



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 11:03 AM GMT

PDB ID : 3NWA
Title : Glycoprotein B from Herpes simplex virus type 1, W174R mutant, low-pH
Authors : Stampfer, S.D.; Lou, H.; Cohen, G.H.; Eisenberg, R.J.; Heldwein, E.E.
Deposited on : 2010-07-09
Resolution : 2.26 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

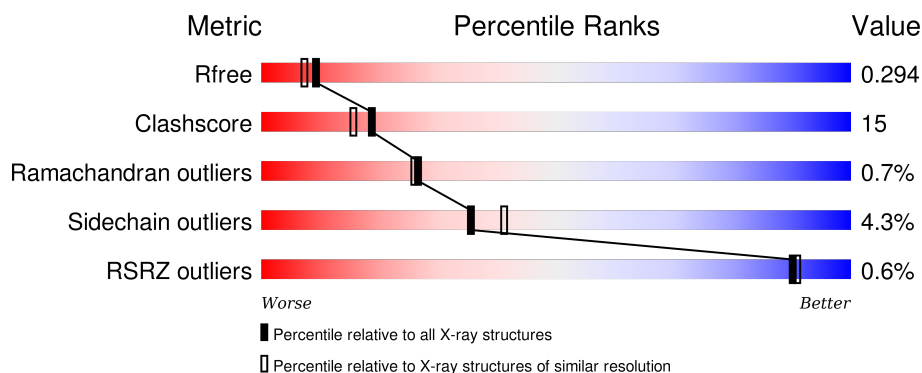
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.26 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	1640 (2.28-2.24)
Clashscore	102246	1095 (2.26-2.26)
Ramachandran outliers	100387	1063 (2.26-2.26)
Sidechain outliers	100360	1063 (2.26-2.26)
RSRZ outliers	91569	1647 (2.28-2.24)

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	703	<div> <div>62%</div> <div>23%</div> <div>•</div> <div>14%</div> </div>
1	B	703	<div> <div>%</div> <div>56%</div> <div>29%</div> <div>•</div> <div>14%</div> </div>
1	C	703	<div> <div>%</div> <div>59%</div> <div>26%</div> <div>•</div> <div>14%</div> </div>
1	D	703	<div> <div>59%</div> <div>26%</div> <div>•</div> <div>14%</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	NAG	A	1398	-	-	-	X
3	MRY	A	2000	-	-	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 21541 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 Envelope glycoprotein B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	607	Total	C	N	O	S	0	1	0
			4896	3086	867	920	23			
1	A	608	Total	C	N	O	S	0	1	0
			4899	3088	867	922	22			
1	C	608	Total	C	N	O	S	0	0	0
			4883	3080	864	917	22			
1	D	607	Total	C	N	O	S	0	1	0
			4900	3087	867	923	23			

There are 24 discrepancies between the modelled and reference sequences:

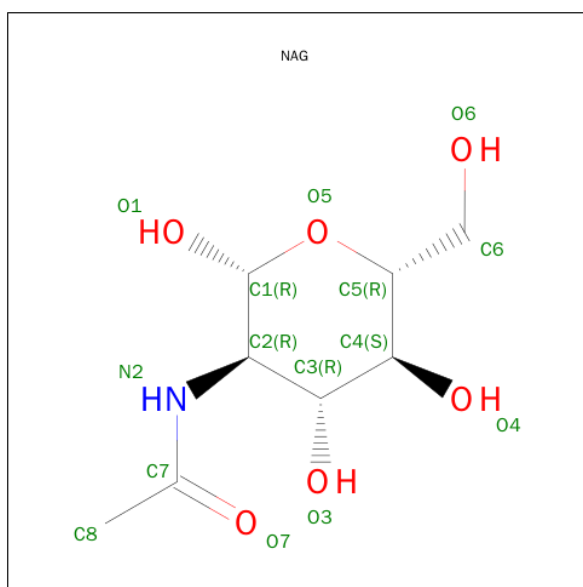
Chain	Residue	Modelled	Actual	Comment	Reference
B	28	ASP	-	EXPRESSION TAG	UNP P06437
B	29	PRO	-	EXPRESSION TAG	UNP P06437
B	58	ALA	PRO	SEE REMARK 999	UNP P06437
B	174	ARG	TRP	ENGINEERED MUTATION	UNP P06437
B	313	SER	THR	SEE REMARK 999	UNP P06437
B	443	LEU	GLN	SEE REMARK 999	UNP P06437
A	28	ASP	-	EXPRESSION TAG	UNP P06437
A	29	PRO	-	EXPRESSION TAG	UNP P06437
A	58	ALA	PRO	SEE REMARK 999	UNP P06437
A	174	ARG	TRP	ENGINEERED MUTATION	UNP P06437
A	313	SER	THR	SEE REMARK 999	UNP P06437
A	443	LEU	GLN	SEE REMARK 999	UNP P06437
C	28	ASP	-	EXPRESSION TAG	UNP P06437
C	29	PRO	-	EXPRESSION TAG	UNP P06437
C	58	ALA	PRO	SEE REMARK 999	UNP P06437
C	174	ARG	TRP	ENGINEERED MUTATION	UNP P06437
C	313	SER	THR	SEE REMARK 999	UNP P06437
C	443	LEU	GLN	SEE REMARK 999	UNP P06437
D	28	ASP	-	EXPRESSION TAG	UNP P06437
D	29	PRO	-	EXPRESSION TAG	UNP P06437
D	58	ALA	PRO	SEE REMARK 999	UNP P06437

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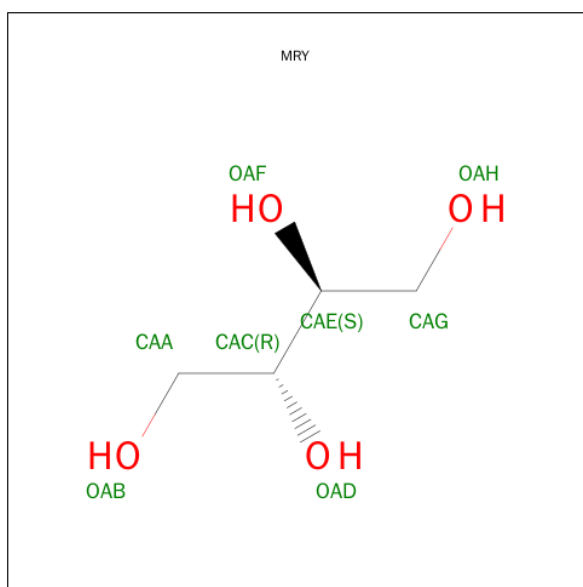
Chain	Residue	Modelled	Actual	Comment	Reference
D	174	ARG	TRP	ENGINEERED MUTATION	UNP P06437
D	313	SER	THR	SEE REMARK 999	UNP P06437
D	443	LEU	GLN	SEE REMARK 999	UNP P06437

- Molecule 2 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	C	1	Total	C	N	O	0	0
			14	8	1	5		
2	D	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 3 is MESO-ERYTHRITOL (three-letter code: MRY) (formula: $C_4H_{10}O_4$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	C	O	0	0
			8	4	4		
3	B	1	Total	C	O	0	0
			8	4	4		
3	A	1	Total	C	O	0	0
			8	4	4		
3	C	1	Total	C	O	0	0
			8	4	4		
3	D	1	Total	C	O	0	0
			8	4	4		

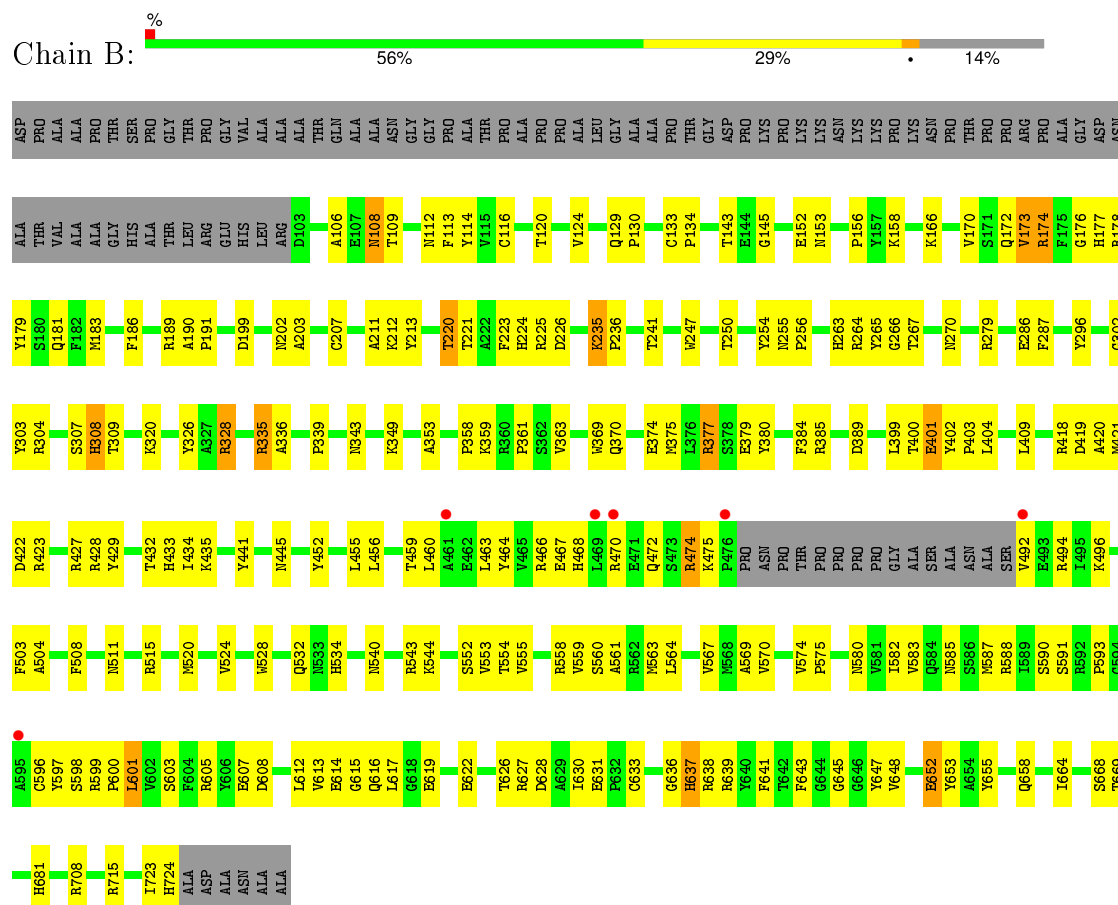
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	444	Total	O	0	0
			444	444		
4	A	478	Total	O	0	0
			478	478		
4	C	462	Total	O	0	0
			462	462		
4	D	483	Total	O	0	0
			483	483		

