HD2	1.96	0.47
2:B:198:LEU:N	2:B:198:LEU:HD23	2.29	0.47
2:B:482:ALA:HB3	2:B:485:ASN:HD21	1.78	0.47
1:A:178:HIS:HA	1:A:202:VAL:HG11	1.95	0.47
1:A:252:ARG:O	1:A:267:PHE:HA	2.14	0.47
2:B:265:LEU:HA	2:B:268:VAL:HG23	1.96	0.47
2:B:56:ILE:HG12	2:B:56:ILE:H	1.60	0.47
2:B:635:HIS:HB2	2:B:657:PRO:HD3	1.97	0.46
2:B:374:ARG:HA	2:B:374:ARG:HD3	1.76	0.46
2:B:16:GLU:O	2:B:17:SER:HB3	2.15	0.46
2:B:286:LEU:HB3	2:B:317:MET:HE3	1.97	0.46
2:B:761:VAL:CG2	2:B:762:GLU:N	2.70	0.46
1:A:267:PHE:CE1	1:A:280:LEU:HB3	2.51	0.46
2:B:629:GLN:O	2:B:639:SER:HB3	2.15	0.46
2:B:244:ASN:O	2:B:248:VAL:HG23	2.16	0.46
2:B:727:LEU:HA	2:B:744:ALA:O	2.16	0.46
2:B:660:ALA:O	2:B:665:LEU:O	2.33	0.46
1:A:216:PHE:HB2	1:A:320:GLU:OE1	2.16	0.46
2:B:730:LEU:CD1	2:B:730:LEU:C	2.79	0.46
2:B:651:PHE:CE2	2:B:672:GLU:HB3	2.51	0.46
2:B:559:ASN:O	2:B:563:ASP:O	2.33	0.46
2:B:303:TRP:HB2	2:B:307:GLU:O	2.15	0.46
1:A:260:PHE:CD1	1:A:260:PHE:N	2.84	0.46
2:B:243:ASN:HD21	2:B:246:VAL:H	1.60	0.46
1:A:187:MET:HB3	1:A:294:VAL:HG11	1.97	0.46
2:B:107:VAL:HA	2:B:112:ARG:HA	1.97	0.46
2:B:276:ARG:NH1	2:B:296:GLU:O	2.38	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:710:VAL:HG11	2:B:743:LEU:HD12	1.98	0.46
2:B:623:ALA:O	2:B:645:GLU:HA	2.15	0.46
1:A:110:LEU:HD11	1:A:322:LEU:HD23	1.96	0.46
2:B:253:MET:HG3	2:B:259:PRO:HA	1.97	0.46
2:B:573:VAL:HG22	2:B:585:LEU:HD13	1.97	0.46
2:B:600:LYS:HG2	2:B:601:GLU:CG	2.44	0.45
2:B:617:PHE:HB3	2:B:622:LEU:O	2.16	0.45
1:A:197:VAL:HG22	1:A:219:LEU:HD11	1.98	0.45
1:A:95:LEU:HA	1:A:95:LEU:HD12	1.73	0.45
1:A:175:LEU:HB3	1:A:203:PHE:CD1	2.50	0.45
2:B:531:LEU:O	2:B:532:LEU:HD13	2.16	0.45
2:B:769:ALA:O	2:B:772:LEU:HB3	2.16	0.45
2:B:219:PHE:HE2	2:B:387:ARG:NE	2.04	0.45
2:B:635:HIS:HB2	2:B:657:PRO:CD	2.46	0.45
2:B:523:ARG:HH11	2:B:523:ARG:CG	2.29	0.45
2:B:692:ALA:HA	2:B:749:PHE:O	2.16	0.45
1:A:349:VAL:O	1:A:349:VAL:CG1	2.65	0.45
2:B:535:ASN:N	2:B:536:PRO:HD3	2.31	0.45
2:B:94:THR:HG22	2:B:96:LEU:HD13	1.99	0.45
2:B:672:GLU:C	2:B:673:LEU:HD22	2.36	0.45
1:A:244:LEU:HA	1:A:244:LEU:HD23	1.74	0.45
2:B:642:VAL:HG23	2:B:651:PHE:HA	1.99	0.45
2:B:105:GLU:HG3	2:B:114:PHE:CD1	2.52	0.45
1:A:154:LEU:HD22	1:A:174:LEU:CA	2.47	0.45
2:B:649:VAL:CG2	2:B:674:ARG:H	2.30	0.45