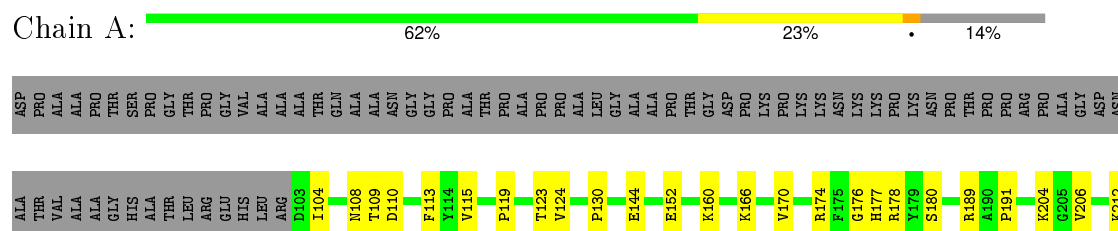
3 Residue-property plots

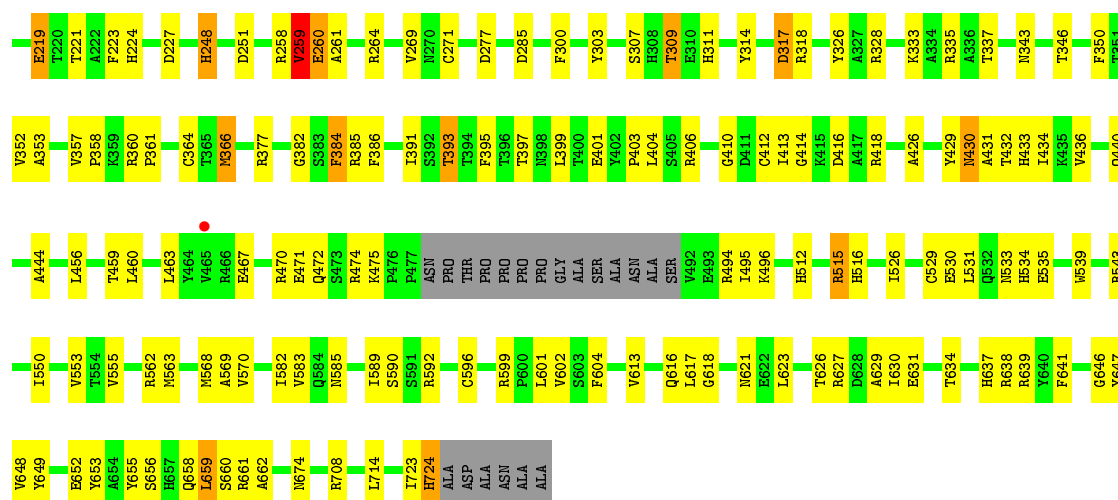
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according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

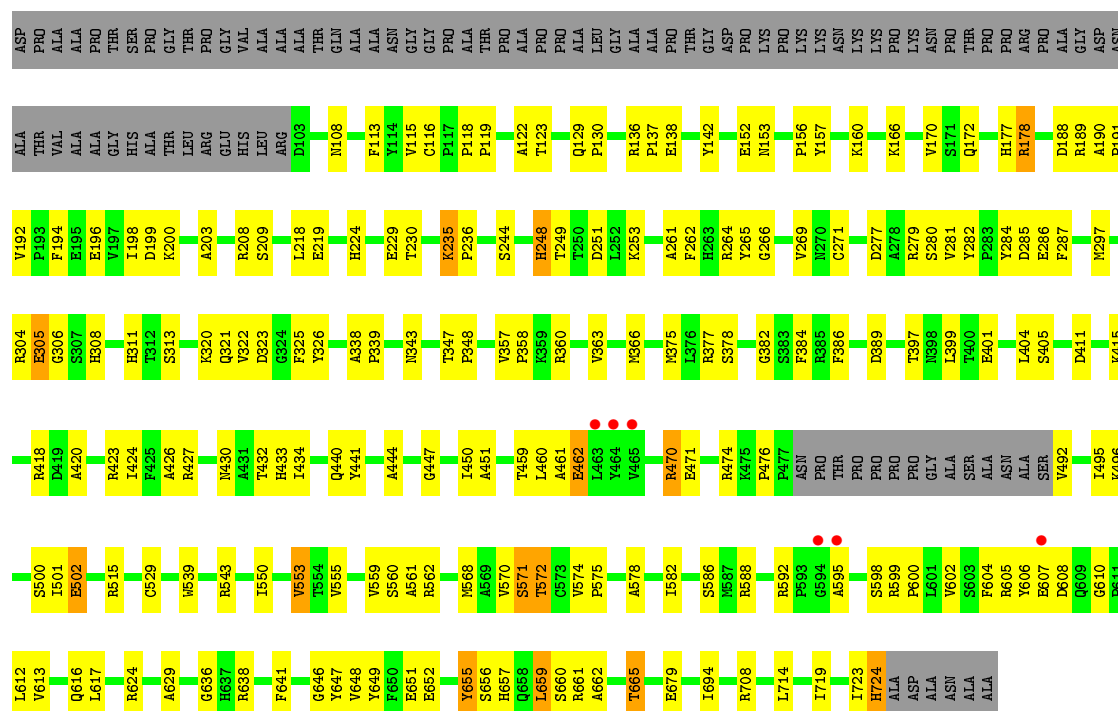


• Molecule 1: Envelope glycoprotein B

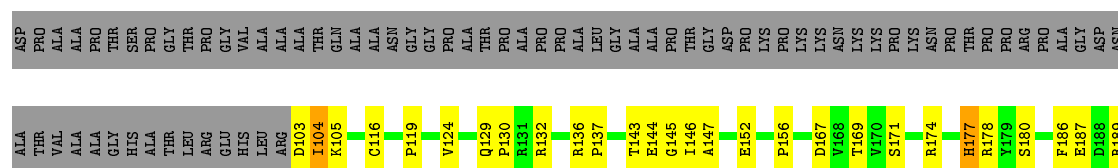




• Molecule 1: Envelope glycoprotein B



• Molecule 1: Envelope glycoprotein B



E607	D608	Q609	V613	Q616	L617	E622	L623	R624	T634	V635	G636	R637	R638	R639	Y640	F650	E651	E652	Y655	L659	S660	R661	I664	H681	E682	F683	V684	R691	S697	D701	E704	R708	H724	ALA	ASP	ALA	ASN	ALA	ALA													
N511	H512	I513	Q514	R515	M520	R523	V524	L531	H534	E535	G536	R537	R538	R539	Y540	F550	E551	E552	V553	V559	S560	A561	R562	M563	L564	V567	N568	A569	V570	A577	M580	V581	I582	M587	R588	I589	S590	S591	R592	P593	Y597	S598	R599	P600	L601	V602	S603	F604	R605	Y606		
H433	I434	K435	Q438	P439	Q440	Y441	Y442	L443	A451	L455	L456	S457	M458	T459	L460	L463	R466	E467	H468	L469	A470	E471	Q472	S473	R474	K475	P476	P477	ASN	PRO	THR	PRO	PRO	PRO	PRO	GLY	ALA	SER	ALA	ASN	ALA	SER	VAL	E493	K496	S499	L424	S500	I501	E502	F503	A504
T332	K333	A334	R335	P339	N343	K349	A353	R360	P361	S362	V363	C364	T365	M366	E379	Y380	F384	R385	F386	S387	S388	I391	S392	I393	T394	L399	T400	E401	Y402	P403	L404	V407	D408	L409	G410	G414	S307	R418	D419	R423	I424	F425	R428	Y429	R328	T432						

4 Data and refinement statistics

Property	Value	Source
Space group	P 3	Depositor
Cell constants a, b, c, α , β , γ	117.09Å 117.09Å 321.38Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	47.32 – 2.26 48.35 – 2.26	Depositor EDS
% Data completeness (in resolution range)	87.1 (47.32-2.26) 87.1 (48.35-2.26)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.45 (at 2.27Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6.1_357)	Depositor
R, R_{free}	0.172 , 0.227 0.253 , 0.294	Depositor DCC
R_{free} test set	11385 reflections (5.98%)	DCC
Wilson B-factor (Å ²)	28.3	Xtriage
Anisotropy	0.493	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	(Not available) , (Not available)	EDS
Estimated twinning fraction	0.020 for -h,-k,l 0.467 for h,-h-k,-l 0.021 for -k,-h,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 227148 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	21541	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 74.87 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 1.4096e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² Theoretical 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: NAG, MRY

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	0.38	0/5021	0.55	0/6822
1	B	0.37	0/5017	0.54	0/6814
1	C	0.37	0/5002	0.53	0/6798
1	D	0.38	0/5020	0.55	0/6820
All	All	0.37	0/20060	0.54	0/27254

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	4899	0	4713	133	0
1	B	4896	0	4717	183	0
1	C	4883	0	4691	134	0
1	D	4900	0	4708	149	0
2	A	14	0	13	0	0
2	B	14	0	13	1	0
2	C	14	0	13	1	0
2	D	14	0	13	1	0
3	A	8	0	10	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	16	0	20	0	0
3	C	8	0	10	0	0
3	D	8	0	10	0	0
4	A	478	0	0	13	0
4	B	444	0	0	12	0
4	C	462	0	0	19	0
4	D	483	0	0	14	0
All	All	21541	0	18931	595	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 (595) 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:D:515:ARG:HH11	1:D:515:ARG:HG3	1.27	0.98
1:D:515:ARG:NH1	1:D:515:ARG:HG3	1.82	0.88
1:C:543:ARG:HB3	1:C:550:ILE:HG21	1.55	0.88
1:B:189:ARG:HB2	1:B:349:LYS:HE2	1.59	0.85
1:D:403:PRO:HG3	1:D:476:PRO:HB3	1.60	0.82
1:D:116:CYS:HB3	1:D:560:SER:HB3	1.63	0.81
1:B:599:ARG:HD3	1:B:617:LEU:O	1.81	0.80
1:D:224:HIS:CE1	1:D:225:ARG:HD3	2.17	0.80
1:B:723:ILE:O	1:B:724:HIS:HB3	1.83	0.78
1:C:129:GLN:HG3	1:C:130:PRO:HD2	1.65	0.77
1:D:599:ARG:HD3	1:D:617:LEU:O	1.85	0.77
1:B:181:GLN:HB3	1:B:183:MET:HE3	1.64	0.77
1:B:605:ARG:HE	1:B:612:LEU:HD13	1.50	0.76
1:C:166:LYS:HE2	1:C:192:VAL:HG22	1.66	0.76
1:D:591:SER:O	1:D:592:ARG:HG2	1.86	0.75
1:A:377:ARG:HD2	1:A:384:PHE:CE1	2.21	0.75
1:C:500:SER:HB2	1:C:502:GLU:HG2	1.68	0.75
1:D:388:SER:HB3	1:D:391:ILE:HG12	1.67	0.75
1:A:563:MET:SD	1:A:568:MET:HG2	2.28	0.74
1:C:115:VAL:HG11	1:C:606:TYR:HE1	1.53	0.74
1:A:674:ASN:HA	4:A:742:HOH:O	1.86	0.74
1:B:459:THR:HG22	1:B:460:LEU:HD23	1.68	0.74
1:A:326:TYR:HE1	1:A:337:THR:O	1.70	0.73
1:B:116:CYS:HB3	1:B:560:SER:HB2	1.71	0.73
1:C:262:PHE:HB2	4:C:1905:HOH:O	1.88	0.72
1:D:379:GLU:HG2	1:D:384:PHE:HE1	1.53	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:387:SER:HB3	1:D:394:THR:OG1	1.89	0.72
1:D:401:GLU:HG2	1:D:441:TYR:O	1.90	0.71
1:D:515:ARG:HH11	1:D:515:ARG:CG	2.03	0.70
1:A:432:THR:HG22	1:A:433:HIS:ND1	2.07	0.69
1:B:427:ARG:O	1:B:427:ARG:HG2	1.91	0.69
1:A:543:ARG:HB3	1:A:550:ILE:HG21	1.73	0.69
1:B:335:ARG:HD2	1:B:336:ALA:O	1.94	0.68
1:C:599:ARG:HD3	1:C:617:LEU:O	1.93	0.68
1:C:285:ASP:HB2	1:C:311:HIS:HB3	1.76	0.68
1:B:304:ARG:HA	1:A:317:ASP:HB2	1.77	0.67
1:A:309:THR:HG22	4:A:915:HOH:O	1.95	0.67
1:C:649:TYR:CE2	1:C:651:GLU:HG3	2.29	0.66
1:C:624:ARG:HD3	4:C:1243:HOH:O	1.94	0.66
1:A:176:GLY:O	1:A:258:ARG:NH2	2.24	0.65
1:A:403:PRO:HG3	1:A:406:ARG:HH21	1.62	0.65
1:A:377:ARG:HD2	1:A:384:PHE:CD1	2.31	0.65
1:C:648:VAL:HG23	1:C:655:TYR:HE1	1.60	0.65
1:A:248:HIS:HA	1:A:271:CYS:O	1.96	0.65
1:C:515:ARG:HB2	4:C:1488:HOH:O	1.96	0.65
1:C:366:MET:HE3	1:C:495:ILE:HB	1.77	0.65
1:A:104:ILE:HD11	1:A:585:ASN:ND2	2.11	0.65
1:B:172:GLN:HG2	1:B:183:MET:HB2	1.79	0.64
1:B:359:LYS:HE2	1:B:409:LEU:HD11	1.78	0.64
1:B:474:ARG:H	1:B:474:ARG:HD2	1.63	0.64
1:A:377:ARG:HD2	1:A:384:PHE:CZ	2.33	0.64
1:C:638:ARG:HD3	1:C:649:TYR:OH	1.98	0.64
1:A:426:ALA:HA	1:A:430:ASN:HB3	1.80	0.64
1:A:152:GLU:N	1:A:366:MET:HE2	2.13	0.64
1:B:647:TYR:CE1	1:B:664:ILE:HD12	2.33	0.63
1:B:614:GLU:HA	1:B:627:ARG:HH21	1.63	0.63
1:B:585:ASN:HA	1:B:655:TYR:HB2	1.80	0.63
1:B:358:PRO:HB2	1:B:361:PRO:HD2	1.81	0.63
1:D:124:VAL:HB	1:D:567:VAL:CG1	2.29	0.63
1:D:177:HIS:HB3	4:D:1538:HOH:O	1.97	0.63
1:D:189:ARG:HH11	1:D:349:LYS:HE3	1.64	0.63
1:B:225:ARG:HH11	1:B:254:TYR:HD1	1.47	0.62
1:B:199:ASP:O	1:B:203:ALA:HB3	1.98	0.62
1:C:194:PHE:CG	1:C:320:LYS:HD2	2.33	0.62
1:B:434:ILE:HD12	1:B:435:LYS:H	1.63	0.62
1:D:432:THR:HB	1:D:433:HIS:ND1	2.14	0.62
1:D:225:ARG:HD2	1:D:254:TYR:HB2	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:189:ARG:NH1	1:D:349:LYS:HE3	2.15	0.62
1:D:428:ARG:HG2	1:D:429:TYR:CD1	2.33	0.62
1:D:399:LEU:O	1:D:474:ARG:HG3	1.99	0.62
1:B:511:ASN:O	1:B:515:ARG:HG2	1.98	0.62
1:A:393:THR:HG21	1:A:395:PHE:CE1	2.34	0.62
1:A:655:TYR:OH	1:A:658:GLN:HG3	2.00	0.62
1:D:434:ILE:HG22	1:D:435:LYS:H	1.65	0.61
1:C:366:MET:CE	1:C:495:ILE:HB	2.30	0.61
1:B:379:GLU:HG2	1:B:384:PHE:CE1	2.35	0.61
1:B:585:ASN:HB2	1:B:655:TYR:HB3	1.82	0.61
1:B:181:GLN:HG2	4:B:779:HOH:O	2.01	0.60
1:D:591:SER:C	1:D:592:ARG:HG2	2.22	0.60
1:D:428:ARG:HG2	1:D:429:TYR:CE1	2.36	0.60
1:D:300:PHE:O	1:D:307:SER:HB2	2.01	0.60
1:D:597:TYR:CE1	1:D:601:LEU:HD11	2.37	0.60
1:C:401:GLU:HG3	1:C:474:ARG:HB3	1.83	0.60
1:C:285:ASP:HB2	1:C:311:HIS:CB	2.31	0.60
1:B:326:TYR:HB3	1:B:335:ARG:HD3	1.84	0.60
1:B:181:GLN:HB3	1:B:183:MET:CE	2.32	0.59
1:B:380:TYR:O	1:B:385:ARG:NH1	2.35	0.59
1:C:605:ARG:HH21	1:C:612:LEU:HB2	1.67	0.59
1:C:198:ILE:HD11	1:C:322:VAL:HG21	1.83	0.59
1:A:204:LYS:HB2	1:A:206:VAL:HG22	1.83	0.59
1:D:199:ASP:O	1:D:203:ALA:HB3	2.03	0.59
1:D:459:THR:HG22	1:D:460:LEU:HD23	1.85	0.59
1:C:153:ASN:HA	4:C:1347:HOH:O	2.03	0.59
1:D:380:TYR:CG	1:D:380:TYR:O	2.55	0.59
1:B:605:ARG:HE	1:B:612:LEU:CD1	2.16	0.59
1:D:434:ILE:HG22	1:D:435:LYS:N	2.17	0.59
1:A:599:ARG:NH1	1:A:618:GLY:O	2.36	0.59
1:A:459:THR:HG22	1:A:460:LEU:HD23	1.84	0.58
1:C:459:THR:HG22	1:C:460:LEU:HD23	1.85	0.58
1:D:256:PRO:HG3	1:D:265:TYR:O	2.03	0.58
1:A:460:LEU:HB3	1:A:463:LEU:HD12	1.85	0.58
1:A:326:TYR:CE1	1:A:337:THR:O	2.54	0.58
1:B:177:HIS:HA	4:B:1460:HOH:O	2.03	0.58
1:A:599:ARG:HD3	1:A:617:LEU:O	2.03	0.58
1:A:472:GLN:O	1:A:475:LYS:HB2	2.03	0.58
1:B:466:ARG:HH11	1:B:470:ARG:HD3	1.69	0.58
1:B:669:THR:O	1:B:669:THR:HG23	2.03	0.58
1:B:116:CYS:HB2	1:B:622:GLU:OE1	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:313:SER:O	4:C:735:HOH:O	2.17	0.58
1:A:659:LEU:HD12	1:A:659:LEU:N	2.18	0.58
1:D:418:ARG:HE	1:D:439:PRO:HG2	1.69	0.58
1:C:559:VAL:HG12	1:C:572:THR:HA	1.86	0.58
1:D:224:HIS:CE1	1:D:250:THR:HG21	2.38	0.57
1:D:664:ILE:N	1:D:664:ILE:HD12	2.19	0.57
1:A:414:GLY:O	1:A:418:ARG:HB2	2.04	0.57
1:C:648:VAL:HG23	1:C:655:TYR:CE1	2.39	0.57
1:C:500:SER:HB2	1:C:502:GLU:CG	2.35	0.57
1:B:145:GLY:HA3	1:B:452:TYR:CZ	2.38	0.57
1:A:555:VAL:O	1:A:555:VAL:HG12	2.05	0.57
1:D:116:CYS:HB2	1:D:622:GLU:OE1	2.04	0.57
1:D:616:GLN:HG3	1:D:624:ARG:HH12	1.68	0.57
1:C:679:GLU:HB2	4:C:878:HOH:O	2.04	0.57
1:D:379:GLU:HG2	1:D:384:PHE:CE1	2.39	0.57
1:A:364:CYS:SG	1:A:410:GLY:HA2	2.45	0.57
1:D:590:SER:O	1:D:593:PRO:HD3	2.05	0.56
1:C:218:LEU:HD12	1:C:219:GLU:N	2.19	0.56
1:A:314:TYR:HB3	1:A:318:ARG:HD2	1.87	0.56
1:A:104:ILE:HB	1:A:583:VAL:HG13	1.88	0.56
1:C:248:HIS:HA	1:C:271:CYS:O	2.05	0.56
1:D:388:SER:HB3	1:D:391:ILE:CG1	2.35	0.56
1:A:648:VAL:HG23	1:A:655:TYR:CE1	2.39	0.56
1:D:511:ASN:O	1:D:515:ARG:HD2	2.05	0.56
1:B:626:THR:HG22	1:B:628:ASP:HB3	1.88	0.56
1:B:363:VAL:HG21	1:B:409:LEU:HD13	1.87	0.56
1:C:694:ILE:HD12	4:C:751:HOH:O	2.05	0.56
1:B:432:THR:HB	1:B:433:HIS:ND1	2.20	0.56
1:B:303:TYR:HD1	1:B:308:HIS:CD2	2.23	0.56
1:D:256:PRO:HG3	1:D:265:TYR:C	2.26	0.56
1:B:343:ASN:O	1:B:353:ALA:HA	2.05	0.56
1:A:589:ILE:HG21	1:A:592:ARG:HG2	1.88	0.56