2:B:669:HIS:O	2:B:670:LEU:HD12	2.17	0.45
2:B:381:GLN:HG3	2:B:386:ALA:O	2.17	0.45
1:A:113:ILE:O	1:A:117:LEU:CD1	2.65	0.45
1:A:94:SER:HB2	2:B:567:ARG:NH2	2.32	0.45
1:A:174:LEU:HD23	1:A:174:LEU:C	2.38	0.45
1:A:256:VAL:HG22	1:A:257:TYR:H	1.82	0.44
2:B:264:ASP:CG	2:B:328:THR:HG23	2.37	0.44
1:A:193:PRO:HB2	2:B:479:PHE:CE1	2.52	0.44
1:A:221:GLY:O	1:A:314:ALA:HA	2.16	0.44
1:A:252:ARG:HE	1:A:268:ALA:HB3	1.82	0.44
2:B:549:PHE:CD1	2:B:550:PRO:N	2.85	0.44
2:B:427:ILE:HG12	2:B:466:ILE:HG21	1.99	0.44
2:B:707:TYR:CE2	2:B:727:LEU:HD22	2.49	0.44
2:B:121:ARG:HA	2:B:126:GLY:O	2.17	0.44
2:B:731:TYR:CE2	2:B:733:GLY:HA2	2.52	0.44
2:B:458:ASP:O	2:B:462:GLU:HG2	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:122:VAL:CG1	2:B:488:VAL:HG13	2.47	0.44
1:A:149:TRP:CD1	1:A:177:THR:CG2	2.98	0.44
2:B:717:ALA:C	2:B:768:VAL:HG22	2.38	0.44
1:A:141:GLU:HG3	1:A:142:HIS:N	2.32	0.44
2:B:775:ARG:HE	2:B:775:ARG:HB3	1.49	0.44
2:B:420:PRO:HG2	2:B:423:GLU:HB2	1.99	0.44
2:B:650:GLY:HA3	2:B:673:LEU:CD1	2.45	0.44
1:A:146:ARG:HB2	1:A:146:ARG:HE	1.66	0.44
2:B:609:LEU:HD21	2:B:671:PHE:CD2	2.52	0.44
2:B:592:GLU:OE1	2:B:592:GLU:N	2.50	0.44
2:B:728:PHE:CE1	2:B:746:HIS:N	2.86	0.44
2:B:163:ASN:O	2:B:452:ASP:HB3	2.18	0.44
2:B:275:ARG:O	2:B:298:LEU:HD23	2.18	0.44
1:A:133:ASN:OD1	1:A:176:ARG:HA	2.17	0.44
2:B:72:VAL:HG22	2:B:73:GLU:N	2.33	0.43
2:B:765:VAL:CG1	2:B:766:SER:N	2.81	0.43
2:B:661:GLN:O	2:B:663:LEU:N	2.51	0.43
2:B:666:PRO:HB2	2:B:667:PRO:HD2	1.97	0.43
2:B:699:VAL:HG12	2:B:773:ARG:NH2	2.33	0.43
2:B:289:VAL:HG12	2:B:291:ARG:HG2	2.00	0.43
2:B:710:VAL:HG11	2:B:743:LEU:CD1	2.49	0.43
2:B:680:LYS:O	2:B:680:LYS:HG2	2.18	0.43
1:A:300:ARG:HG3	1:A:300:ARG:O	2.19	0.43
2:B:548:LEU:HD12	2:B:548:LEU:HA	1.88	0.43
2:B:523:ARG:HH11	2:B:523:ARG:HG3	1.81	0.43
2:B:647:GLU:HA	2:B:647:GLU:OE1	2.18	0.43
2:B:515:PHE:CE1	2:B:533:LEU:HD21	2.54	0.43
2:B:652:LEU:HD12	2:B:653:GLY:N	2.33	0.43
1:A:238:TYR:C	1:A:238:TYR:CD1	2.91	0.43
2:B:75:VAL:CG1	2:B:108:ILE:HG21	2.33	0.43
2:B:161:THR:HG22	2:B:162:PRO:CD	2.47	0.43
1:A:270:TRP:O	1:A:272:PRO:HD3	2.18	0.43
2:B:548:LEU:HD13	2:B:576:VAL:HG12	1.99	0.43
1:A:262:GLU:OE1	2:B:458:ASP:HA	2.18	0.43
1:A:317:LEU:O	1:A:317:LEU:HD23	2.17	0.43
2:B:141:PRO:HG2	2:B:144:THR:CG2	2.49	0.43
2:B:88:ALA:O	2:B:117:ALA:HA	2.19	0.43
2:B:609:LEU:CD2	2:B:652:LEU:CD1	2.97	0.43
1:A:280:LEU:HD12	1:A:280:LEU:HA	1.75	0.43
2:B:486:ARG:HA	2:B:486:ARG:HD3	1.66	0.43
2:B:600:LYS:CD	2:B:600:LYS:H	2.32	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:675:LEU:HB3	2:B:676:PRO:HA	2.01	0.43
2:B:514:SER:O	2:B:545:ARG:HG2	2.19	0.43
2:B:40:PRO:HA	2:B:152:GLU:OE2	2.19	0.43
2:B:447:PRO:HB2	2:B:449:HIS:CE1	2.54	0.43
2:B:548:LEU:HD22	2:B:584:HIS:CB	2.49	0.42
2:B:768:VAL:O	2:B:772:LEU:N	2.51	0.42
2:B:600:LYS:N	2:B:600:LYS:CD	2.82	0.42
1:A:101:HIS:CD2	1:A:103:ILE:HB	2.55	0.42
2:B:668:VAL:HG12	2:B:669:HIS:N	2.34	0.42
2:B:761:VAL:C	2:B:763:GLU:H	2.21	0.42
2:B:766:SER:O	2:B:770:GLU:HB3	2.19	0.42
2:B:572:GLU:HG3	2:B:573:VAL:N	2.35	0.42
2:B:258:GLN:NE2	5:B:854:HOH:O	2.48	0.42
1:A:105:LEU:HD22	1:A:349:VAL:CG1	2.49	0.42
2:B:642:VAL:HG23	2:B:651:PHE:CA	2.49	0.42
2:B:44:GLY:O	2:B:91:LEU:HD12	2.20	0.42
2:B:365:ASP:HA	2:B:366:PRO:HD2	1.76	0.42
2:B:421:GLU:O	2:B:425:ILE:HG12	2.19	0.42
2:B:285:THR:OG1	2:B:286:LEU:N	2.52	0.42
1:A:117:LEU:N	1:A:117:LEU:HD12	2.35	0.42
2:B:725:LEU:CD2	2:B:725:LEU:C	2.88	0.42
2:B:707:TYR:O	2:B:707:TYR:CD1	2.72	0.42
2:B:731:TYR:HD1	2:B:742:SER:HG	1.59	0.42
2:B:754:ARG:HD2	2:B:755:THR:O	2.19	0.42
1:A:327:TYR:HB3	1:A:346:PHE:HE2	1.85	0.42
2:B:707:TYR:O	2:B:708:GLY:C	2.58	0.42
2:B:300:ILE:HD12	2:B:314:ALA:HB2	2.02	0.42
2:B:46:VAL:HB	2:B:143:GLY:O	2.19	0.42
2:B:145:PRO:O	2:B:148:GLU:HB2	2.20	0.42
2:B:286:LEU:HD13	2:B:320:ALA:HA	2.01	0.42
2:B:297:ASP:OD1	2:B:346:THR:HG23	2.20	0.42
1:A:237:ILE:O	1:A:240:LEU:HB3	2.20	0.42
2:B:265:LEU:HD23	2:B:268:VAL:CG2	2.48	0.42
2:B:263:PHE:O	2:B:331:ILE:HB	2.20	0.42
1:A:265:ALA:HB2	2:B:469:TYR:CE2	2.52	0.42
2:B:533:LEU:HB2	2:B:536:PRO:HG3	2.02	0.42
2:B:557:LYS:HE3	2:B:664:GLU:OE2	2.20	0.42
2:B:490:ALA:HB3	2:B:491:PRO:CD	2.41	0.42
2:B:548:LEU:C	2:B:550:PRO:HD2	2.41	0.41
2:B:35:ILE:C	2:B:36:GLU:HG2	2.41	0.41
2:B:634:LEU:HB3	2:B:639:SER:OG	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:175:LEU:O	1:A:176:ARG:C	2.58	0.41
1:A:238:TYR:HA	1:A:251:VAL:HG11	2.01	0.41
2:B:702:PRO:O	2:B:741:LYS:HE2	2.20	0.41
2:B:773:ARG:HB2	2:B:773:ARG:HH11	1.85	0.41