1:A:360:ARG:HB2	1:A:361:PRO:HD3	1.87	0.56
1:C:649:TYR:O	1:C:656:SER:HB3	2.05	0.55
1:C:714:LEU:HG	4:C:870:HOH:O	2.04	0.55
1:B:615:GLY:N	1:B:627:ARG:HE	2.04	0.55
1:B:428:ARG:HG2	1:B:429:TYR:CE1	2.42	0.55
1:A:539:TRP:CH2	1:A:553:VAL:HG11	2.41	0.55
1:C:426:ALA:O	1:C:430:ASN:HB3	2.06	0.55
1:A:634:THR:HB	1:A:637:HIS:ND1	2.21	0.55
1:C:198:ILE:HG22	1:C:199:ASP:OD1	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:256:PRO:HD3	1:B:266:GLY:HA3	1.88	0.55
1:C:326:TYR:CZ	1:C:339:PRO:HG3	2.41	0.55
1:D:225:ARG:CD	1:D:254:TYR:HB2	2.37	0.55
1:A:123:THR:HB	1:A:570:VAL:HG23	1.89	0.55
1:B:174:ARG:HG3	1:B:174:ARG:O	2.01	0.55
1:D:616:GLN:HG3	1:D:624:ARG:NH1	2.20	0.54
1:D:119:PRO:HG2	1:D:562:ARG:HG2	1.88	0.54
1:B:173:VAL:HG21	1:B:256:PRO:HD2	1.90	0.54
1:A:649:TYR:O	1:A:656:SER:HB3	2.07	0.54
1:D:407:VAL:HG11	1:D:410:GLY:HA3	1.89	0.54
1:B:320:LYS:HG3	1:A:303:TYR:HB3	1.89	0.54
1:B:564:LEU:HD11	1:B:569:ALA:HB2	1.89	0.54
1:D:456:LEU:HD22	1:D:467:GLU:OE2	2.07	0.54
1:A:467:GLU:O	1:A:471:GLU:HG2	2.08	0.54
1:A:391:ILE:HG13	1:A:393:THR:HB	1.90	0.54
1:A:515:ARG:HG2	1:A:516:HIS:N	2.22	0.54
1:B:637:HIS:HB3	1:B:652:GLU:HA	1.90	0.54
1:A:589:ILE:CG2	1:A:592:ARG:HG2	2.38	0.54
1:D:634:THR:HG22	1:D:635:VAL:H	1.72	0.54
1:D:531:LEU:O	1:D:535:GLU:HG2	2.08	0.54
1:A:223:PHE:HB3	1:A:227:ASP:O	2.08	0.54
1:D:225:ARG:HD2	1:D:254:TYR:CB	2.38	0.53
1:C:129:GLN:HG3	1:C:130:PRO:CD	2.37	0.53
1:C:377:ARG:HD2	1:C:384:PHE:CE2	2.44	0.53
1:C:582:ILE:O	1:C:602:VAL:HA	2.08	0.53
1:B:464:TYR:O	1:B:468:HIS:HB2	2.07	0.53
1:D:187:GLU:HG2	4:D:812:HOH:O	2.07	0.53
1:B:379:GLU:HG2	1:B:384:PHE:HE1	1.72	0.53
1:A:176:GLY:O	1:A:178:ARG:HA	2.07	0.53
1:C:249:THR:HG23	1:C:271:CYS:HB3	1.91	0.53
1:D:456:LEU:HD11	1:D:460:LEU:HB2	1.90	0.53
1:B:374:GLU:HG3	1:B:428:ARG:NH2	2.23	0.53
1:B:561:ALA:HA	1:B:569:ALA:O	2.08	0.53
1:A:261:ALA:HA	1:A:264:ARG:CZ	2.38	0.53
1:B:176:GLY:HA3	1:B:179:TYR:CE2	2.44	0.53
1:C:116:CYS:HB3	1:C:560:SER:HB3	1.89	0.53
1:B:428:ARG:HG3	1:B:428:ARG:O	2.08	0.53
1:C:515:ARG:HD2	4:C:768:HOH:O	2.09	0.52
1:B:614:GLU:HB3	1:B:627:ARG:NH2	2.24	0.52
1:B:638:ARG:O	1:B:639:ARG:NE	2.41	0.52
1:C:321:GLN:NE2	1:C:343:ASN:OD1	2.40	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:136:ARG:NH1	1:D:523:ARG:HH21	2.07	0.52
1:B:603:SER:HA	1:B:613:VAL:O	2.09	0.52
1:A:335[B]:ARG:HD3	4:A:1755:HOH:O	2.10	0.52
1:A:531:LEU:O	1:A:535:GLU:HG3	2.09	0.52
1:D:605:ARG:HD3	1:D:607:GLU:O	2.10	0.52
1:C:177:HIS:CE1	1:C:178:ARG:HG2	2.44	0.52
1:A:115:VAL:HG22	1:A:623:LEU:HB2	1.91	0.52
1:A:224:HIS:HB2	1:A:269:VAL:HB	1.91	0.52
1:D:171:SER:O	1:D:265:TYR:HA	2.09	0.52
1:B:636:GLY:O	1:B:638:ARG:HG3	2.09	0.52
1:B:613:VAL:HG12	1:B:614:GLU:N	2.24	0.52
1:D:332:THR:O	1:D:333:LYS:HB2	2.09	0.52
1:D:640:TYR:HE2	1:D:659:LEU:HD13	1.75	0.52
1:A:144:GLU:CD	1:A:433:HIS:HE2	2.13	0.52
1:A:436:VAL:HG12	1:A:471:GLU:HG3	1.92	0.52
1:D:391:ILE:CD1	1:D:393:THR:HB	2.40	0.52
1:B:224:HIS:CD2	1:B:225:ARG:HG2	2.45	0.52
1:B:429:TYR:CZ	1:B:455:LEU:HD13	2.45	0.52
1:B:108:ASN:HB3	1:B:645:GLY:H	1.75	0.52
1:B:225:ARG:NH1	4:B:1467:HOH:O	2.39	0.51
1:D:577:ALA:HB3	1:D:580:ASN:HB2	1.92	0.51
1:A:531:LEU:O	1:A:534:HIS:HB3	2.10	0.51
1:B:156:PRO:HG2	1:B:279:ARG:NH2	2.24	0.51
1:D:167:ASP:OD1	1:D:272:ILE:HD11	2.10	0.51
1:B:166:LYS:HE3	4:B:849:HOH:O	2.11	0.51
1:D:661:ARG:NH1	1:D:661:ARG:HB3	2.26	0.51
1:B:588:ARG:HG3	1:B:653:TYR:HB2	1.91	0.51
1:C:122:ALA:HB3	4:C:947:HOH:O	2.10	0.51
1:D:543:ARG:HG3	1:D:544:LYS:N	2.25	0.51
1:A:590:SER:HB3	4:A:1622:HOH:O	2.11	0.51
1:B:225:ARG:HD3	1:B:254:TYR:CD1	2.46	0.51
1:C:586:SER:OG	1:C:588:ARG:HG3	2.11	0.51
1:B:235:LYS:HE3	4:B:784:HOH:O	2.09	0.51
1:B:129:GLN:HB3	1:B:130:PRO:HD2	1.92	0.51
1:D:224:HIS:CE1	1:D:225:ARG:HH11	2.29	0.51
1:A:366:MET:HE1	1:A:495:ILE:HB	1.92	0.51
1:A:328:ARG:HH12	1:A:333:LYS:HB3	1.76	0.51
1:B:558:ARG:NH2	1:B:622:GLU:HB2	2.27	0.50
1:C:322:VAL:HG12	1:C:325:PHE:HB2	1.93	0.50
1:B:641:PHE:HB2	1:B:648:VAL:HG12	1.93	0.50
1:C:423:ARG:NH1	1:C:423:ARG:HB3	2.26	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:652:GLU:O	1:A:653:TYR:HB2	2.10	0.50
1:C:108:ASN:HB2	1:C:646:GLY:N	2.26	0.50
1:B:302:GLY:N	1:B:307:SER:HB3	2.26	0.50
1:C:382:GLY:HA2	1:C:399:LEU:HD11	1.93	0.50
1:B:129:GLN:HB3	1:B:130:PRO:CD	2.41	0.50
1:D:137:PRO:HG2	4:D:1281:HOH:O	2.11	0.50
1:D:250:THR:HB	4:D:905:HOH:O	2.10	0.50
1:D:432:THR:HB	1:D:433:HIS:CE1	2.46	0.50
1:B:429:TYR:HB3	1:B:433:HIS:HB2	1.92	0.50
1:C:142:TYR:CD2	1:C:378:SER:HB3	2.46	0.50
1:D:177:HIS:CE1	1:D:178:ARG:HE	2.30	0.50
1:A:401:GLU:HG3	1:A:474:ARG:O	2.12	0.50
1:A:124:VAL:HG22	1:A:569:ALA:HA	1.94	0.50
1:A:191:PRO:HB2	1:A:346:THR:HG23	1.93	0.50
1:D:365:THR:O	1:D:366:MET:HE2	2.12	0.50
1:B:211:ALA:O	1:B:221:THR:HA	2.12	0.50
1:D:380:TYR:O	1:D:380:TYR:CD2	2.65	0.49
1:A:403:PRO:HG3	1:A:406:ARG:NH2	2.26	0.49
1:B:153:ASN:O	1:B:494:ARG:NH2	2.46	0.49
1:D:388:SER:CB	1:D:391:ILE:HG12	2.40	0.49
1:B:599:ARG:HH21	1:B:619:GLU:HG2	1.76	0.49
1:A:562:ARG:O	1:A:569:ALA:N	2.43	0.49
1:C:592:ARG:HD2	1:C:595:ALA:HB3	1.93	0.49
1:B:639:ARG:HB3	1:B:641:PHE:CZ	2.48	0.49
1:A:212:LYS:HG3	1:A:221:THR:OG1	2.13	0.49
1:C:188:ASP:OD1	1:C:189:ARG:N	2.43	0.49
1:B:590:SER:HA	4:B:1191:HOH:O	2.13	0.49
1:C:119:PRO:HG3	1:C:561:ALA:HA	1.93	0.49
1:A:358:PRO:HA	4:A:1493:HOH:O	2.12	0.49
1:C:555:VAL:O	1:C:555:VAL:HG12	2.12	0.49
1:B:429:TYR:CE2	1:B:455:LEU:HD13	2.48	0.48
1:B:389:ASP:OD2	1:B:508:PHE:HZ	1.96	0.48
1:D:324:GLY:HA2	1:D:339:PRO:HB2	1.94	0.48
1:C:209:SER:HB2	1:C:224:HIS:HB3	1.95	0.48
1:D:553:VAL:HG23	4:D:1670:HOH:O	2.13	0.48
1:A:160:LYS:HE2	1:A:277:ASP:OD1	2.13	0.48
1:B:404:LEU:HD22	1:B:441:TYR:CE1	2.48	0.48
1:C:196:GLU:O	1:C:200:LYS:HB2	2.12	0.48
1:B:614:GLU:CA	1:B:627:ARG:HH21	2.27	0.48
1:C:113:PHE:HD1	1:C:578:ALA:HA	1.77	0.48
1:D:401:GLU:HB3	1:D:476:PRO:HG3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:225:ARG:HA	1:B:254:TYR:CD2	2.47	0.48
1:A:393:THR:CG2	1:A:395:PHE:CE1	2.97	0.48
1:D:407:VAL:CG1	1:D:410:GLY:HA3	2.43	0.48
1:B:320:LYS:HE3	1:A:303:TYR:O	2.13	0.48
1:C:235:LYS:NZ	1:C:251:ASP:OD1	2.44	0.48
1:D:438:GLN:HA	4:D:826:HOH:O	2.13	0.48
1:B:580:ASN:OD1	1:B:608:ASP:HA	2.12	0.48
1:D:391:ILE:HD12	1:D:393:THR:HB	1.95	0.48
1:C:471:GLU:O	1:C:474:ARG:HB2	2.14	0.48
1:B:226:ASP:OD2	1:B:267:THR:HB	2.13	0.48
1:B:560:SER:O	1:B:570:VAL:HA	2.13	0.48
1:C:447:GLY:HA3	1:C:496:LYS:O	2.13	0.48
1:A:366:MET:CE	1:A:495:ILE:HB	2.44	0.47
1:B:124:VAL:HG13	1:B:567:VAL:HB	1.96	0.47
1:A:674:ASN:N	1:A:674:ASN:OD1	2.46	0.47
1:A:429:TYR:C	1:A:431:ALA:H	2.17	0.47
1:B:599:ARG:HB3	1:B:600:PRO:CD	2.44	0.47
1:A:377:ARG:HD3	1:A:386:PHE:CZ	2.49	0.47
1:C:441:TYR:HA	1:C:450:ILE:O	2.14	0.47
1:A:177:HIS:HA	1:A:178:ARG:HA	1.51	0.47
1:A:589:ILE:HG21	1:A:592:ARG:CG	2.44	0.47
1:D:328:ARG:NH2	4:D:842:HOH:O	2.46	0.47
1:D:708:ARG:NH1	4:D:1852:HOH:O	2.48	0.47
1:C:655:TYR:CZ	1:C:657:HIS:HA	2.50	0.47
1:B:178:ARG:O	1:B:179:TYR:HB3	2.15	0.47
1:C:360:ARG:NH2	1:C:411:ASP:OD1	2.46	0.47
1:D:681:HIS:HD2	4:D:894:HOH:O	1.97	0.47
1:C:659:LEU:HD23	1:C:659:LEU:N	2.30	0.47
1:C:599:ARG:O	1:C:616:GLN:NE2	2.40	0.47
1:B:580:ASN:HB3	1:B:605:ARG:O	2.14	0.47
1:C:285:ASP:HB3	4:C:803:HOH:O	2.15	0.47
1:B:434:ILE:HG13	1:B:435:LYS:N	2.30	0.47
1:B:374:GLU:HG2	1:B:429:TYR:OH	2.15	0.47
1:C:377:ARG:HD2	1:C:384:PHE:CD2	2.49	0.47
1:C:304:ARG:NH1	1:C:323:ASP:OD1	2.47	0.47
1:C:424:ILE:HG12	1:C:427:ARG:HH21	1.79	0.47
1:C:470:ARG:CG	1:C:470:ARG:HH11	2.28	0.47
1:A:259:VAL:O	1:A:261:ALA:N	2.48	0.47
1:D:540:ASN:O	1:D:543:ARG:HG2	2.14	0.47
1:C:347:THR:HB	1:C:348:PRO:HD2	1.96	0.47
1:B:286:GLU:HB2	1:B:296:TYR:HA	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:582:ILE:O	1:A:602:VAL:HA	2.15	0.47
1:B:585:ASN:CB	1:B:655:TYR:HB3	2.44	0.47
1:D:308:HIS:HE1	4:D:1651:HOH:O	1.97	0.47
1:C:224:HIS:HB2	1:C:269:VAL:HB	1.97	0.47
1:A:429:TYR:C	1:A:431:ALA:N	2.69	0.47
1:D:129:GLN:HB3	1:D:130:PRO:CD	2.45	0.47
1:C:501:ILE:O	1:C:501:ILE:HG13	2.14	0.47
1:B:358:PRO:HB2	1:B:361:PRO:CD	2.44	0.46
1:A:456:LEU:HA	4:A:1754:HOH:O	2.14	0.46
1:A:212:LYS:HE2	1:A:219:GLU:OE1	2.15	0.46
1:D:472:GLN:HG2	1:D:475:LYS:HE3	1.96	0.46
1:B:460:LEU:O	1:B:463:LEU:HD12	2.15	0.46
1:C:599:ARG:H	1:C:616:GLN:NE2	2.13	0.46
1:D:443:LEU:O	2:D:1398:NAG:H81	2.14	0.46
1:A:382:GLY:O	1:A:399:LEU:HG	2.15	0.46
1:D:425:PHE:CD1	1:D:429:TYR:HB2	2.50	0.46
1:B:434:ILE:CD1	1:B:435:LYS:H	2.25	0.46
1:A:343:ASN:O	1:A:353:ALA:HA	2.14	0.46
1:D:684:VAL:HG12	4:D:1589:HOH:O	2.16	0.46
1:C:160:LYS:HE3	1:C:277:ASP:OD1	2.16	0.46
1:D:147:ALA:HA	1:D:451:ALA:O	2.16	0.46
1:D:561:ALA:HB2	1:D:570:VAL:HG12	1.97	0.46
1:B:605:ARG:HH21	1:B:612:LEU:HD22	1.81	0.46
1:A:456:LEU:HD21	1:A:463:LEU:HB2	1.98	0.46
1:D:105:LYS:HG2	1:D:582:ILE:HG12	1.96	0.46
1:B:114:TYR:HA	1:B:574:VAL:O	2.15	0.46
1:C:177:HIS:HA	1:C:178:ARG:HA	1.40	0.46
1:C:172:GLN:HB2	1:C:265:TYR:CE2	2.50	0.46
1:A:412:CYS:O	1:A:416:ASP:N	2.24	0.46
1:B:212:LYS:HA	1:B:220:THR:O	2.15	0.46
1:B:421:MET:O	1:B:422:ASP:C	2.54	0.46
1:D:211:ALA:O	1:D:221:THR:HA	2.15	0.46
1:A:723:ILE:HG22	1:A:724:HIS:N	2.31	0.46
1:D:428:ARG:HG3	1:D:428:ARG:O	2.14	0.46
1:B:587:MET:HE3	1:B:597:TYR:O	2.15	0.46
1:C:543:ARG:HB2	1:C:568:MET:CE	2.46	0.46
1:B:599:ARG:NH2	1:B:619:GLU:HG2	2.31	0.46
1:A:377:ARG:HA	1:A:385:ARG:O	2.16	0.46
1:B:456:LEU:HD22	1:B:467:GLU:OE1	2.16	0.46
1:A:649:TYR:HD2	1:A:656:SER:HB3	1.81	0.46
1:B:558:ARG:HD2	1:B:558:ARG:HA	1.78	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:598:SER:OG	1:C:629:ALA:HB1	2.15	0.45
1:C:647:TYR:HB2	1:C:659:LEU:HG	1.99	0.45
1:C:123:THR:HB	1:C:570:VAL:O	2.16	0.45
1:A:714:LEU:HG	4:A:782:HOH:O	2.15	0.45
1:B:601:LEU:HD12	1:B:616:GLN:HB3	1.98	0.45
1:B:304:ARG:HA	1:A:317:ASP:CB	2.45	0.45
1:C:119:PRO:HA	1:C:571:SER:OG	2.15	0.45
1:A:277:ASP:HB3	4:A:952:HOH:O	2.15	0.45
1:A:596:CYS:O	1:A:630:ILE:HG23	2.16	0.45
1:B:120:THR:HG23	4:B:1454:HOH:O	2.16	0.45
1:D:514:GLN:OE1	1:D:515:ARG:NH1	2.49	0.45
1:B:420:ALA:O	1:B:423:ARG:HB3	2.16	0.45
1:C:253:LYS:HE2	4:C:1080:HOH:O	2.17	0.45
1:D:638:ARG:O	1:D:639:ARG:NE	2.40	0.45
1:B:564:LEU:CD1	1:B:569:ALA:HB2	2.46	0.45
1:A:300:PHE:HD2	1:A:357:VAL:O	2.00	0.45
1:A:300:PHE:O	1:A:307:SER:HB2	2.17	0.45
1:A:377:ARG:HD2	1:A:384:PHE:CG	2.51	0.45
1:D:600:PRO:O	1:D:616:GLN:HB2	2.17	0.45
1:D:366:MET:HE3	4:D:848:HOH:O	2.16	0.45
1:A:429:TYR:O	1:A:431:ALA:N	2.49	0.45
1:B:626:THR:CG2	1:B:628:ASP:HB3	2.46	0.45
1:C:305:GLU:HA	4:C:1244:HOH:O	2.15	0.45
1:D:259:VAL:O	1:D:261:ALA:N	2.50	0.45
1:D:360:ARG:N	1:D:361:PRO:CD	2.79	0.45
1:C:152:GLU:HA	1:C:366:MET:HE2	1.99	0.45
1:B:256:PRO:HG3	1:B:265:TYR:O	2.17	0.45
1:B:223:PHE:HB2	1:B:226:ASP:HA	1.99	0.45
1:C:357:VAL:HB	1:C:358:PRO:HD2	1.97	0.45
1:D:324:GLY:HA2	1:D:339:PRO:CB	2.47	0.44
1:B:708:ARG:NH1	4:B:791:HOH:O	2.50	0.44
1:D:502:GLU:HG3	1:D:503:PHE:N	2.32	0.44
1:A:634:THR:O	1:A:637:HIS:HB2	2.17	0.44
1:D:104:ILE:HD13	1:D:655:TYR:CE2	2.52	0.44
1:D:200:LYS:HZ1	1:D:208:ARG:HH21	1.65	0.44
1:D:143:THR:HG22	1:D:144:GLU:O	2.18	0.44
1:C:208:ARG:NH1	1:C:229:GLU:OE2	2.47	0.44
1:B:445:ASN:OD1	2:B:1398:NAG:H83	2.16	0.44
1:D:254:TYR:N	1:D:268:THR:OG1	2.44	0.44
1:C:199:ASP:O	1:C:203:ALA:HB3	2.18	0.44
1:D:691:ARG:NH1	4:D:908:HOH:O	2.39	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:363:VAL:CG2	1:B:409:LEU:HD13	2.47	0.44
1:B:614:GLU:HB3	1:B:627:ARG:CZ	2.47	0.44
1:B:434:ILE:CG1	1:B:435:LYS:N	2.80	0.44
1:C:177:HIS:ND1	1:C:178:ARG:HG2	2.32	0.44
1:A:119:PRO:HG2	1:A:562:ARG:HB3	1.99	0.44
1:A:599:ARG:NH2	1:A:641:PHE:HD2	2.16	0.44
1:D:152:GLU:OE1	1:D:496:LYS:HA	2.18	0.44
1:A:660:SER:C	1:A:662:ALA:H	2.20	0.44
1:D:145:GLY:HA2	1:D:455:LEU:HG	1.99	0.44
1:D:552:SER:HA	1:D:559:VAL:HG22	1.99	0.44
1:C:249:THR:CG2	1:C:271:CYS:HB3	2.47	0.44
1:A:526:ILE:O	1:A:530:GLU:HG3	2.17	0.44
1:C:236:PRO:HD3	4:C:844:HOH:O	2.18	0.44
1:A:377:ARG:HD2	1:A:384:PHE:CE2	2.52	0.44
1:B:255:ASN:HA	1:B:256:PRO:HD3	1.88	0.44
1:C:433:HIS:HB3	1:C:434:ILE:H	1.67	0.44
1:D:520:MET:O	1:D:524:VAL:HG23	2.17	0.44
1:D:386:PHE:O	1:D:394:THR:HA	2.18	0.44
1:B:520:MET:O	1:B:524:VAL:HG23	2.18	0.44
1:B:600:PRO:O	1:B:616:GLN:HB2	2.18	0.43
1:B:404:LEU:HA	1:B:404:LEU:HD12	1.77	0.43
1:D:208:ARG:NH1	4:D:1618:HOH:O	2.48	0.43
1:A:494:ARG:HB2	1:A:496:LYS:NZ	2.32	0.43
1:B:591:SER:C	1:B:593:PRO:HD3	2.38	0.43
1:A:601:LEU:HD13	1:A:627:ARG:NH1	2.33	0.43
1:B:463:LEU:O	1:B:464:TYR:C	2.57	0.43
1:B:235:LYS:O	1:B:247:TRP:HA	2.18	0.43
1:C:280:SER:HB2	1:C:287:PHE:HB3	1.99	0.43
1:B:264:ARG:HD3	1:B:264:ARG:HA	1.79	0.43
1:B:681:HIS:HD2	4:B:1022:HOH:O	2.01	0.43
1:C:649:TYR:HE2	1:C:651:GLU:HG3	1.78	0.43
1:C:604:PHE:O	1:C:613:VAL:N	2.49	0.43
1:C:170:VAL:HA	1:C:266:GLY:O	2.18	0.43
1:B:369:TRP:CD2	1:B:370:GLN:HG2	2.53	0.43
1:D:402:TYR:HA	1:D:403:PRO:HD3	1.81	0.43
1:B:636:GLY:O	1:B:637:HIS:C	2.55	0.43
1:D:241:THR:O	1:D:243:THR:HG23	2.18	0.43
1:B:583:VAL:HG23	1:B:643:PHE:CZ	2.54	0.43
1:B:106:ALA:HA	1:B:658:GLN:HE22	1.82	0.43
1:B:225:ARG:HD3	1:B:254:TYR:CG	2.54	0.43
1:B:563:MET:O	1:B:564:LEU:HD23	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:133:CYS:HA	1:B:134:PRO:HD3	1.86	0.43
1:B:152:GLU:OE1	1:B:496:LYS:HA	2.18	0.43
1:B:503:PHE:CG	1:B:504:ALA:N	2.86	0.43
1:C:405:SER:O	1:C:492:VAL:HG12	2.19	0.43
1:D:466:ARG:NH1	1:D:470:ARG:HB2	2.34	0.43
1:B:399:LEU:O	1:B:474:ARG:HG2	2.19	0.43
1:A:475:LYS:NZ	4:A:1433:HOH:O	2.52	0.43
1:D:343:ASN:O	1:D:353:ALA:HA	2.18	0.43
1:A:285:ASP:O	1:A:311:HIS:HD2	2.01	0.43
1:D:286:GLU:HB2	1:D:296:TYR:HA	1.99	0.43
1:D:587:MET:SD	1:D:650:PHE:CD2	3.11	0.43