2:B:141:PRO:HA	2:B:142:PRO:HD2	1.94	0.41
2:B:450:ARG:HA	2:B:450:ARG:HD2	1.64	0.41
2:B:250:ASN:O	2:B:254:LEU:HG	2.20	0.41
1:A:183:GLN:NE2	1:A:220:GLU:OE2	2.52	0.41
2:B:532:LEU:N	2:B:532:LEU:HD22	2.35	0.41
2:B:700:VAL:CG1	2:B:736:LEU:HD13	2.50	0.41
2:B:688:SER:HB3	2:B:752:PRO:O	2.20	0.41
2:B:253:MET:O	2:B:256:ARG:O	2.39	0.41
2:B:537:LEU:HA	2:B:537:LEU:HD23	1.69	0.41
2:B:83:LYS:HG2	2:B:84:GLY:N	2.35	0.41
2:B:617:PHE:CE2	2:B:644:VAL:HG23	2.55	0.41
1:A:348:GLY:C	1:A:350:LEU:N	2.74	0.41
1:A:152:PHE:CE1	1:A:205:PHE:HD2	2.39	0.41
2:B:151:PRO:HD2	2:B:232:ARG:NE	2.36	0.41
2:B:219:PHE:N	2:B:219:PHE:CD1	2.88	0.41
2:B:598:TRP:CZ3	2:B:599:ALA:HB2	2.56	0.41
2:B:566:GLU:CG	2:B:592:GLU:HG2	2.51	0.41
2:B:505:LEU:HD12	2:B:505:LEU:HA	1.67	0.41
2:B:530:ARG:NH1	2:B:530:ARG:HB2	2.36	0.41
2:B:755:THR:CG2	2:B:756:LEU:N	2.84	0.41
2:B:733:GLY:HA3	2:B:736:LEU:HD21	2.02	0.41
2:B:523:ARG:NH1	2:B:523:ARG:CG	2.84	0.41
1:A:184:VAL:O	1:A:185:ARG:C	2.59	0.41
2:B:304:ARG:O	2:B:307:GLU:HB2	2.21	0.41
2:B:119:SER:HB2	2:B:129:GLY:HA2	2.03	0.41
2:B:3:VAL:HA	2:B:4:PRO:HD3	1.83	0.41
2:B:509:GLU:HB2	2:B:571:PHE:CE1	2.56	0.41
2:B:176:ASP:O	2:B:179:ALA:HB3	2.21	0.41
2:B:751:HIS:HE1	5:B:811:HOH:O	2.04	0.41
1:A:242:GLN:OE1	1:A:247:PRO:HB3	2.20	0.41
2:B:557:LYS:HG3	2:B:557:LYS:HZ2	1.82	0.41
2:B:556:LEU:C	2:B:556:LEU:HD12	2.41	0.40
1:A:94:SER:O	2:B:594:VAL:HG12	2.22	0.40
1:A:128:GLU:HG3	1:A:129:SER:N	2.36	0.40
2:B:404:ILE:HG12	2:B:454:ARG:O	2.21	0.40
2:B:535:ASN:N	2:B:535:ASN:OD1	2.54	0.40
2:B:758:ASP:CA	2:B:761:VAL:HG22	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:82:ARG:HH12	2:B:134:GLU:CD	2.24	0.40
2:B:487:GLY:O	2:B:489:GLU:N	2.55	0.40
1:A:301:LEU:HD23	1:A:301:LEU:HA	1.84	0.40
2:B:509:GLU:CA	2:B:571:PHE:CE1	3.04	0.40
2:B:198:LEU:HA	2:B:199:PRO:HD2	1.74	0.40
2:B:294:HIS:CD2	2:B:296:GLU:N	2.70	0.40
2:B:761:VAL:C	2:B:763:GLU:N	2.74	0.40
2:B:346:THR:O	2:B:349:ARG:HB3	2.22	0.40
2:B:14:GLU:H	2:B:14:GLU:HG3	1.73	0.40
2:B:301:ALA:HB1	2:B:309:PHE:O	2.21	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	263/350 (75%)	243 (92%)	13 (5%)	7 (3%)	6	16
2	B	773/785 (98%)	684 (88%)	70 (9%)	19 (2%)	7	18
All	All	1036/1135 (91%)	927 (90%)	83 (8%)	26 (2%)	7	18