1:B:605:ARG:NE	1:B:612:LEU:HD13	2.27	0.43
1:C:285:ASP:CB	1:C:311:HIS:HB3	2.47	0.43
1:D:442:TYR:OH	1:D:474:ARG:HG2	2.18	0.43
1:A:592:ARG:H	1:A:592:ARG:HG2	1.62	0.43
1:B:401:GLU:HG2	1:B:441:TYR:O	2.18	0.43
1:C:261:ALA:HA	1:C:264:ARG:NH1	2.34	0.43
1:D:637:HIS:HB3	1:D:652:GLU:HA	2.00	0.43
1:B:375:MET:HB3	1:B:452:TYR:HE1	1.83	0.43
1:C:415:LYS:HA	1:C:418:ARG:NH1	2.34	0.43
1:B:552:SER:HA	1:B:559:VAL:HG22	2.00	0.43
1:D:434:ILE:N	1:D:434:ILE:HD12	2.34	0.43
1:B:628:ASP:C	1:B:630:ILE:HD12	2.39	0.43
1:B:404:LEU:HD22	1:B:441:TYR:CZ	2.53	0.43
1:A:660:SER:C	1:A:662:ALA:N	2.71	0.43
1:B:170:VAL:HB	1:B:186:PHE:HB3	2.01	0.43
1:A:108:ASN:OD1	1:A:646:GLY:HA3	2.19	0.43
1:D:169:THR:HA	1:D:186:PHE:O	2.19	0.43
1:D:403:PRO:CG	1:D:476:PRO:HB3	2.40	0.42
1:B:612:LEU:HA	1:B:612:LEU:HD12	1.67	0.42
1:B:588:ARG:HA	1:B:596:CYS:SG	2.59	0.42
1:A:350:PHE:CD1	1:A:352:VAL:HG22	2.54	0.42
1:D:603:SER:HA	1:D:613:VAL:O	2.19	0.42
1:B:254:TYR:OH	1:B:263:HIS:HE1	2.02	0.42
1:B:113:PHE:O	1:B:575:PRO:HA	2.18	0.42
1:B:379:GLU:O	1:B:380:TYR:HB3	2.19	0.42
1:D:661:ARG:HH11	1:D:661:ARG:HB3	1.85	0.42
1:D:363:VAL:HG23	1:D:409:LEU:HD13	2.01	0.42
1:C:306:GLY:O	1:C:308:HIS:N	2.53	0.42
1:C:281:VAL:O	1:C:282:TYR:C	2.56	0.42
1:C:156:PRO:HG2	1:C:279:ARG:NH2	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:596:CYS:O	1:B:630:ILE:HG23	2.20	0.42
1:D:129:GLN:HB3	1:D:130:PRO:HD2	2.01	0.42
1:B:583:VAL:CG2	1:B:643:PHE:CZ	3.02	0.42
1:C:138:GLU:OE2	2:C:1141:NAG:H5	2.19	0.42
1:C:607:GLU:HB2	1:C:610:GLY:HA3	2.01	0.42
1:B:553:VAL:CG1	1:B:554:THR:N	2.82	0.42
1:D:414:GLY:O	1:D:418:ARG:HG3	2.18	0.42
1:B:582:ILE:HG22	1:B:583:VAL:N	2.34	0.42
1:B:540:ASN:O	1:B:543:ARG:HG2	2.19	0.42
1:B:377:ARG:NH2	1:B:474:ARG:NH1	2.67	0.42
1:A:366:MET:HE1	1:A:495:ILE:CG2	2.49	0.42
1:B:587:MET:HE2	1:B:653:TYR:CD2	2.55	0.42
1:D:543:ARG:HD2	1:D:563:MET:SD	2.60	0.42
1:A:616:GLN:NE2	1:A:629:ALA:HB3	2.35	0.42
1:A:434:ILE:HD11	4:A:1498:HOH:O	2.19	0.42
1:B:402:TYR:HA	1:B:403:PRO:HD3	1.84	0.42
1:D:589:ILE:HG12	1:D:597:TYR:CE1	2.55	0.42
1:B:470:ARG:C	1:B:472:GLN:H	2.23	0.42
1:C:600:PRO:HD3	1:C:641:PHE:CE1	2.55	0.42
1:D:592:ARG:O	1:D:593:PRO:C	2.58	0.42
1:D:425:PHE:CZ	1:D:434:ILE:HA	2.55	0.42
1:C:440:GLN:O	1:C:451:ALA:HA	2.20	0.42
1:B:543:ARG:HG3	1:B:544:LYS:HG3	2.02	0.42
1:D:156:PRO:HG2	1:D:279:ARG:NH2	2.35	0.42
1:D:404:LEU:HD22	1:D:441:TYR:CE1	2.55	0.41
1:B:143:THR:HB	1:B:377:ARG:HB3	2.01	0.41
1:A:393:THR:O	1:A:393:THR:HG22	2.20	0.41
1:D:701:ASP:OD1	1:D:704:GLU:HG3	2.20	0.41
1:C:500:SER:CB	1:C:502:GLU:HG2	2.44	0.41
1:D:393:THR:HG23	1:D:504:ALA:HB3	2.02	0.41
1:A:471:GLU:HA	1:A:474:ARG:HD2	2.01	0.41
1:A:259:VAL:O	1:A:260:GLU:C	2.59	0.41
1:A:382:GLY:HA2	1:A:399:LEU:HD11	2.02	0.41
1:B:250:THR:HB	1:B:270:ASN:HA	2.02	0.41
1:C:723:ILE:HG22	1:C:724:HIS:N	2.34	0.41
1:D:458:ASN:N	1:D:458:ASN:OD1	2.53	0.41
1:C:338:ALA:HA	1:C:339:PRO:HD3	1.87	0.41
1:B:156:PRO:O	1:B:158:LYS:HG3	2.20	0.41
1:C:708:ARG:NH1	4:C:1077:HOH:O	2.39	0.41
1:C:115:VAL:HG11	1:C:606:TYR:CE1	2.44	0.41
1:A:596:CYS:N	1:A:631:GLU:O	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:512:HIS:CE1	4:A:759:HOH:O	2.73	0.41
1:B:202:ASN:O	1:B:328:ARG:HD3	2.20	0.41
1:C:136:ARG:HA	1:C:137:PRO:HD3	1.84	0.41
1:C:539:TRP:CH2	1:C:553:VAL:HG11	2.54	0.41
1:C:401:GLU:OE2	1:C:440:GLN:HG2	2.21	0.41
1:B:472:GLN:HA	1:B:475:LYS:HG3	2.02	0.41
1:B:630:ILE:HG22	1:B:631:GLU:N	2.34	0.41
1:B:433:HIS:HA	1:B:456:LEU:O	2.21	0.41
1:D:146:ILE:HG13	1:D:455:LEU:HD11	2.01	0.41
1:B:553:VAL:HG13	1:B:554:THR:N	2.35	0.41
1:D:174:ARG:HG2	1:D:174:ARG:HH11	1.86	0.41
1:C:119:PRO:HG2	1:C:562:ARG:N	2.35	0.41
1:D:103:ASP:N	1:D:582:ILE:HD13	2.35	0.41
1:C:665:THR:HG22	4:C:1358:HOH:O	2.19	0.41
1:C:574:VAL:HA	1:C:575:PRO:HD3	1.89	0.41
1:C:190:ALA:HA	1:C:191:PRO:HD2	1.91	0.41
1:C:460:LEU:O	1:C:462:GLU:N	2.54	0.41
1:A:360:ARG:N	1:A:361:PRO:CD	2.83	0.41
1:B:265:TYR:HB2	4:B:1048:HOH:O	2.19	0.41
1:A:440:GLN:HE22	1:A:471:GLU:HB3	1.85	0.41
1:C:304:ARG:HG3	4:C:752:HOH:O	2.20	0.41
1:A:647:TYR:HB2	1:A:659:LEU:HD13	2.01	0.41
1:A:223:PHE:HB2	4:A:814:HOH:O	2.21	0.41
1:D:640:TYR:CE2	1:D:659:LEU:HD13	2.55	0.41
1:C:420:ALA:HA	1:C:423:ARG:HH12	1.85	0.41
1:D:466:ARG:HD2	1:D:466:ARG:O	2.20	0.41
1:C:375:MET:SD	1:C:386:PHE:HB3	2.60	0.41
1:D:419:ASP:O	1:D:423:ARG:HB3	2.21	0.41
1:B:459:THR:HG22	1:B:460:LEU:CD2	2.46	0.41
1:A:432:THR:HG22	1:A:433:HIS:CE1	2.55	0.41
1:B:466:ARG:HH11	1:B:470:ARG:CG	2.34	0.41
1:A:440:GLN:NE2	1:A:471:GLU:HB3	2.36	0.41
1:B:419:ASP:OD1	1:B:423:ARG:NH1	2.53	0.41
1:A:397:THR:HG22	1:A:444:ALA:HA	2.02	0.41
1:A:113:PHE:CD2	1:A:621:ASN:HB3	2.56	0.41
1:B:213:TYR:N	1:B:213:TYR:CD2	2.89	0.41
1:A:130:PRO:HA	1:A:533:ASN:OD1	2.20	0.41
1:D:404:LEU:HD12	1:D:404:LEU:HA	1.89	0.41
1:B:723:ILE:O	1:B:724:HIS:CB	2.61	0.41
1:A:648:VAL:HG23	1:A:655:TYR:HE1	1.83	0.41
1:B:428:ARG:HG2	1:B:429:TYR:CZ	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:119:PRO:HB2	1:A:569:ALA:HB1	2.03	0.41
1:D:152:GLU:HA	1:D:366:MET:HE1	2.02	0.41
1:B:715:ARG:HD3	4:B:1860:HOH:O	2.20	0.41
1:C:389:ASP:N	4:C:791:HOH:O	2.50	0.41
1:A:604:PHE:O	1:A:613:VAL:N	2.39	0.40
1:C:616:GLN:NE2	1:C:629:ALA:HB3	2.36	0.40
1:D:189:ARG:HD3	1:D:349:LYS:NZ	2.35	0.40
1:D:463:LEU:O	1:D:467:GLU:HG3	2.22	0.40
1:B:145:GLY:HA3	1:B:452:TYR:CE1	2.55	0.40
1:B:302:GLY:C	1:B:307:SER:HB2	2.42	0.40
1:B:236:PRO:HB3	4:B:836:HOH:O	2.21	0.40
1:A:638:ARG:C	1:A:639:ARG:HG2	2.42	0.40
1:A:639:ARG:NH1	4:A:836:HOH:O	2.55	0.40
1:B:279:ARG:O	1:B:287:PHE:HB2	2.21	0.40
1:C:113:PHE:CD1	1:C:578:ALA:HA	2.55	0.40
1:C:286:GLU:HA	1:C:297:MET:O	2.21	0.40
1:C:397:THR:HG22	1:C:444:ALA:HA	2.03	0.40
1:D:609:GLN:OE1	1:D:609:GLN:N	2.55	0.40
1:C:636:GLY:N	1:C:652:GLU:OE2	2.52	0.40
1:D:564:LEU:CD1	1:D:569:ALA:HB2	2.52	0.40
1:B:307:SER:C	1:B:309:THR:H	2.24	0.40
1:C:157:TYR:HB2	1:C:284:TYR:CE2	2.56	0.40
1:B:528:TRP:O	1:B:532:GLN:HG2	2.21	0.40
1:D:311:HIS:HE2	1:D:313:SER:HG	1.69	0.40
1:C:719:ILE:HD11	4:C:793:HOH:O	2.22	0.40
1:D:501:ILE:HD12	1:D:501:ILE:HA	1.92	0.40
1:C:660:SER:OG	1:C:662:ALA:HB3	2.21	0.40
1:C:166:LYS:HB2	1:C:190:ALA:HB3	2.03	0.40
1:B:515:ARG:N	1:B:515:ARG:HD3	2.36	0.40
1:A:467:GLU:O	1:A:470:ARG:HB2	2.22	0.40
1:C:420:ALA:HA	1:C:423:ARG:NH1	2.36	0.40
1:D:200:LYS:HB3	1:D:206:VAL:O	2.21	0.40
1:A:166:LYS:O	1:A:189:ARG:HA	2.21	0.40
1:B:190:ALA:HA	1:B:191:PRO:HD3	1.92	0.40
1:D:469:LEU:C	1:D:469:LEU:HD12	2.42	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	605/703 (86%)	558 (92%)	43 (7%)	4 (1%)	26	26
1	B	604/703 (86%)	555 (92%)	46 (8%)	3 (0%)	34	34
1	C	604/703 (86%)	543 (90%)	55 (9%)	6 (1%)	19	16
1	D	604/703 (86%)	571 (94%)	29 (5%)	4 (1%)	26	26
All	All	2417/2812 (86%)	2227 (92%)	173 (7%)	17 (1%)	26	26

All (17) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	259	VAL
1	A	260	GLU
1	D	177	HIS
1	C	118	PRO
1	C	655	TYR
1	C	461	ALA
1	D	260	GLU
1	D	577	ALA
1	B	633	CYS
1	A	413	ILE
1	A	430	ASN
1	C	305	GLU
1	B	637	HIS
1	C	572	THR
1	C	476	PRO
1	B	339	PRO
1	D	104	ILE

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	526/593 (89%)	504 (96%)	22 (4%)	36	42
1	B	526/593 (89%)	501 (95%)	25 (5%)	31	35
1	C	522/593 (88%)	503 (96%)	19 (4%)	42	51
1	D	527/593 (89%)	502 (95%)	25 (5%)	32	36
All	All	2101/2372 (89%)	2010 (96%)	91 (4%)	35	41

All (91) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	108	ASN
1	B	109	THR
1	B	112	ASN
1	B	173	VAL
1	B	174	ARG
1	B	207	CYS
1	B	220	THR
1	B	235	LYS
1	B	241	THR
1	B	308	HIS
1	B	328	ARG
1	B	335	ARG
1	B	377	ARG
1	B	400	THR
1	B	401	GLU
1	B	418	ARG
1	B	474	ARG
1	B	492	VAL
1	B	534	HIS
1	B	555	VAL
1	B	598	SER
1	B	601	LEU
1	B	607	GLU
1	B	652	GLU
1	B	668	SER
1	A	109	THR
1	A	110	ASP
1	A	170	VAL