All (26) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	138	ASN
2	B	488	VAL
2	B	664	GLU
1	A	94	SER
1	A	338	GLY
2	B	128	TYR
2	B	645	GLU
2	B	708	GLY

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Mol	Chain	Res	Type
2	B	772	LEU
2	B	486	ARG
2	B	525	ARG
2	B	600	LYS
2	B	735	PRO
2	B	199	PRO
2	B	557	LYS
1	A	330	PRO
1	A	349	VAL
2	B	196	LEU
2	B	737	PRO
2	B	752	PRO
2	B	770	GLU
1	A	273	GLU
2	B	761	VAL
2	B	702	PRO
2	B	710	VAL
1	A	247	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	213/277 (77%)	173 (81%)	40 (19%)	2	5
2	B	623/630 (99%)	494 (79%)	129 (21%)	1	4
All	All	836/907 (92%)	667 (80%)	169 (20%)	1	4

All (169) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	86	VAL
1	A	95	LEU
1	A	115	ARG
1	A	122	VAL
1	A	129	SER

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Mol	Chain	Res	Type
1	A	138	ASN
1	A	143	HIS
1	A	146	ARG
1	A	147	ASP
1	A	151	THR
1	A	154	LEU
1	A	168	GLU
1	A	174	LEU
1	A	177	THR
1	A	178	HIS
1	A	182	MET
1	A	183	GLN
1	A	204	ARG
1	A	209	ASP
1	A	213	GLU
1	A	230	MET
1	A	237	ILE
1	A	245	PHE
1	A	250	LYS
1	A	252	ARG
1	A	260	PHE
1	A	266	GLN
1	A	276	LYS
1	A	280	LEU
1	A	292	GLN
1	A	299	GLU
1	A	303	LEU
1	A	317	LEU
1	A	321	ARG
1	A	326	ARG
1	A	339	ARG
1	A	340	LEU
1	A	341	LYS
1	A	347	LYS
1	A	350	LEU
2	B	2	ARG
2	B	33	ASP
2	B	37	ARG
2	B	43	ARG
2	B	49	ARG
2	B	56	ILE
2	B	59	THR

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Mol	Chain	Res	Type
2	B	60	ARG
2	B	70	ARG
2	B	89	LEU
2	B	95	GLU
2	B	96	LEU
2	B	99	LEU
2	B	106	ARG
2	B	108	ILE
2	B	109	GLN
2	B	111	VAL
2	B	127	GLU
2	B	144	THR
2	B	148	GLU
2	B	152	GLU
2	B	157	ASP
2	B	161	THR
2	B	171	LEU
2	B	176	ASP
2	B	186	GLU
2	B	188	GLU
2	B	196	LEU
2	B	203	LYS
2	B	208	GLU
2	B	222	ARG
2	B	226	SER
2	B	230	MET
2	B	235	PHE
2	B	239	MET
2	B	243	ASN
2	B	256	ARG
2	B	282	ARG
2	B	283	LEU
2	B	284	LYS
2	B	285	THR
2	B	286	LEU
2	B	293	LEU
2	B	298	LEU
2	B	307	GLU
2	B	308	SER
2	B	313	LEU
2	B	326	GLU
2	B	329	GLU

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Mol	Chain	Res	Type
2	B	331	ILE
2	B	339	ASP
2	B	345	LYS
2	B	357	SER
2	B	361	GLU
2	B	397	SER
2	B	438	GLU
2	B	441	THR
2	B	459	LEU
2	B	461	GLU
2	B	486	ARG
2	B	494	LYS
2	B	497	ARG
2	B	499	ARG
2	B	509	GLU
2	B	512	THR
2	B	523	ARG
2	B	525	ARG
2	B	526	LEU
2	B	541	LYS
2	B	545	ARG
2	B	548	LEU
2	B	554	ARG
2	B	556	LEU
2	B	558	GLU
2	B	562	LEU
2	B	567	ARG
2	B	570	LEU
2	B	572	GLU
2	B	575	ARG
2	B	579	GLU
2	B	588	LEU
2	B	590	PHE
2	B	592	GLU
2	B	600	LYS
2	B	601	GLU
2	B	602	ARG
2	B	603	LEU
2	B	609	LEU
2	B	613	LEU
2	B	624	PHE
2	B	633	PHE