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Mol	Chain	Res	Type
1	A	174	ARG
1	A	180	SER
1	A	219	GLU
1	A	248	HIS
1	A	251	ASP
1	A	259	VAL
1	A	309	THR
1	A	317	ASP
1	A	366	MET
1	A	384	PHE
1	A	393	THR
1	A	404	LEU
1	A	515	ARG
1	A	529	CYS
1	A	626	THR
1	A	659	LEU
1	A	661	ARG
1	A	708	ARG
1	A	724	HIS
1	C	178	ARG
1	C	230	THR
1	C	235	LYS
1	C	244	SER
1	C	248	HIS
1	C	363	VAL
1	C	404	LEU
1	C	432	THR
1	C	462	GLU
1	C	470	ARG
1	C	502	GLU
1	C	529	CYS
1	C	553	VAL
1	C	571	SER
1	C	608	ASP
1	C	659	LEU
1	C	661	ARG
1	C	665	THR
1	C	724	HIS
1	D	132	ARG
1	D	180	SER
1	D	200	LYS
1	D	225	ARG

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Mol	Chain	Res	Type
1	D	241	THR
1	D	305	GLU
1	D	317	ASP
1	D	335	ARG
1	D	380	TYR
1	D	418	ARG
1	D	458	ASN
1	D	469	LEU
1	D	474	ARG
1	D	499	SER
1	D	512	HIS
1	D	515	ARG
1	D	534	HIS
1	D	588	ARG
1	D	592	ARG
1	D	603	SER
1	D	608	ASP
1	D	634	THR
1	D	682	GLU
1	D	697	SER
1	D	724	HIS

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

Mol	Chain	Res	Type
1	B	181	GLN
1	B	609	GLN
1	B	674	ASN
1	B	681	HIS
1	A	585	ASN
1	C	657	HIS
1	C	709	ASN
1	D	308	HIS
1	D	511	ASN
1	D	681	HIS
1	D	706	GLN

5.3.3 RNA ⓘ

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](#)

9 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
2	NAG	A	1398	1	14,14,15	0.51	0	15,19,21	1.49	1 (6%)
3	MRY	A	2000	-	7,7,7	0.46	0	6,8,8	0.55	0
2	NAG	B	1398	1	14,14,15	0.45	0	15,19,21	1.08	1 (6%)
3	MRY	B	2000	-	7,7,7	0.32	0	6,8,8	0.63	0
3	MRY	B	3000	-	7,7,7	0.89	0	6,8,8	1.55	0
2	NAG	C	1141	1	14,14,15	0.55	0	15,19,21	0.90	1 (6%)
3	MRY	C	2000	-	7,7,7	0.19	0	6,8,8	0.82	0
2	NAG	D	1398	1	14,14,15	0.54	0	15,19,21	0.93	1 (6%)
3	MRY	D	2000	-	7,7,7	0.45	0	6,8,8	0.74	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	A	1398	1	-	0/6/23/26	0/1/1/1
3	MRY	A	2000	-	-	0/8/8/8	0/0/0/0
2	NAG	B	1398	1	-	0/6/23/26	0/1/1/1
3	MRY	B	2000	-	-	0/8/8/8	0/0/0/0
3	MRY	B	3000	-	-	0/8/8/8	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	C	1141	1	-	0/6/23/26	0/1/1/1
3	MRY	C	2000	-	-	0/8/8/8	0/0/0/0
2	NAG	D	1398	1	-	0/6/23/26	0/1/1/1
3	MRY	D	2000	-	-	0/8/8/8	0/0/0/0

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	1141	NAG	C1-O5-C5	2.03	114.82	112.25
2	D	1398	NAG	C1-O5-C5	2.14	114.97	112.25
2	B	1398	NAG	C1-O5-C5	3.30	116.44	112.25
2	A	1398	NAG	C1-O5-C5	4.99	118.58	112.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1398	NAG	1	0
2	C	1141	NAG	1	0
2	D	1398	NAG	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	608/703 (86%)	-0.23	1 (0%) 95 96	21, 33, 55, 75	0
1	B	607/703 (86%)	-0.17	6 (0%) 84 85	21, 36, 63, 90	0
1	C	608/703 (86%)	-0.17	6 (0%) 84 85	22, 35, 64, 88	0
1	D	607/703 (86%)	-0.23	1 (0%) 95 96	23, 34, 55, 88	0
All	All	2430/2812 (86%)	-0.20	14 (0%) 90 91	21, 34, 60, 90	0

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	463	LEU	3.2
1	D	476	PRO	3.1
1	B	492	VAL	3.0
1	C	464	TYR	3.0
1	A	465	VAL	3.0
1	B	470	ARG	2.5
1	B	476	PRO	2.5
1	C	465	VAL	2.5
1	C	594	GLY	2.4
1	B	461	ALA	2.2
1	B	469	LEU	2.2
1	B	595	ALA	2.2
1	C	595	ALA	2.1
1	C	607	GLU	2.0

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

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
2	NAG	A	1398	14/15	0.87	0.25	9.47	49,65,76,81	0
3	MRY	A	2000	8/8	0.97	0.14	2.11	27,33,36,37	0
2	NAG	D	1398	14/15	0.85	0.13	0.40	40,58,64,64	0
3	MRY	B	2000	8/8	0.95	0.13	0.37	29,35,39,44	0
3	MRY	C	2000	8/8	0.98	0.12	-0.07	27,29,33,38	0
3	MRY	D	2000	8/8	0.98	0.12	-0.17	27,27,32,32	0
3	MRY	B	3000	8/8	0.95	0.10	-1.57	39,41,43,47	0
2	NAG	B	1398	14/15	0.93	0.09	-2.94	46,59,65,66	0
2	NAG	C	1141	14/15	0.93	0.23	-	84,89,92,95	0

6.5 Other polymers [i](#)

There are no such residues in this entry.