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Mol	Chain	Res	Type
2	B	634	LEU
2	B	635	HIS
2	B	638	VAL
2	B	639	SER
2	B	645	GLU
2	B	648	GLU
2	B	649	VAL
2	B	661	GLN
2	B	662	GLU
2	B	663	LEU
2	B	670	LEU
2	B	674	ARG
2	B	682	LEU
2	B	685	GLN
2	B	688	SER
2	B	689	ARG
2	B	700	VAL
2	B	701	VAL
2	B	707	TYR
2	B	711	GLU
2	B	713	LEU
2	B	715	ARG
2	B	716	GLU
2	B	727	LEU
2	B	728	PHE
2	B	730	LEU
2	B	731	TYR
2	B	732	GLN
2	B	736	LEU
2	B	738	GLU
2	B	741	LYS
2	B	746	HIS
2	B	748	ARG
2	B	757	ARG
2	B	759	GLU
2	B	767	ARG
2	B	770	GLU
2	B	775	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	101	HIS
1	A	120	GLN
1	A	138	ASN
1	A	142	HIS
1	A	178	HIS
1	A	183	GLN
1	A	232	HIS
1	A	287	HIS
2	B	101	GLN
2	B	109	GLN
2	B	178	HIS
2	B	231	GLN
2	B	243	ASN
2	B	258	GLN
2	B	294	HIS
2	B	656	HIS

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 ⓘ

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	PHE	A	352	-	9,12,12	0.71	0	9,15,15	0.50	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	PHE	A	352	-	-	0/4/8/8	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	265/350 (75%)	0.03	6 (2%) 64 64	30, 62, 101, 121	0
2	B	775/785 (98%)	0.15	40 (5%) 31 30	28, 66, 115, 130	0
All	All	1040/1135 (91%)	0.12	46 (4%) 38 37	28, 65, 114, 130	0

All (46) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	99	LEU	5.6
2	B	768	VAL	4.5
2	B	718	ALA	4.4
2	B	769	ALA	4.2
2	B	696	ASP	4.1
2	B	743	LEU	3.8
2	B	731	TYR	3.7
2	B	753	LYS	3.7
2	B	762	GLU	3.6
2	B	659	ILE	3.5
2	B	637	GLY	3.4
2	B	736	LEU	3.2
2	B	98	GLY	3.1
2	B	688	SER	3.1
2	B	699	VAL	3.0
2	B	101	GLN	3.0
2	B	704	PRO	3.0
1	A	158	GLY	2.9
2	B	752	PRO	2.9
2	B	700	VAL	2.9
2	B	100	GLY	2.8
2	B	734	PRO	2.8
2	B	638	VAL	2.8
2	B	739	GLY	2.7

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Mol	Chain	Res	Type	RSRZ
2	B	772	LEU	2.7
2	B	703	ALA	2.6
2	B	759	GLU	2.6
2	B	695	ARG	2.5
1	A	99	GLY	2.4
2	B	443	ARG	2.4
2	B	732	GLN	2.3
2	B	630	ALA	2.3
2	B	763	GLU	2.3
2	B	733	GLY	2.3
1	A	142	HIS	2.2
1	A	143	HIS	2.2
2	B	698	ALA	2.2
2	B	756	LEU	2.2
2	B	277	ALA	2.2
1	A	169	VAL	2.2
1	A	350	LEU	2.1
2	B	435	VAL	2.1
2	B	775	ARG	2.1
2	B	738	GLU	2.0
2	B	744	ALA	2.0
2	B	633	PHE	2.0

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
4	PHE	A	352	12/12	0.95	0.22	3.51	58,64,87,87	0
3	MG	A	351	1/1	0.94	0.18	1.26	36,36,36,36	0

6.5 Other polymers [i](#)

There are no such residues in this entry.